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=> d his

(FILE 'HOME' ENTERED AT 11:33:14 ON 19 JUN 2002)
SET COST OFF

FILE 'REGISTRY' ENTERED AT 11:33:30 ON 19 JUN 2002

E CHOLESTERYL ESTER TRANSFER PROTEIN/CN
L1 1 S E4
E CETP/CN
E CHOLESTER? (L) ESTER (L) TRANSFER? (L) PROTEIN
L2 13 S CHOLESTER? (L) ESTER (L) TRANSFER? (L) PROTEIN
L3 13 S CETP
L4 13 S CHOLESTER? (L) ESTER (L) EXCHANG? (L) PROTEIN
L5 1 S L1 AND L2-L4
L6 24 S L2-L4 NOT L5

FILE 'HCAPLUS' ENTERED AT 11:37:36 ON 19 JUN 2002

L7 876 S CHOLESTER? (L) ESTER (L) EXCHANG? (L) PROTEIN
E CHOLESTER? (L) ESTER (L) TRANSFER? (L) PROTEIN
L8 883 S CETP
L9 1325 S CHOLESTER? (L) ESTER (L) TRANSFER? (L) PROTEIN
L10 16 S L5 OR L6
L11 16 S L7-L9 AND L10
L12 57 S ?ARTHEROSCLERO?
L13 34932 S ?ATHEROSCLERO?
L14 19 S ?ARTHERIOSCLERO?
L15 13496 S ?ARTERIOSCLERO?
L16 9 S L11 AND L12-L15
L17 4 S L11 AND VACCIN?
L18 4 S L17 AND L16
E ATHEROSCLEROSIS/CT
E E3+ALL
L19 20165 S E7-E9,E6
L20 32452 S E6,E8,E9/BI
E E5+ALL

Jan Delaval
Reference Librarian
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L21 22555 S E5+NT
 L22 8925 S E5/BI
 L23 9 S L11 AND L19-L22
 L24 4 S L16,L23 AND VACCIN?
 L25 5 S L16,L23 NOT L24
 L26 9 S L23-L25
 L27 331 S L7-L9 AND L12-L15,L19-L22
 L28 9 S L27 AND VACCIN?
 L29 24 S L7-L9,L10 AND EPITOP?
 L30 5 S L29 AND (TETANUS OR DIPHTHER? OR TOXOID OR TOXIN OR BCG OR BA
 L31 15 S L26,L28,L30
 L32 19 S L29 NOT L31
 E RITTERSHAUS C/AU
 L33 20 S E3-E6
 E THOMAS L/AU
 L34 219 S E3,E14,E15
 E THOMAS LARRY/AU
 L35 4 S E3
 L36 23 S E26,E29
 L37 6 S L33-L36 AND L7-L10
 L38 6 S L31 AND L37
 L39 9 S L31 NOT L38
 L40 15 S L38,L39
 L41 5 S L40 AND (PY<=1995 OR PRY<=1995 OR AY<=1995)
 L42 15 S L40,L41

FILE 'HCAPLUS' ENTERED AT 11:52:33 ON 19 JUN 2002

=> d all tot 142

L42 ANSWER 1 OF 15 HCAPLUS COPYRIGHT 2002 ACS
 AN 2002:4125 HCAPLUS
 TI An immunotherapeutic approach for the treatment of low plasma
 HDL-Cholesterol
 AU Ryan, Una S.; Rittershaus, Charles W.
 CS AVANT Immunotherapeutics, Inc., Needham, MA, 02494-2725, USA
 SO NATO Science Series, Series I: Life and Behavioural Sciences (2001),
 330(Vascular Endothelium), 26-33
 CODEN: NSSSC9; ISSN: 1566-7693
 PB IOS Press
 DT Journal
 LA English
 CC 15-2 (Immunochemistry)
 Section cross-reference(s): 14
 AB One determinant of plasma HDL-Cholesterol concn. is
cholesteryl ester transfer protein (CETP) activity. Inhibition of **CETP** activity increases
 plasma HDL-C, thus providing a potential therapeutic target for the
 treatment of **atherosclerosis**. Using a **vaccine**
 approach, we immunized New Zealand White rabbits with a peptide contg. a
 region of **CETP** known to be required for neutral lipid
transfer function. **CETP-vaccinated** rabbits
 had significantly reduced plasma **CETP** activity and an altered
 lipoprotein profile compared with control rabbits. In a
cholesterol-fed rabbit model of **atherosclerosis**, the
 fraction of plasma **cholesterol** in HDL was 42% higher, and the
 fraction of plasma **cholesterol** in LDL was 24% lower in the
CETP-vaccinated group compared with the control-
vaccinated group. Moreover, the percentage of the aorta surface
 exhibiting **atherosclerotic** lesion was 39.6% smaller in the
CETP-vaccinated rabbits compared with controls. The
 data reported here demonstrate that **CETP** activity can be reduced
 in vivo by **vaccination** with a peptide derived from **CETP**



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:05:51 : Search time 26.94 Seconds
(without alignments)
92.737 Million cell updates/sec

Title: US-09-943-334-1
Perfect score: 134
Sequence: 1 RDGFLLQMDFGFPEHLVDPLQSL S 26

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 28338 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 28338

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	134	100.0	493	2 A53176	cholesteryl ester
2	134	100.0	493	2 A26941	cholesteryl ester
3	131	97.8	289	2 A38700	cholesteryl ester
4	117	87.3	497	2 I46692	cholesteryl ester
5	56	41.8	587	2 D95247	aspartyl-LRNA synt
6	54	40.3	310	2 A98112	aspartate--trNA 11
7	54	39.6	426	2 D82199	conserved hypotet
8	53	39.6	426	2 A81904	hypothetical prote
9	53	39.6	426	2 A86870	aspartate--trNA 11
10	51	38.1	274	2 C83497	conserved hypotet
11	50	37.3	311	1 C64884	gamma protein - Esc
12	50	37.3	311	2 A85749	hypothetical prote
13	50	37.3	311	2 H90869	hypothetical prote
14	49.5	36.9	559	2 D90291	permease, multiru
15	48	35.8	348	1 ADECH	2-dehydro-3-deoxy
16	48	35.8	348	2 C90930	hypothetical prote
17	48	35.8	348	2 G85778	hypothetical prote
18	48	35.8	348	2 AD0704	3-deoxy-D-arabinoh
19	48	35.8	348	2 AD0294	2-dehydro-3-deoxy
20	48	35.8	348	2 D83853	cystathionine beta
21	48	35.8	348	2 C96633	probable serine/th
22	48	35.8	682	1 C71299	conserved hypotet
23	47	35.1	311	2 AC0663	conserved hypotet
24	46.5	34.7	110	2 A11860	hypothetical prote
25	46.5	34.7	1952	2 A96002	hypothetical prote
26	46	34.3	104	2 A96002	hypothetical prote
27	46	34.3	312	2 G82791	conserved hypotet
28	46	34.3	356	2 H90168	3TP-binding protel
29	46	34.3	374	2 G97057	coproporphyrinogen

30	46	34.3	422	2 A49837	clathrin-associate
31	46	34.3	425	2 T23603	hypothetical prote
32	46	34.3	428	2 G86240	hypothetical prote
33	46	34.3	567	2 S60985	probable membrane
34	46	34.3	849	1 T05181	S-receptor kinase
35	46	34.3	886	2 T10890	cysteine proteinas
36	46	34.3	1071	2 T51224	related to small s
37	45.5	34.0	293	2 AF3393	Apases of the pp
38	45.5	34.0	738	2 S40992	hypothetical prote
39	45	33.6	177	2 T04228	ribosomal protein
40	45	33.6	265	2 F71119	probable diaphthine
41	45	33.6	496	2 B96674	hypothetical prote
42	45	33.6	531	2 B83422	probable serine/th
43	45	33.6	700	2 E69146	sensory transducti
44	45	33.6	779	1 MNVZAL	ribonucleoside-dip
45	45	33.6	900	2 A95340	cation transport p

ALIGNMENTS

RESULT 1
A53176
Cholesteryl ester transfer protein - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 07-May-1999
C:Accession: A53176
R:Pape, M.E.; Rehberg, E.F.; Marotti, K.R.; Melchior, G.W.
Arterioscler. Thromb. 11, 1759-1771, 1991
A:Title: Molecular cloning, sequence, and expression of cynomolgus monkey cholesteryl
asana high density lipoprotein levels.
A:Reference number: A53176; MUID:92031355
A:Accession: A53176
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-493 <PAP>
A:Cross-references: GB:M66343

Query Match 100.0%; Score 134; DB 2; Length 493;
Best Local Similarity 100.0%; Pred. No. 5.5e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGFLLQMDFGFPEHLVDPLQSL S 26
Db 468 RDGFLLQMDFGFPEHLVDPLQSL S 493

RESULT 2
A26941
cholesteryl ester transfer protein precursor - human
C:Species: Homo sapiens (man)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 21-Jul-2000
C:Accession: A26941
R:Drayna, D.; Jernaglin, A.S.; Mclean, J.; Henzel, W.; Kohr, W.; Fielding, C.; Lavn, R
Nature 327, 632-634, 1987
A:Title: Cloning and sequencing of human cholesteryl ester transfer protein cDNA.
A:Reference number: A26941; MUID:87258172
A:Accession: A26941
A:Molecule type: mRNA
A:Residues: 1-493 <DRA>
A:Cross-references: EMBL:M30185; NID:g180259; PIDN:AAA51977.1; PID:g180260
C:Genetics:
A:Gene: GDB:CEP
A:Cross-references: GDB:119773; OMIM:118470
A:Map position: 16q13-16q13
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-493/Product: cholesteryl ester transfer protein #status predicted <MAT>

Query Match 100.0%; Score 134; DB 2; Length 493;
Best Local Similarity 100.0%; Pred. No. 5.5e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLQMDGFPFPHLVDFLOSL 26
Db 468 RDGFLQMDGFPFPHLVDFLOSL 493

RESULT 3
A38700
cholesteryl ester transfer protein - golden hamster (fragment)
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 28-Feb-1992 #sequence_revision 10-Apr-1992 #text_change 05-Nov-1999
C:Accession: A38700
R:Jiang, X.C.; Moulin, P.; Quinet, E.; Goldberg, I.J.; Yacoub, L.K.; Agellon, L.B.; Comp
J. Biol. Chem. 266, 4631-4639, 1991
A:Title: Mammalian adipose tissue and muscle are major sources of lipid transfer protein
A:Reference number: A38700; MUID:91154277
A:Accession: A38700
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-289 <TAA>
A:Cross-references: GB:M63992; NID:9191342; PIDN:AA37066.1; PID:9191343
A:Note: the authors translated the codon CTG for residue 68 as Gly, GCG for residue 69 as
as Ser, and TTC for residue 267 as Ser

Query Match 97.8%; Score 131; DB 2; Length 289;
Best Local Similarity 96.2%; Pred. No. 8.7e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLQMDGFPFPHLVDFLOSL 26
Db 264 RDGFLQMDGFPFPHLVDFLOSL 289

RESULT 4
14692
cholesteryl ester transfer protein - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 05-Nov-1999
C:Accession: I46692
R:Nagashima, M.; McLean, J.W.; Lamn, R.M.
J. Lipid Res. 29, 1643-1649, 1988
A:Title: Cloning and mRNA tissue distribution of rabbit cholesteryl ester transfer prote
A:Reference number: I46692; MUID:89215620
A:Accession: I46692
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-497 <NAG>
A:Cross-references: GB:M27486; NID:9530906; PIDN:AA31199.1; PID:9530907
C:Genetics:
A:Gene: CERP

Query Match 87.3%; Score 117; DB 2; Length 497;
Best Local Similarity 92.0%; Pred. No. 2.5e-10;
Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DGFLLQMDGFPFPHLVDFLOSL 26
Db 473 DGFLLQMDGFPFPHLVDFLOSL 497

RESULT 5
D95247
aspartyl-tRNA synthetase [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C:Accession: D95247
R:Rettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Ventler, J.C.; Dougherty, B.A.; Morrison,

A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: D95247
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-587 <KUR>
A:Cross-references: GB:AE005672; PIDN:AAK76173.1; PID:914973626; GSPDB:GN00164; TIGR:
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP2114
C:Superfamily: lysine--tRNA ligase

Query Match 41.8%; Score 56; DB 2; Length 587;
Best Local Similarity 71.4%; Pred. No. 1.1;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 GFLLQMDGFPFPH 16
Db 510 GFLLQMDGFPFPH 523

RESULT 6
A98112
aspartate--tRNA ligase (EC 6.1.1.12) [imported] - Streptococcus pneumoniae (strain R6
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C:Accession: A98112
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: A98112
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-587 <KUR>
A:Cross-references: GB:AE007317; PIDN:AAL00726.1; PID:915459621; GSPDB:GN00174
C:Genetics:
A:Gene: asps
A:Superfamily: lysine--tRNA ligase
C:Keywords: ligase

Query Match 41.8%; Score 56; DB 2; Length 587;
Best Local Similarity 71.4%; Pred. No. 1.1;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 GFLLQMDGFPFPH 16
Db 510 GFLLQMDGFPFPH 523

RESULT 7
D82199
conserved hypothetical protein VC1432 [imported] - Vibrio cholerae (strain N16961 ser
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: D82199
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers
1, R.R.; Mekalanos, J.J.; Ventler, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833
A:Accession: D82199
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-310 <HEI>
A:Cross-references: GB:AE004222; GB:AE003852; NID:9655930; PIDN:AAF94589.1; GSPDB:GN
A:Experimental source: serogroup O1, strain N16961; biotype El Tor

C:Genetics:
A:Gene: VC1432
A:Map position: 1
C:Superfamily: conserved hypothetical protein MJ1157

Query Match 40.3%; Score 54; DB 2; Length 110;
Best Local Similarity 64.3%; Pred. No. 1.1;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 12 GFEHLVDFLOSL 25
|||||:|::|:|
Db 84 GFEHLVDFLOSL 97

RESULT 8
A:1904
hypothetical protein NMA1350 [imported] - Neisseria meningitidis (strain Z2491 serogroup
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: A81904
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holtroyd, S.; Jørgensen, K.; Leach, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:20222556
A:Accession: A81904
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-426 <PAR>
A:Cross-references: GB:AL162755; GB:AL157959; NID:97379742; PIDN:CAB84597.1; PID:9738001
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA1350
C:Superfamily: hypothetical protein H10404

Query Match 39.6%; Score 53; DB 2; Length 426;
Best Local Similarity 62.5%; Pred. No. 2.2;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 3 GFLLOMDPPEHL 18
|||:|::|:|
Db 331 GFLLOMDPPEHL 346

RESULT 9
E86870
aspartate--tRNA ligase (EC 6.1.1.12) [imported] - Lactococcus lactis subsp. lactis (stra
N:Alternate names: aspartyl-tRNA synthetase
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: E86870
R:Botolm, A.; Winkler, P.; Mauger, S.; Jallion, O.; Malarte, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: E86870
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-590 <STO>
A:Cross-references: GB:AE005176; PID:912725007; PIDN:AAK0663.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: asps
C:Superfamily: lysine--tRNA ligase
C:Keywords: ligase

Query Match 39.6%; Score 53; DB 2; Length 590;
Best Local Similarity 64.3%; Pred. No. 3.2;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 3 GFLLOMDPPEHL 16
|||||:|::|:|
Db 517 GFLLOMDPPEHL 530

RESULT 10
C83497
conserved hypothetical protein PA1192 [imported] - Pseudomonas aeruginosa (strain PAO
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: C83497
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;
Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapid, K.; L
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pa
A:Reference number: A82950; MUID:20437337
A:Accession: C83497
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-274 <STO>
A:Cross-references: GB:AE004549; GB:AE004091; NID:99947110; PIDN:ACG04581.1; GSPDB:GN
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: PA1192
C:Superfamily: conserved hypothetical protein MJ1157

Query Match 38.1%; Score 51; DB 2; Length 274;
Best Local Similarity 57.1%; Pred. No. 2.7;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 12 GFEHLVDFLOSL 25
|||||:|::|:|
Db 76 GFEHLVDFLOSL 89

RESULT 11
C64884
ydao protein - Escherichia coli
N:Alternate names: conserved hypothetical protein b1344
C:Species: Escherichia coli
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: C64884
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: C64884
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-311 <BLAT>
A:Cross-references: GB:AE000232; GB:U00096; NID:91787600; PIDN:ACG4426.1; PID:917876
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: ydao
C:Superfamily: conserved hypothetical protein MJ1157

Query Match 37.3%; Score 50; DB 1; Length 311;
Best Local Similarity 57.1%; Pred. No. 4.5;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 12 GFEHLVDFLOSL 25
|||||:|::|:|
Db 83 GFEHLVDFLOSL 96

RESULT 12
A85749
hypothetical protein ydao [imported] - Escherichia coli (strain O157:H7, substrain ED
C:Species: Escherichia coli

C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Nov-2001
C:Accession: A85749
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grothbeck, E.J.; Davis, N.W.; Lim, A.; Dimmlanta, E.; Potamocitis, K.; Apodaca,
Nature 409, 529-533, 2001
A>Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A85749
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-311 <STO>
A:Cross-references: GB:AE005174; NID:g12515408; PIDN:AA656453.1; GSPDB:GN00145; UWGP:224
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: ydao
C:Superfamily: conserved hypothetical protein MJ1157

Query Match 37.3%; Score 50; DB 2; Length 311;
Best Local Similarity 57.1%; Pred. No. 4.5;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 12 GPEHLLVDFLOSL 25
|||||:|:|:|:|
DB 83 GPEHVLPEYLEKL 96

RESULT 13
H90869
hypothetical protein ECS1928 [imported] - *Escherichia coli* (strain O157:H7, substrain R1
C:Species: *Escherichia coli*
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 27-Nov-2001
C:Accession: H90869
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shibata, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A>Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: H90869
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-311 <HAV>
A:Cross-references: GB:BA000007; PIDN:BA835351.1; PID:g13361393; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain R1MD 0509552
C:Genetics:
A:Gene: ECS1928
C:Superfamily: conserved hypothetical protein MJ1157

Query Match 37.3%; Score 50; DB 2; Length 311;
Best Local Similarity 57.1%; Pred. No. 4.5;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 12 GPEHLLVDFLOSL 25
|||||:|:|:|:|
DB 83 GPEHVLPEYLEKL 96

RESULT 14
D90291
permease, multidrug efflux [imported] - *Sulfolobus solfataricus*
C:Species: *Sulfolobus solfataricus*
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C:Accession: D90291
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, V.; Allard, G.; Awaize, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Mgoc, H.P.; Redder, F.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: *Sulfolobus solfataricus* complete genome.
A:Reference number: A89139
A:Accession: D90291
A>Status: Preliminary
A:Molecule type: DNA

A:Residues: 1-559 <KUR>
A:Cross-references: GB:AE006641; NID:g13814561; PIDN:AAK41587.1; GSPDB:GN00155
C:Genetics:
A:Gene: SSO1351

Query Match 36.9%; Score 49.5; DB 2; Length 559;
Best Local Similarity 42.3%; Pred. No. 11;
Matches 11; Conservative 5; Mismatches 7; Indels 3; Gaps 1;

OY 3 GFLLLQM--DEGPEHLLVDFLOSL 25
|||||:|:|:|:|
DB 360 GFLLLTLIPYNNPEYDEFALITPMGL 385

RESULT 15
AD6CH
2-dehydro-3-deoxyphosphopentate aldolase (EC 4.1.2.15) (Trp-sensitive) - *Escherichia*
N:Alternate names: 3-deoxy-D-arabino-hepulosonate-7-phosphate synthase; phospho-2-de
C:Species: *Escherichia coli*
C>Date: 22-May-1991 #sequence_revision 31-Oct-1997 #text_change 18-Jun-1999
C:Accession: H64928; J01131; A31384; A01107
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A>Title: The complete genome sequence of *Escherichia coli* K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: H64928
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-348 <BIAT>
A:Cross-references: GB:AE000265; GB:U00096; NID:g2367122; PIDN:AACT4774.1; PID:g17879
A:Experimental source: strain K-12, substrain MG1655
R:Hudson, G.S.; Relloso, P.; Davidson, B.E.
Gene 102, 87-91, 1991
A>Title: Two promoters control the *aroH* gene of *Escherichia coli*.
A:Reference number: J01131; MUID:91323737
A:Accession: J01131
A:Molecule type: DNA
A:Residues: 1-332, 'S', '334-348 <HND>
A:Cross-references: GB:M38266; NID:g145376; PIDN:AAA23497.1; PID:g145378
R:Ray, J.M.; Yanofsky, C.; Baerle, R.
J. Bacteriol. 170, 5500-5506, 1988
A>Title: Mutational analysis of the catalytic and feedback sites of the tryptophan-se
A:Reference number: A31384; MUID:89053867
A:Accession: A31384
A:Molecule type: DNA
A:Residues: 1-122, 'A', '124-202, '204', 'Q', '206-332', 'RQ', '335-348 <RAY>
A:Cross-references: GB:J04221
R:Zurawski, G.; Gunsalus, R.P.; Brown, K.D.; Yanofsky, C.
J. Mol. Biol. 145, 47-73, 1981
A>Title: Structure and regulation of *aroH*, the structural gene for the tryptophan-rep
A:Reference number: A01107; MUID:81263314
A:Accession: A01107
A:Molecule type: DNA
A:Residues: 1-36; '231-332', 'RQ', '335-348 <QUR>
A:Cross-references: GB:J01592; GB:J01593
C:Genetics:
A:Gene: *aroH*
A:Map position: 37 min
C:Function:
A:Description: aldehyde-lyase; carbon-carbon lyase; this is one of the DAP synthases
ic acid-7-phosphate
A:Pathway: aromatic amino acid biosynthesis; shikimate pathway
A>Note: the first reaction in aromatic amino acid biosynthesis
A>Note: feedback-inhibited by tryptophan; the other two DAP synthases are tyrosine-
C:Superfamily: phospho-2-dehydro-3-deoxyheptone aldolase
C:Keywords: aldehyde-lyase; aromatic amino acid biosynthesis; carbon-carbon lyase; sh

Query Match 35.8%; Score 48; DB 1; Length 348;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy	10	DRGFEHLVDF	21
	:	1	:
Db	254	EFDLPEHLVDF	265

Search completed: June 18, 2002, 08:06:29
Job time: 38 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:07:01 ; Search time 13.5 Seconds

(without alignments)
74.571 Million cell updates/sec

Title: US-09-943-334-1

Perfect score: 134
Sequence: 1 RDGFLLLQMDGEPPEHLVDFLOSL 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105324

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	134	100.0	493 1	CEP_HUMAN
2	134	100.0	493 1	CEP_MACFA
3	131	97.8	289 1	CEP_MESAU
4	117	87.3	497 1	CEP_RABIT
5	52	38.8	313 1	YDAO_HABIN
6	50	37.3	180 1	R102_ARATH
7	50	37.3	311 1	YDAO_ECOLI
8	50	37.3	311 1	TSDI_ABIGR
9	48	35.8	348 1	AROH_ECOLI
10	46.5	34.7	377 1	OP52_HEMSA
11	46	34.3	422 1	AP47_CABEL
12	46	34.3	868 1	PRPT_PORGI
13	45.5	34.0	1246 1	YMW2_CAREL
14	45	33.6	177 1	R101_ARATH
15	45	33.6	423 1	AIM2_HUMAN
16	45	33.6	423 1	AIM2_MOUSE
17	45	33.6	779 1	RIR1_ASFPM2
18	44.5	33.2	428 1	GDF2_MOUSE
19	44.5	33.2	782 1	CP8B_MOUSE
20	44.5	33.2	901 1	POLG_ENMG3
21	44.5	33.2	2290 1	POLG_EMEV
22	44.5	33.2	2292 1	POLG_EMCVB
23	44.5	33.2	2292 1	POLG_EMCVD
24	44.5	33.2	439 1	AP50_DICDI
25	44	32.8	472 1	C901_ARATH
26	44	32.8	516 1	LEF9_NPVAC
27	43.5	32.5	317 1	PLSX_BACHD
28	43.5	32.5	340 1	TCPE_VIBCH
29	43.5	32.5	496 1	MSS1_SCHPO
30	43	32.1	131 1	YD94_ARCFU
31	43	32.1	210 1	FTM2_SALTU
32	43	32.1	407 1	RRC_SALTU
33	43	32.1	421 1	SMAA_STRRR

34	43	32.1	423 1	AIM1_HUMAN	Q9bx5 h adaptor-t
35	43	32.1	423 1	AIM1_MOUSE	P35585 m adaptor-t
36	43	32.1	702 1	SYT_MYCLE	O07151 mycobacteri
37	43	32.1	778 1	RIR1_ASFB7	P42491 african swi
38	42.5	31.7	190 1	YPA1_BACSU	P50726 bacillus su
39	42.5	31.7	358 1	PKX1_HUMAN	P51817 homo sapien
40	42.5	31.7	1816 1	LM44_MOUSE	P97927 mus musculi
41	42.5	31.7	3097 1	CADN_DROME	O15943 drosophila
42	42	31.3	383 1	Y628_MYCTU	P96918 mycobacteri
43	42	31.3	387 1	DHAT_KLEPN	O59477 klebsiella
44	42	31.3	437 1	EP1G_HUMAN	P26641 homo sapien
45	42	31.3	437 1	EP1G_MOUSE	Q908n0 mus musculi

ALIGNMENTS

RESULT 1	CEP_HUMAN	STANDARD:	PRT: 493 AA.
ID	CEP_HUMAN	013987; 013988;	
AC	P1597; 013987; 013988;		
DT	01-OCT-1989 (Rel. 12; Created)		
DT	01-OCT-1989 (Rel. 12; Last sequence update)		
DT	16-OCT-2001 (Rel. 40; Last annotation update)		
DE	Cholesteryl ester transfer protein precursor (lipid transfer protein 1).		
GN	CEP.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.		
RX	MEDLINE=87258172; PubMed=3600759;		
RA	Drayna D., Jarnagin A.S., McLean J., Henzel W., Kohr W., Fielding C.,		
RA	Lawn R.,		
RT	"Cloning and sequencing of human cholesteryl ester transfer protein		
RT	CDNA."		
RL	Nature 327:632-634(1987).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=90241928; PubMed=2334701;		
RA	Agellon L.B., Quinet E.M., Gillette T.G., Drayna D.T., Brown M.L.,		
RA	Tall A.R.;		
RT	"Organization of the human cholesteryl ester transfer protein gene."		
RT	Biochemistry 29:1372-1376(1990).		
RN	[3]		
RP	SEQUENCE OF 1-15 FROM N.A.		
RX	MEDLINE=97112972; PubMed=8943225;		
RA	Oliveira C.F.O., Chouinard R.A., Agellon L.B., Bruce C., Ma L.,		
RA	Walsh A., Breslow J.L., Tall A.R.;		
RT	"Human cholesteryl ester transfer protein gene proximal promoter		
RT	contains dietary cholesterol positive responsive elements and mediates		
RT	expression in small intestine and periphery while predominant liver		
RT	and spleen expression is controlled by 5'-distal sequences. Cis-acting		
RT	sequences mapped in transgenic mice."		
RL	J. Biol. Chem. 271:31831-31838(1996).		
RN	[4]		
RP	SEQUENCE OF 1-27 FROM N.A.		
RX	MEDLINE=97473500; PubMed=8332354;		
RA	Williams S., Hayes L., Eisenbos L., Williams A., Andre C.,		
RA	Abramson R., Thompson J.F., Milos P.M.;		
RT	"Sequencing of the cholesteryl ester transfer protein 5' regulatory		
RT	region using artificial transposons."		
RL	Gene 197:101-107(1997).		
RN	[5]		
RP	SEQUENCE OF 9-493 FROM N.A.		
RC	TISSUE=liver.		
RA	Dinichuk J.E., Hart J.T., Mirak D.O.;		
RL	Submitted (Feb-1992) to the EMBL/GenBank/DBJ databases.		
RN	[6]		
RP	VARIANT GUY-459.		
RX	MEDLINE=94013514; PubMed=8408659;		

```

RA Takahashi K., Jiang X.-C., Sakai N., Yamashita S., Hirano K., Bujo H.,
RA Yamazaki H., Kusunoki J., Miura T., Kussie P., Matsuzawa Y., Saito Y.,
RA Tall A.:
RT "A missense mutation in the cholesteryl ester transfer protein gene
RT with possible dominant effects on plasma high density lipoproteins";
RL J. Clin. Invest. 92:2060-2064(1993).
CC -1- FUNCTION: CETP IS AN EXTREMELY HYDROPHOBIC PROTEIN INVOLVED IN THE
CC TRANSFER OF INSOLUBLE CHOLESTERYL ESTERS IN THE REVERSE TRANSPORT
CC OF CHOLESTEROL.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED MAINLY IN THE LIVER.
CC -1- DISEASE: PROBABLY INVOLVED IN THE DEVELOPMENT OF ATHEROSCLEROSIS.
CC -1- SIMILARITY: BELONGS TO THE BPI/CETP/LBP/PLTP FAMILY.
CC -----
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CC -----
DR EMBL: M30185; AA51977.1; -.
DR EMBL: M32998; AA51978.1; -.
DR EMBL: M32993; AA51978.1; JOINED.
DR EMBL: M32994; AA51978.1; JOINED.
DR EMBL: M32995; AA51978.1; JOINED.
DR EMBL: M32996; AA51978.1; JOINED.
DR EMBL: M32997; AA51978.1; JOINED.
DR EMBL: M32997; AA51978.1; JOINED.
DR EMBL: AF027656; AAB86604.1; -.
DR EMBL: M83573; AAB59388.1; -.
DR PIR: A26941; A26941.
DR InterPro: IPR001124; LBP_BPI_CETP.
DR Pfam: PF01273; LBP_BPI_CETP.1.
DR SMART: SM00328; BPI1; 1.
DR SMART: SM00329; BPI2; 1.
DR PROSITE: PS00400; LBP_BPI_CETP.1.
KW Lipid transport; Cholesterol metabolism; Glycoprotein; Signal;
KW Atherosclerosis; Disease mutation.
FT SIGNAL 1 17
FT CHAIN 18 493 CHOLESTERYL ESTER TRANSFER PROTEIN.
FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 358 358 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 413 413 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 459 459 D -> G (IN CETP DEFICIENCY).
FT CONFLICT 251 310 /FTID=VAR.004172.
FT CONFLICT 422 422 MISSING (IN REF. 5).
FT SEQUENCE 493 AA: 54770 MW: 16d47ACDC99B063C CRC64:
SQ
Query Match 100.0%; Score 134; DB 1; Length 493;
Best Local Similarity 100.0%; Pred. No. 2,7e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RDGFLLLQMDFGPEPHLLVDFLOSL 26
DB 468 RDGFLLLQMDFGPEPHLLVDFLOSL 493
RESULT 2
CETP_MACFA STANDARD; PRT; 493 AA.
ID CETP_MACFA
AC P47896;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Cholesteryl ester transfer protein precursor (Lipid transfer protein

```

```

DE 1).
GN CETP.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92031355; PubMed=1931878;
RA Page M.E., Rehberg E.F., Marotti K.R., Melchior G.W.;
RT "Molecular cloning, sequence, and expression of cynomolgus monkey
RT cholesteryl ester transfer protein. Inverse correlation between
RT hepatic cholesteryl ester transfer protein mRNA levels and plasma
RT high density lipoprotein levels";
RL Atheroscler. Thromb. 11:1759-1771(1991).
CC -1- FUNCTION: CETP IS AN EXTREMELY HYDROPHOBIC PROTEIN INVOLVED IN THE
CC TRANSFER OF INSOLUBLE CHOLESTERYL ESTERS IN THE REVERSE TRANSPORT
CC OF CHOLESTEROL.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED MAINLY IN THE LIVER.
CC -1- SIMILARITY: BELONGS TO THE BPI/CETP/LBP/PLTP FAMILY.
CC -----
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CC -----
DR EMBL: M86343; AAA36840.1; -.
DR InterPro: IPR001124; LBP_BPI_CETP.
DR Pfam: PF01273; LBP_BPI_CETP.1.
DR SMART: SM00328; BPI1; 1.
DR SMART: SM00329; BPI2; 1.
DR PROSITE: PS00400; LBP_BPI_CETP.1.
KW Lipid transport; Cholesterol metabolism; Glycoprotein; Signal.
FT SIGNAL 1 17
FT CHAIN 18 493
FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 358 358 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 413 413 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 493 AA: 54743 MW: 7E82BE3C2A8FAED CRC64:
SQ
Query Match 100.0%; Score 134; DB 1; Length 493;
Best Local Similarity 100.0%; Pred. No. 2,7e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RDGFLLLQMDFGPEPHLLVDFLOSL 26
DB 468 RDGFLLLQMDFGPEPHLLVDFLOSL 493
RESULT 3
CETP_MESAU STANDARD; PRT; 289 AA.
ID CETP_MESAU
AC P25914;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cholesteryl ester transfer protein (lipid transfer protein 1)
DE (Fragment).
GN CETP.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;

```



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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91154277; PubMed=1999438;
RA Jiang X.C., Moulin P., Quinet E., Goldberg I.J., Yacoub L.K.,
RA Agellon L.B., Compton D., Scholtzer-Polokoff R., Tall A.R.;
RT "Mammalian adipose tissue and muscle are major sources of lipid
RT transfer protein mRNA.";
RL J. Biol. Chem. 266:4631-4639(1991).
CC -1- FUNCTION: CETP IS AN EXTREMELY HYDROPHOBIC PROTEIN INVOLVED IN THE
CC TRANSFER OF INSOLUBLE CHOLESTERYL ESTERS IN THE REVERSE TRANSPORT
CC OF CHOLESTEROL.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- SIMILARITY: BELONGS TO THE BPI/CETP/LBP/PLTP FAMILY.
CC -----
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CC -----
CC EMBL: M63992; AAA37066.1; -.
CC PIR: A38700; A38700.
CC InterPro: IPR001124; LBP_BPI_CETP.
CC Pfam: PF01273; LBP_BPI_CETP; 1.
CC SMART: SM00328; BPI2; 1.
CC SMART: SM00329; BPI2; 1.
CC PROSITE: PS00400; LBP_BPI_CETP; PARTIAL.
CC Lipid transport; Cholesterol metabolism; Glycoprotein.
CC KW NON_TER 1 1
CC CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 289 AA; 32330 MW; CA91A06D83927747 CRC64;

Query Match 97.8%; Score 131; DB 1; Length 289;
Best Local Similarity 96.2%; Pred. No. 4.5e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DGGFLLQMDGFRPHLVDFLOSL 26
DB 264 RDGFLQMDGFRPHLVDFLOSLN 289

RESULT 4
CETP_RABIT STANDARD; PRT; 497 AA.
AC P22687;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cholesteryl ester transfer protein precursor (Lipid transfer protein
DE 1) (Fragment).
GN CETP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_Taxid=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9215620; PubMed=3244015;
RA Nagashima M., McLean J.W., Lahn R.M.;
RT "Cloning and mRNA tissue distribution of rabbit cholesteryl ester
RT transfer protein.";
RL J. Lipid Res. 29:1643-1649(1988).
CC -1- FUNCTION: CETP IS AN EXTREMELY HYDROPHOBIC PROTEIN INVOLVED IN THE
CC TRANSFER OF INSOLUBLE CHOLESTERYL ESTERS IN THE REVERSE TRANSPORT
CC OF CHOLESTEROL.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED MAINLY IN THE LIVER.
CC -1- SIMILARITY: BELONGS TO THE BPI/CETP/LBP/PLTP FAMILY.
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CC -----
CC EMBL: M27486; AAA31199.1; -.
CC InterPro: IPR001124; LBP_BPI_CETP.
CC Pfam: PF01273; LBP_BPI_CETP; 1.
CC SMART: SM00328; BPI2; 1.
CC SMART: SM00329; BPI2; 1.
CC PROSITE: PS00400; LBP_BPI_CETP; 1.
CC Lipid transport; Cholesterol metabolism; Glycoprotein; Signal.
CC KW NON_TER 1 1
CC SIGNAL 1 1
CC CHAIN 2 497
CC CARBOHYD 89 89 CHOLESTERYL ESTER TRANSFER PROTEIN.
CC CARBOHYD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 417 417 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 497 AA; 54513 MW; EB2944E1821D0332 CRC64;

Query Match 87.3%; Score 117; DB 1; Length 497;
Best Local Similarity 92.0%; Pred. No. 1.2e-10;
Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DGGFLLQMDGFRPHLVDFLOSL 26
DB 473 DGGFLLQMDGFRPHLVDFLOSL 497

RESULT 5
YDAO_HAEIN STANDARD; PRT; 313 AA.
AC Q57184; 005059;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein H11371.1.
GN H11371.1.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellales;
OC Haemophilus.
OX NCBI_Taxid=727;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fieischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kierlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uitterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Georgagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
RT influenzae Rd.";
RL Science 269:496-512(1995).
RN [2]
RP REVISIONS.
RA White O., Clayton R.A., Kierlavage A.R., Fieischmann R.D.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: STRONG, TO E.COLI YDAO.
CC -----
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 CC -----
 DR EMBL: U32817; AAC23019.1; -
 DR TIGR: H11371.1; -
 DR InterPro: IPR000541; UPF0021.
 DR Pfam: PF01171; UPF0021; 1.
 DR Hypothetical protein: Complete proteome.
 SO SEQUENCE 313 AA; 35703 MW; 646717CB802F7252 CRC64;

Query Match 38.8%; Score 52; DB 1; Length 313;
 Best Local Similarity 57.1%; Pred. No. 0.93;
 Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 QY 12 GFEPHLVDFLOSL 25
 DB 86 GFEPHLVDFLOSL 99

RESULT 6
 ID R102_ARATH STANDARD; PRT; 180 AA.
 AC Q9F58;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE 40S ribosomal protein S10-2.
 GN RPS10B OR AT5G41520 OR MBK23.4.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosida II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=97471969; PubMed=9330910;
 RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
 RA Miyajima N., Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
 RT features of the 1.6 Mb regions covered by twenty physically assigned
 RT clones.";
 RL DNA Res. 4:215-230(1997).
 [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Shin P.,
 RA Tracy S.E., Ban J., Bowser L., Carlucci P., Chung M.K.,
 RA Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,
 RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Pham P.K., Quach H.L.,
 RA Sakano H., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C.,
 RA Toriumi M., Yamada K., Yu G., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE S10E FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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 CC -----
 DR EMBL: AB005233; BAB11458.1; -
 DR EMBL: AY037240; AAK59840.1; -

DR EMBL: AF375440; AAK53024.1; -
 KW Ribosomal protein: Multigene family.
 SO SEQUENCE 180 AA; 19733 MW; 9D8C1E2FED5CA28B CRC64;

Query Match 37.3%; Score 50; DB 1; Length 180;
 Best Local Similarity 32.0%; Pred. No. 1.1;
 Matches 8; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
 QY 1 RKGFLQMDGEPHLLVDFLOSL 25
 DB 17 KKGVLAKKDFMLPQHPLEISVPL 41

RESULT 7
 ID YDAO_ECOLI STANDARD; PRT; 311 AA.
 AC P76055; Q47558;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein ydao.
 GN YDAO OR B1344.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 [2]
 RN SEQUENCE OF 1-40 FROM N.A.
 RC STRAIN=K12 / W3110;
 RX MEDLINE=94162733; PubMed=7764507;
 RA Yamada M., Yanai S., Talkner A.;
 RT "Analysis of products of the Escherichia coli genomic genes and
 RT regulation of their expressions: an applicable procedure for genomic
 RT analysis of other microorganisms.";
 RL Biosci. Biotechnol. Biochem. 58:117-120(1994).
 CC -1- SIMILARITY: STRONG, TO H. INFLUENZAE H11371.1.
 CC -----
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 CC -----
 DR EMBL: AE000232; AAC74426.1; -
 DR EMBL: D21139; BAA04675.1; -
 DR EcoGene: EG13357; ydao.
 DR InterPro: IPR000541; UPF0021.
 DR Pfam: PF01171; UPF0021; 1.
 KW Hypothetical protein: Complete proteome.
 FT CONFLICT 11 E -> A (IN REF. 2).
 FT SEQUENCE 311 AA; 35561 MW; D696057B7C092D79 CRC64;

Query Match 37.3%; Score 50; DB 1; Length 311;
 Best Local Similarity 57.1%; Pred. No. 1.9;
 Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 12 GFEPHLVDFLOSL 25
 DB 83 GFEPHLVDFLOSL 96

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RESULT      8
ID          TSD1_ABIGR      STANDARD:      PRT:      628 AA.
AC          024475:
DT          01-MAR-2002 (Rel. 41, Created)
DT          01-MAR-2002 (Rel. 41, Last sequence update)
DT          01-MAR-2002 (Rel. 41, Last annotation update)
DE          Pinene synthase, chloroplast precursor (EC 4.2.3.14) (Beta-geraniolene
DE          synthase) ((-)-(1S,5S)-pinene synthase).
GN          AG3.18.
OS          Abies grandis (Grand fir).
OC          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC          Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
OX          NCBI_TaxID=46611;
RN          [1]
RP          SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX          MEDLINE=97413772; PubMed=9268308;
RA          Bohlmann J., Steele C.L., Croteau R.;
RT          *Monoterpene synthases from grand fir (Abies grandis): cDNA isolation,
RT          characterization, and functional expression of myrcene synthase, (-)-
RT          (4S)-limonene synthase, and (-)-(1S,5S)-pinene synthase.*;
RL          J. Biol. Chem. 272:21784-21792(1997).
CC          -1- FUNCTION: Involved in defensive oleoresin formation in conifers in
CC          response to insect attack or other injury. Involved in monoterpene
CC          (C10) olefins biosynthesis. A mixture of alpha-and beta-pinene is
CC          produced by this enzyme.
CC          -1- CATALYTIC ACTIVITY: Geranyl diphosphate = pinene + diphosphate.
CC          -1- COFACTOR: Manganese and potassium.
CC          -1- PATHWAY: Oleoresinosis.
CC          -1- SUBCELLULAR LOCATION: Chloroplast.
CC          -1- INDUCTION: By wounding.
CC          -1- SIMILARITY: BELONGS TO THE TERPENE SYNTHASE FAMILY.
CC          -----
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CC          -----
DR          EMBL: U87909; AB071085.1; -.
DR          HSSP: Q40577; SEAT.
DR          Mendel: 27004; ADIgr:2508;27004.
DR          InterPro: IPR001906; Terp_synth_fam.
DR          Pfam: PF01397; Terpene_synth_1.
KW          Lyase; Manganese; Transit peptide; Chloroplast.
FT          TRANSIT      1      ?      CHLOROPLAST (POTENTIAL).
FT          CHAIN        628      PINENE SYNTHASE.
FT          ACT_SITE     524      524      BY SIMILARITY.
FT          ACT_SITE     601      601      BY SIMILARITY.
FT          ACT_SITE     605      605      BY SIMILARITY.
SQ          SEQUENCE 628 AA: 71505 MW: 23DBB786F3C8072C CXC64:

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DE          Phospho-2-dehydro-3-deoxyheptanate aldolase, Trp-sensitive
DE          (EC 4.1.2.15) (Phospho-2-keto-3-deoxyheptanate aldolase) (DAH
DE          synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase).
GN          AROH OR B1704.
OS          Escherichia coli.
OC          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC          Escherichia.
OX          NCBI_TaxID=562;
RN          [1]
RP          SEQUENCE FROM N.A.
RX          MEDLINE=91323737; PubMed=1677907;
RA          Hudson G.S., Reilios P., Davidson B.E.;
RT          *Two promoters control the aroH gene of Escherichia coli.*;
RT          Gene 102:87-91(1991).
RL          [2]
RN          [2]
RP          SEQUENCE FROM N.A.
RX          MEDLINE=89053867; PubMed=2903857;
RA          Ray J.M., Yanofsky C., Baerle R.;
RT          *Mutational analysis of the catalytic and feedback sites of the
RT          tryptophan-sensitive 3-deoxy-D-arabino-heptulosonate-7-phosphate
RT          synthase of Escherichia coli.*;
RL          J. Bacteriol. 170:5500-5506(1988).
RN          [3]
RP          SEQUENCE FROM N.A.
RX          STRAIN=K12 / MG1655;
RA          MEDLINE=97426617; PubMed=9278503;
RA          Balthner F.R., Plunkett G., Ili, Bloch C.A., Perna N.T., Burland V.,
RA          Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA          Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA          Mau B., Shao Y.;
RT          *The complete genome sequence of Escherichia coli K-12.*;
RT          Science 277:1453-1474(1997).
RL          [4]
RN          [4]
RP          SEQUENCE FROM N.A.
RX          STRAIN=K12;
RA          MEDLINE=97251357; PubMed=9097039;
RA          Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA          Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA          Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA          Nakade S., Nakamura Y., Nishimoto S., Nishio Y., Oshima T., Saito N.,
RA          Sempel G., Seki Y., Sivasubramanian S., Tagami H., Takeda J.,
RA          Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horikuchi T.;
RT          *A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT          corresponding to the 28.0-40.1 min region on the linkage map.*;
RL          DNA Res. 3:363-377(1996).
RN          [5]
RP          SEQUENCE OF 1-36 AND 232-348 FROM N.A.
RX          MEDLINE=91267314; PubMed=6167722;
RA          Zurawski G., Gunsalus R.P., Brown K.D., Yanofsky C.;
RT          *Structure and regulation of aroH, the structural gene for the
RT          tryptophan-repressible 3-deoxy-D-arabino-heptulosonic
RT          acid-7-phosphate synthetase of Escherichia coli.*;
RL          J. Mol. Biol. 145:47-73(1981).
CC          -1- FUNCTION: STEREOSPECIFIC CONDENSATION OF PHOSPHOENOLPYRUVATE (PEP)
CC          AND D-ERYTHROSE-4-PHOSPHATE (E4P) GIVING RISE TO 3-DEOXY-D-
CC          ARABINO-HEPTULOSONATE-7-PHOSPHATE (DAH).
CC          -1- CATALYTIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptanate 7-
CC          phosphate + phosphate = phosphoenolpyruvate + D-erythrose 4-
CC          phosphate + H(2)O.
CC          -1- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN
CC          THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
CC          -1- MISCELLANEOUS: THERE ARE 3 DAHP SYNTHASES. AROH IS
CC          FEEDBACK-INHIBITED BY TRP. THE OTHER 2 DAHP SYNTHASES ARE TYR- AND
CC          PHE-SENSITIVE, RESPECTIVELY.
CC          -1- SIMILARITY: BELONGS TO CLASS-I DAHP SYNTHETASE FAMILY.
CC          -----
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CC -----
DR EMBL: M38266; AAA23497.1; -.
DR EMBL: J04221; AAA23493.1; -.
DR EMBL: AE00265; AAC74774.1; -.
DR EMBL: D90813; BAA15473.1; -.
DR EMBL: V00261; CAA23510.1; -.
DR EMBL: X04373; CAA27956.1; -.
DR PIR: J01131; ADECH.
DR HSSP: P00886; 1QR7.
DR EcoGene: EG10080; arch.
DR InterPro: IPR001785; DAHP_synth_1.
DR Pfam: PF00793; DAHP_synth_1.1.
DR ProDom: PD005060; DAHP_synth_1.1.
DR Aromatic amino acid biosynthesis; Lyase; Complete proteome.
KW CONFLICT 123 123 E -> G (IN REF. 2).
FT CONFLICT 203 205 RAS -> AQ (IN REF. 2).
FT CONFLICT 333 333 S -> T (IN REF. 3 AND 4).
FT CONFLICT 333 334 SE -> RQ (IN REF. 2 AND 5).
SQ SEQUENCE 348 AA; 38721 MW; F293C462447226E6 CRC64;

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Query Match 35.8%; Score 48; DB 1; Length 348;
Best Local Similarity 66.7%; Pred. No. 4.3;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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QY 10 MDGFEHLVDF 21
   : 1111:111
Db 254 EFDLPHELVDF 265

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RESULT 10
OPS2_HEMSA STANDARD; PRT; 377 AA.
ID OPS2_HEMSA
AC 025158;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Compound eye opsin BCRH2.
OS Hemigrapsus sanguineus (Crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Grapsoidea; Varunidae; Hemigrapsus.
OX NCBI_TaxID=40176;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Eye;
RA Sakamoto K., Hisatomi O., Tokunaga F., Eguchi E.;
RT "Two opsins from the compound eye of the crab Hemigrapsus
   sanguineus.";
RL J. Exp. Biol. 199;441-450(1996).
CC -1- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT
CC MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
CC LINKED TO CIS-RETINAL. THIS OPSIN PRODUCES VISUAL PIGMENTS WITH
CC MAXIMAL ABSORPTION IN THE BLUE-GREEN REGION OF THE SPECTRUM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL OF THE SEVEN RETINULAR CELLS
CC (R1-R7) FORMING THE MAIN RABDOM IN EACH OMATIDUM.
CC -1- PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SRR OR THR RESIDUES MAY
CC BE PHOSPHORYLATED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC OPSIN SUBFAMILY.
CC -----
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CC -----
CC EMBL: D50584; BAA09133.1; -.
CC DR GCRDB: GCR 1067; -.
CC DR InterPro: IPR000276; GPCR_Rhodpsn.

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DR InterPro: IPR001760; Opsin.
DR Pfam: PF00001; 7em_1; 1.
DR PRINTS: PR00237; GPCR_RHODPSN.
DR PROSITE: PS00237; G-PROTEIN_RECIP_FL_1; 1.
DR PROSITE: PS00262; G-PROTEIN_RECIP_FL_2; 1.
DR PROSITE: PS00238; OPSIN_1.
KW Photoreceptor; Retinal protein; Transmembrane; Glycoprotein; Vision;
KW Phosphorylation; G-protein coupled receptor.
FT DOMAIN 1 53 EXTRACELLULAR.
FT TRANSMEM 54 78 1 (POTENTIAL).
FT DOMAIN 79 90 CYTOPLASMIC.
FT TRANSMEM 91 115 2 (POTENTIAL).
FT DOMAIN 116 131 EXTRACELLULAR.
FT TRANSMEM 132 151 3 (POTENTIAL).
FT DOMAIN 152 170 CYTOPLASMIC.
FT TRANSMEM 171 194 4 (POTENTIAL).
FT DOMAIN 195 218 EXTRACELLULAR.
FT TRANSMEM 219 246 5 (POTENTIAL).
FT DOMAIN 247 281 CYTOPLASMIC.
FT TRANSMEM 282 305 6 (POTENTIAL).
FT DOMAIN 306 313 EXTRACELLULAR.
FT TRANSMEM 314 338 7 (POTENTIAL).
FT DOMAIN 339 377 CYTOPLASMIC.
FT DISULFD 128 205 BY SIMILARITY.
FT BINDING 325 325 RETINAL CHROMOPHORE (BY SIMILARITY).
FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 377 AA; 42114 MW; FD6CC2E0E199A256 CRC64;

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Query Match 34.7%; Score 46.5; DB 1; Length 377;
Best Local Similarity 56.2%; Pred. No. 8.1;
Matches 9; Conservative 5; Mismatches 1; Indels 1; Gaps 1;

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QY 9 MDGFEHL-LVDFIQ 23
   : 111:11 : : 111:11
Db 17 MDGFEHGVSYDFVR 32

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RESULT 11
ID AP47_CAEEL STANDARD; PRT; 422 AA.
AC P35602;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Clathrin coat assembly protein AP47 (Clathrin coat associated protein
   AP47) (Golgi adaptor AP-1 47 kDa protein) (HA1 47 kDa subunit)
DE (Clathrin assembly protein assembly protein complex 1 medium chain).
DE UNC-101.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=94116859; PubMed=8288128;
RA Lee J., Jongeward G.D., Sternberg P.W.;
RT "unc-101, a gene required for many aspects of Caenorhabditis elegans
   development and behavior, encodes a clathrin-associated protein.";
RL Genes Dev. 8:60-73(1994).
CC -1- FUNCTION: COMPONENT OF THE ADAPTOR COMPLEXES WHICH LINK CLATHRIN
CC TO RECEPTORS IN COATED VESICLES. CLATHRIN-ASSOCIATED PROTEIN
CC COMPLEXES ARE BELIEVED TO INTERACT WITH THE CYTOPLASMIC TAILS OF
CC MEMBRANE PROTEINS, LEADING TO THEIR SELECTION AND CONCENTRATION.
CC AP47 IS A SUBUNIT OF THE PLASMA MEMBRANE ADAPTOR.
CC -1- FUNCTION: REQUIRED FOR MANY ASPECTS OF DEVELOPMENT AND BEHAVIOR,
CC INCLUDING NEGATIVE REGULATION OF VULVAL DIFFERENTIATION.
CC -1- SUBUNIT: ASSEMBLY PROTEIN COMPLEX 1 (AP-1) IS A HETEROTETRAMER
CC COMPOSED OF TWO LARGE CHAINS (GAMMA AND BETA'), A MEDIUM CHAIN
CC (AP47) AND A SMALL CHAIN (AP19).
CC -1- SUBCELLULAR LOCATION: COMPONENT OF THE COAT SURROUNDING THE
CC CYTOPLASMIC FACE OF COATED VESICLES LOCATED AT THE GOLGI COMPLEX.

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CC -1- SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES MEDIUM SUBUNITS
CC FAMILY.
CC -----
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CC -----
DR EMBL: L26291; AAA72418.1; -
DR InterPro: IPR001392; Adap_comp_sub.
DR Pfam: PF00928; Adap_comp_sub; 1.
DR PRINTS: PR00314; CLATHRINADPT.
DR PROSITE: PS00990; CLAT_ADAPTOR_M.1; 1.
DR PROSITE: PS00991; CLAT_ADAPTOR_M.2; 1.
DR Coated pits.
DR SEQUENCE 422 AA; 48297 MW; D57BF5D1EF496D50 CRC64;

Query Match 34.3%; Score 46; DB 1; Length 422;
Best Local Similarity 42.9%; Pred. No. 11;
Matches 9; Conservative 4; Mismatches 2; Indels 6; Gaps 1;

QY 1 RDGFLL-----QMDGFPE 15
Db 104 RDNFVYIYELDMDGFPE 124
|||||: |||||:
PRTT_PORGI STANDARD; PRT; 868 AA.
ID P43158;
AC 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Thiol protease/hemagglutinin prt precursor (EC 3.4.22.-).
GN PRTT.
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; CF8 group; Bacteroidetes; Bacteroidales; Porphyromonadaceae;
OC Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN-ATCC 53977;
RX MEDLINE-93114862; PubMed-8093357;
RA Ologoto J.-I., Kuramitsu H.K.;
RT "Isolation and characterization of the Porphyromonas gingivalis prt
RT gene, coding for protease activity."
RL Infect. Immun. 61:117-123(1993).
RN [2]
RP REVISIONS, SEQUENCE FROM N.A.
RC STRAIN-ATCC 53977;
RX MEDLINE-95105001; PubMed-7806362;
RA Madden T.E., Clark V.L., Kuramitsu H.K.;
RT "Revised sequence of the Porphyromonas gingivalis prt cysteine
RT exoeloxin B/streptococcal proteinase."
RL Infect. Immun. 63:238-247(1995).
CC -1- FUNCTION: APPEARS TO BE SPECIFIC FOR ARGININE-CONTAINING PEPTIDE
CC BONDS. POSSESSES HEMAGGLUTININ ACTIVITY.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C10.
CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-17 IS THE INITIATOR.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----

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DR EMBL: M83096; -; NOT_ANNOTATED_CDS.
DR MEROPS: C10.002; -.
DR InterPro: IPR000200; Peptidase_C10.
DR Pfam: PF01640; Peptidase_C10; 1.
DR PRINTS: PR00797; STREPTOPALIN.
KW Hydrolyase; Thiol protease; Signal; Hemagglutinin.
FT SIGNAL 1 27
FT PROPEP 28 ? POTENTIAL.
FT CHAIN 7 868 THIOL PROTEASE/HEMAGGLUTININ PRTT.
FT ACT_SITE 184 184 BY SIMILARITY.
FT ACT_SITE 327 327 BY SIMILARITY.
DR SEQUENCE 868 AA; 96444 MW; 45436FEF32779323 CRC64;

Query Match 34.3%; Score 46; DB 1; Length 868;
Best Local Similarity 60.0%; Pred. No. 23;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RDGFLLQMDGFPE 15
Db 74 KDGFLVAADDFPE 88
|||||: |||
PRTT_PORGI STANDARD; PRT; 1246 AA.
ID YWV2_CAEEL
AC P4504; P34505; P34506; P90907;
DT 01-FEB-1994 (Rel. 28, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Hypothetical 130.6 kDa protein K04H4.2 in chromosome III.
GN K04H4.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE-94150718; PubMed-7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berts M.,
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Sims M., Smaildon N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Woldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
RN [2]
RP REVISIONS.
RC Dubinin R.;
RA Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOPFORMS: K04H_2A (SHOW HERE) AND
CC K04H_2B. ARE PROBABLY PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: TO CHITIN-BINDING MOTIFS.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Z27078; CAAB1587.1; -
DR EMBL: Z27078; CAAB1588.1; -
DR PIR: S40992;

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DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adaptor-related protein complex 1 mu 2 subunit (Clathrin coat
DE assembly protein AP47 2) (Clathrin coat associated protein AP47 2)
DE (Golgi adaptor AP-1 47 kDa protein) (HA1 47 kDa subunit 2) (Clathrin
DE assembly protein assembly protein complex 1 medium chain 2) (AP-mu
DE chain family member muB).
GN APIM2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=99268457; PubMed=10338135;
RA Ohno H., Tomemori T., Nakatsu F., Okazaki Y., Aguilar R.C.,
RA Foerisch H., Melman I., Saito T., Shirasawa T., Bonifacio J.S.;
RT "muB, a novel adaptor medium chain expressed in polarized epithelial
RT cells."
RL FEBS Lett. 449:215-220(1999).
CC -1- FUNCTION: COMPONENT OF THE ADAPTOR COMPLEXES WHICH LINK CLATHRIN
CC TO RECEPTORS IN COATED VESICLES. CLATHRIN-ASSOCIATED PROTEIN
CC COMPLEXES ARE BELIEVED TO INTERACT WITH THE CYTOPLASMIC TAILS OF
CC MEMBRANE PROTEINS, LEADING TO THEIR SELECTION AND CONCENTRATION.
CC AP47 IS A SUBUNIT OF THE PLASMA MEMBRANE ADAPTOR.
CC -1- SUBUNIT: ASSEMBLY PROTEIN COMPLEX 1 (AP-1) IS A HETEROTETRAMER
CC COMPOSED OF TWO LARGE CHAINS (GAMMA AND BETA'), A MEDIUM CHAIN
CC (AP47) AND A SMALL CHAIN (API9).
CC -1- SUBCELLULAR LOCATION: COMPONENT OF THE COAT SURROUNDING THE
CC CYTOPLASMIC FACE OF COATED VESICLES LOCATED AT THE GOLGI COMPLEX.
CC -1- PTM: AUTOPHOSPHORYLATED (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES MEDIUM SUBUNITS
CC FAMILY.
CC -----
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CC or send an email to license@lsb-slb.ch).
CC -----
CC EMBL: AF020797; AAD25870.2; -
DR InterPro: IPR001392; Adap_comp_sub.
DR Pfam: PF00928; Adap_comp_sub; 1.
DR PRINTS: PR00314; CLATHRINADPT.
DR PROSITE: PS00980; CLAT_ADAPTOR_M.1; 1.
DR PROSITE: PS00991; CLAT_ADAPTOR_M.2; 1.
KW Coated pits; Phosphorylation.
SQ SEQUENCE 423 AA; 48108 MW; A3F6FDF8659DD6F7 CRC64;

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Query Match          33.6%; Score 45; DB 1; Length 423;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 9; Conservative 4; Mismatches 2; Indels 6; Gaps 1;

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QY 1 RDGFLLQ-----MDFGPE 15
   |||:::|||||:
Db 104 RDNFVIVYELLDLMDFGFPQ 124

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Search completed: June 18, 2002, 08:13:08
 Job time: 367 sec

10

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:06:36 ; Search time 41.39 Seconds
(without alignments)
108.670 Million cell updates/sec

Title: US-09-943-334-1
Perfect score: 134
Sequence: 1 RDGFLLQMDFGFPEHLLVDFLOSL 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL-19-
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	123	91.8	485	6	Q9BG59	Q9BG59 tupala gilis
2	56	41.8	314	16	Q9CN39	Q9CN39 pasteurrella
3	56	41.8	582	16	Q9SXLO	Q9SXLO streptococc
4	56	41.8	587	16	Q9XND6	Q9XND6 streptococc
5	54	40.3	310	16	Q9KS29	Q9KS29 vldrio chol
6	53	39.6	426	16	Q9JUE9	Q9JUE9 neisseria m
7	53	39.6	590	16	Q9CE80	Q9CE80 lactococcus
8	51	38.1	274	16	Q9JAE6	Q9JAE6 pseudomonas
9	50	37.3	180	10	Q9FFS8	Q9FFS8 arabidopsis
10	50	37.3	623	10	Q94FW0	Q94FW0 abies grand
11	49.5	36.9	559	17	Q97YH0	Q97YH0 sulfolobus
12	49	36.6	416	2	Q9F2A1	Q9F2A1 chromatum
13	49	36.6	426	3	Q9HFE5	Q9HFE5 schizosacch
14	48	35.8	390	16	Q9KCE3	Q9KCE3 bacillus ha
15	48	35.8	428	10	Q22715	Q22715 arabidopsis
16	48	35.8	429	10	Q94UG7	Q94UG7 oryza sativ

17	48	35.8	438	10	Q23140	Q23140 arabidopsis
18	48	35.8	442	13	Q90YC0	Q90YC0 carassius a
19	48	35.8	682	16	Q83654	Q83654 treponema p
20	48	35.8	1173	5	Q9V7J8	Q9V7J8 drosophila
21	47.5	35.4	227	16	Q92KY0	Q92KY0 rhizobium m
22	47.5	35.4	306	16	Q99ZM1	Q99ZM1 streptococc
23	47	35.1	165	5	Q15887	Q15887 trypanosoma
24	47	35.1	311	2	Q93E30	Q93E30 salmoneilla
25	47	35.1	618	10	Q94820	Q94820 abies grand
26	46.5	34.7	1992	3	Q9P6T1	Q9P6T1 neurospora
27	46	34.3	104	16	Q92U58	Q92U58 rhizobium m
28	46	34.3	312	16	Q9PT8	Q9PT8 xyella fas
29	46	34.3	356	17	Q980M3	Q980M3 sulfolobus
30	46	34.3	374	16	Q97J35	Q97J35 clostridium
31	46	34.3	422	5	Q02282	Q02282 ceenorhabdi
32	46	34.3	428	10	Q9SAC9	Q9SAC9 arabidopsis
33	46	34.3	567	3	Q12108	Q12108 saccharomyc
34	46	34.3	694	10	Q9SVK2	Q9SVK2 arabidopsis
35	46	34.3	849	10	Q81906	Q81906 arabidopsis
36	46	34.3	886	2	Q53481	Q53481 porphyromon
37	46	34.3	1071	3	Q9P388	Q9P388 neurospora
38	46	34.3	1252	5	Q9VTV9	Q9VTV9 drosophila
39	45.5	34.0	628	10	Q9SE51	Q9SE51 arabidopsis
40	45	33.6	78	1	Q97773	Q97773 uncultured
41	45	33.6	177	10	Q9SW09	Q9SW09 arabidopsis
42	45	33.6	265	17	Q58456	Q58456 pyrococcus
43	45	33.6	313	16	Q92PH1	Q92PH1 rhizobium m
44	45	33.6	425	4	Q9BS18	Q9BS18 homo sapien
45	45	33.6	425	11	Q9CMP7	Q9CMP7 mus musculu

ALIGNMENTS

RESULT 1
ID Q9BG59 PRELIMINARY; PRT; 485 AA.
AC Q9BG59;
DC 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CHOLESTERYL ESTER TRANSFER PROTEIN (FRAGMENT).
OS Tupala gilis (tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupala.
OX NCBI_TaxID=9395;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Zeng W.W., Chen B.S., Zhang J.;
RT "Cloning and sequencing of tree shrew cholesterol ester transfer
protein (CETP) cDNA";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF34033; AK06086.1; -;
DR InterPro: IPR001124; LBP_BPL_CETP.
DR Pfam: PF01273; LBP_BPL_CETP.1.
DR Pfam: PF02886; LBP_BPL_CETP_C.1.
DR SMART: SM00328; BP11.1.
DR SMART: SM00329; BP12.1.
DR PROSITE: PS00400; LBP_BPL_CETP.1.
FT NON_TER
SQ SEQUENCE 485 AA: 53993 MW: 2605E76D2635C367 CRC64;

Query Match 91.8%; Score 123; DB 6; Length 485;
Best Local Similarity 92.3%; Pred. No. 8.6e-11;
Matches 24; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RDGFLLQMDFGFPEHLLVDFLOSL 26
DB 460 QDGFLLQMDFGFPEHLLVDFLOSL 485

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RESULT 2
ID 09CN39 PRELIMINARY; PRT; 314 AA.
AC 09CN39;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HYPOTHETICAL PROTEIN PM0606.
GN PM0606.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PM70;
RC MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whitam T.S., Kapur V.;
RT Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
RL EMBL; AE006096; AAK02690.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 314 AA; 36080 MW; 3C0EA33486CF62ED CRC64;

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Query Match 41.8%; Score 56; DB 16; Length 314;
Best Local Similarity 64.3%; Pred. No. 1.3;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
OY 12 GFPEHLVDFPSTL 25
DB 85 GFPEHLVDFPSTL 98

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RESULT 3
ID 099XL0 PRELIMINARY; PRT; 582 AA.
AC 099XL0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PUTATIVE ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12).
GN ASPS OR SPY2156.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / SPROTYPE M1;
RC MEDLINE=21192684; PubMed=11296396;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren O., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT *Complete genome sequence of an M1 strain of Streptococcus pyogenes.*;
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
CC -1 CATALYTIC ACTIVITY: ATP, L-AMINO ACID + TRNA(AMINO ACID) = AMP +
CC PYROPHOSPHATE + L-AMINOCYL-TRNA(AMINO ACID).
CC -1 CATALYTIC ACTIVITY: ATP + L-ASPARTATE (OR L-ASPARAGINE) +
CC TRNA(ASN) = AMP + PYROPHOSPHATE (OR L-ASPARAGINE) +
CC ASPARAGINYL-TRNA(ASN).
CC -1 SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1 SUBCELLULAR LOCATION: CYTOSOLAMIC (BY SIMILARITY).
CC -1 SIMILARITY: BELONGS TO CLASS-II AMINOCYL-TRNA SYNTHETASE FAMILY.
CC -1 SIMILARITY: BELONGS TO ASPARTYL-TRNA SYNTHETASE FAMILY.
DR EMBL; AE006633; AAK34793.1; -.
DR HSSP; P36419; 1EFW.
DR InterPro; IPR002106; AA_trna_ligase_II.
DR InterPro; IPR004115; GAD.
DR InterPro; IPR004364; trna-synt_2.
DR InterPro; IPR002312; trna-synt_asp.
DR InterPro; IPR002313; trna-synt_lys_2.

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DR InterPro; IPR004365; trna_antl.
DR Pfam; PF02938; GAD; 1.
DR Pfam; PF00152; trna-synt_2; 2.
DR Pfam; PF01336; trna_antl; 1.
DR PRINTS; PR01042; TRNASYNTHASP.
DR PRINTS; PR00982; TRNASYNTHLVS.
DR PROSITE; PS00179; AA_TRNA_LIGASE_II_1; 1.
DR PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
KW ATP-binding; Aminocyl-TRNA synthetase; Complete proteome; Ligase;
KW protein biosynthesis.
SQ SEQUENCE 582 AA; 66028 MW; DBA8ADEDE49F4FBC CRC64;

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Query Match 41.8%; Score 56; DB 16; Length 582;
Best Local Similarity 71.4%; Pred. No. 2.5;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 3 GFLLIQMDGFPEH 16
DB 510 GFLLEAMDYGFPFH 523

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RESULT 4
ID 097ND6 PRELIMINARY; PRT; 587 AA.
AC 097ND6;
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ASPARTYL-TRNA SYNTHETASE.
GN SP2114.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TIGR4;
RC MEDLINE=21357209; PubMed=11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Mayhew L.A., White O., Salzberg S.L., Lewis M.R., Radue D.,
RA Holtzapple E., Khoult H., Wolf A.M., Uetebach T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT *Complete genome sequence of a virulent isolate of Streptococcus
RL pneumoniae.*;
RL Science 293:498-506(2001).
DR EMBL; AE007500; AAK76173.1; -.
DR TIGR; SP2114; -.
DR InterPro; IPR002106; AA_trna_ligase_II.
DR InterPro; IPR004115; GAD.
DR InterPro; IPR004364; trna-synt_2.
DR InterPro; IPR002312; trna-synt_asp.
DR InterPro; IPR002313; trna-synt_lys_2.
DR InterPro; IPR004365; trna_antl.
DR Pfam; PF02938; GAD; 1.
DR Pfam; PF00152; trna-synt_2; 2.
DR Pfam; PF01336; trna_antl; 1.
DR PRINTS; PR01042; TRNASYNTHASP.
DR PRINTS; PR00982; TRNASYNTHLVS.
DR PROSITE; PS00179; AA_TRNA_LIGASE_II_1; 1.
DR PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
KW Aminocyl-TRNA synthetase; Complete proteome.
SQ SEQUENCE 587 AA; 66297 MW; AECF6B31C94432A CRC64;

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Query Match 41.8%; Score 56; DB 16; Length 587;
Best Local Similarity 71.4%; Pred. No. 2.5;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY 3 GFLLQMDGFFPEH 16
|||||:|:|:|:|
Db 510 GFLLQMDGFFPEH 523

RESULT 5
Q9KS29 PRELIMINARY: PRT: 310 AA.
AC Q9KS29: SEQUENCE FROM N.A.
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHETICAL PROTEIN VC1432.
GN VC1432.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR N16961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gelin M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermoлаeva M.D., Vamathevan J., Bass S., Qin H., Drygas I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.C., Venter J.C.,
Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
cholerae."
RL Nature 406:477-483(2000).
DR EMBL: AE004222; AAF94589.1; -.
DR TIGR: VC1432; -.
KM Complete proteome.
SQ SEQUENCE 310 AA; 35120 MW; 13FE328403241448 CRC64;

Query Match 40.3%; Score 54; DB 16; Length 310;
Best Local Similarity 64.3%; Pred. No. 2.5;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 12 GFPEHVLDFLOSL 25
|||||:|:|:|:|
Db 84 GFPEHVLDFLOSL 97

RESULT 6
Q9JUE9 PRELIMINARY: PRT: 426 AA.
AC Q9JUE9: SEQUENCE FROM N.A.
RC STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Felkell T., Hamlin N., Holtroyd S.,
Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrall B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis 22491."
RL Nature 404:502-506(2000).
DR EMBL: AL162755; CAB84597.1; -.
DR InterPro: IPR001064; Crystallin.

DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
KM Hypothetical protein: Complete proteome.
SQ SEQUENCE 426 AA; 47732 MW; 623B51BC8212A9E CRC64;

Query Match 39.6%; Score 53; DB 16; Length 426;
Best Local Similarity 62.5%; Pred. No. 5.2;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 GFLLQMDGFFPEH 18
|||||:|:|:|:|
Db 331 GFLLQMDGFFPEH 346

RESULT 7
Q9CE80 PRELIMINARY: PRT: 590 AA.
AC Q9CE80: SEQUENCE FROM N.A.
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12).
GN ASPs.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Lactococcus.
OX NCBI_TaxID=1360;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471;
RA Bolotin A., Wincker P., Manger S., Jallion O., Malarne K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
lactis ssp. lactis IL1403."
RL Genome Res. 11:731-753(2001).
CC -1- CATALYTIC ACTIVITY: ATP + L-AMINO ACID + TRNA(AMINO ACID) = AMP +
PYROPHOSPHATE + L-AMINOACYL-TRNA(AMINO ACID).
CC -1- CATALYTIC ACTIVITY: ATP + L-ASPARTATE (OR L-ASPARAGINE) +
TRNA(ASN) = AMP + PYROPHOSPHATE + L-ASPARTYL-TRNA(ASP) (OR L-
ASPARAGINYL-TRNA(ASN)).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -1- SIMILARITY: BELONGS TO ASPARTYL-TRNA SYNTHETASE FAMILY.
DR EMBL: AE006426; AAK06063.1; -.
DR HSP: P36419; IEFV.
DR InterPro: IPR002106; AA_trna_ligase-II.
DR InterPro: IPR002312; trna-synt_asp.
DR InterPro: IPR002313; trna-synt_lys_2.
DR InterPro: IPR004365; trna-antl.
DR pfam: PF01336; trna-antl_1.
DR PRINTS: PRO1042; TRNASYNTHASP.
DR PRINTS: PRO0962; TRNASYNTHLTS.
DR PROSITE: PS00179; AA_trna_ligase-II_1.
KM ATP-binding: Aminoacyl-trna synthetase; Complete proteome; Ligase;
KM Protein biosynthesis.
SQ SEQUENCE 590 AA; 66544 MW; A323DA770459BE0E CRC64;

Query Match 39.6%; Score 53; DB 16; Length 590;
Best Local Similarity 64.3%; Pred. No. 7.4;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 GFLLQMDGFFPEH 16
|||||:|:|:|:|
Db 517 GFLLQMDGFFPEH 530

RESULT 8
Q914E6 PRELIMINARY: PRT: 274 AA.
AC Q914E6: SEQUENCE FROM N.A.
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12).
GN ASPs.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Lactococcus.
OX NCBI_TaxID=1360;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471;
RA Bolotin A., Wincker P., Manger S., Jallion O., Malarne K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
lactis ssp. lactis IL1403."
RL Genome Res. 11:731-753(2001).
CC -1- CATALYTIC ACTIVITY: ATP + L-AMINO ACID + TRNA(AMINO ACID) = AMP +
PYROPHOSPHATE + L-AMINOACYL-TRNA(AMINO ACID).
CC -1- CATALYTIC ACTIVITY: ATP + L-ASPARTATE (OR L-ASPARAGINE) +
TRNA(ASN) = AMP + PYROPHOSPHATE + L-ASPARTYL-TRNA(ASP) (OR L-
ASPARAGINYL-TRNA(ASN)).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -1- SIMILARITY: BELONGS TO ASPARTYL-TRNA SYNTHETASE FAMILY.
DR EMBL: AE006426; AAK06063.1; -.
DR HSP: P36419; IEFV.
DR InterPro: IPR002106; AA_trna_ligase-II.
DR InterPro: IPR002312; trna-synt_asp.
DR InterPro: IPR002313; trna-synt_lys_2.
DR InterPro: IPR004365; trna-antl.
DR pfam: PF01336; trna-antl_1.
DR PRINTS: PRO1042; TRNASYNTHASP.
DR PRINTS: PRO0962; TRNASYNTHLTS.
DR PROSITE: PS00179; AA_trna_ligase-II_1.
KM ATP-binding: Aminoacyl-trna synthetase; Complete proteome; Ligase;
KM Protein biosynthesis.
SQ SEQUENCE 590 AA; 66544 MW; A323DA770459BE0E CRC64;

DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, last sequence update)
DT 01-OCT-2001 (TReMBLrel. 18, last annotation update)
DE HYPOHETICAL PROTEIN PA1192.
GN PA1192.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Huffnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Mong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL: AE004549; AAG04581.1;
DR InterPro: IPR000541; UPP0021.
DR Pfam: PF01171; UPP0021; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 274 AA; 31260 MW; 4C042FA0198FA4F6 CRC64;

Query Match 38.1%; Score 51; DB 16; Length 274;
Best Local Similarity 57.1%; Pred. No. 6.5;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 12 GFPEHLVDFLQSL 25
|||||:|::|:
Db 76 GFPEHVLPEYLKSI 89

RESULT 9
Q9FFS8 PRELIMINARY; PRT; 180 AA.
ID Q9FFS8
AC Q9FFS8;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
DE SIMILARITY TO 40S RIBOSOMAL PROTEIN S10 (A15G41520/MBR23_4).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RX MEDLINE=97471969; PubMed=9330910;
RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
RA Miyajima N., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
RT features of the 1.6 Mb regions covered by twenty physically assigned
RT pl clones.";
RL DNA Res. 4:215-230(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Shinn P.,
RA Tracy S.E., Ban J., Bowser L., Carninci P., Chung M.K.,
RA Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Natusaka M., Nguyen M., Palm C.D., Pham P.K., Quach H.L.,
RA Sakurai H., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C.,
RA Toriumi M., Yamada K., Yu G., Shinozaki K., Davis R.W., Theologis A.,
RA Becker J.R.;
RT "Arabidopsis cDNA clones.";
RT Submitted (MAY-2001) to the EMBL/GenBank/DBD databases.

DR EMBL: AB005233; BAB11458.1;
DR EMBL: AY037240; AAK59840.1;
DR EMBL: AF375440; AAK53024.1;
KW Ribosomal protein.
SQ SEQUENCE 180 AA; 19733 MW; 9D8C1EF2ED5CA28E CRC64;

Query Match 37.3%; Score 50; DB 10; Length 180;
Best Local Similarity 32.0%; Pred. No. 5.8;
Matches 8; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

OY 1 RDGFLQLQMDGFPPEHLVDFLQSL 25
::| | : | | 1 : | : : |
Db 17 KEGVLFAKKDFMLPQHPLIESVPL 41

RESULT 10

Q94FW0 PRELIMINARY; PRT; 623 AA.

ID Q94FW0
AC Q94FW0;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
DE PINENE SYNTHASE (FRAGMENT).
OS Abies grandis (Grand fir).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
OX NCBI_TaxID=46611;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21297238; PubMed=11404343;
RA Trepp S.C., Croteau R.B.;
RT "Genomic organization of plant terpene synthases and molecular
RT evolutionary implications.";
RL Genetics 158:811-832(2001).
DR EMBL: AF326517; AAK83564.1;
FT NON_TER 1
SQ SEQUENCE 623 AA; 70948 MW; 823B82B38113467B CRC64;

Query Match 37.3%; Score 50; DB 10; Length 623;
Best Local Similarity 47.8%; Pred. No. 23;
Matches 11; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

OY 6 ILQMDGFPPEHLVDFLQSL 26
: | | | | : | | | | :
Db 485 ILTMDIPFDHLKKEVDPSKLN 507

RESULT 11

Q97YH0 PRELIMINARY; PRT; 559 AA.

ID Q97YH0
AC Q97YH0;
DT 01-OCT-2001 (TReMBLrel. 18, Created)
DT 01-OCT-2001 (TReMBLrel. 18, last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
DE PERLEASE, MULTIDRUG EFFLUX.
GN SSO1351.
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=11427726;
RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Aweyer M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moors A., Eruaso G., Fletcher C., Gordon P.M.R.,
RA Helkamp-de Jong I., Jeffries A.C., Kozeza C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gassterland T.,
RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
 DR EMBL: AE006749; AKK41587.1; -.
 KW Complete proteome.
 SQ SEQUENCE 559 AA; 60430 MW; ADC0C903F6DB157F CRC64;

Query Match 36.9%; Score 49.5; DB 17; Length 559;
 Best Local Similarity 42.3%; Pred. NO. 24;
 Matches 11; Conservative 5; Mismatches 7; Indels 3; Gaps 1;

QY 3 GFLLQMDGFPPEHLVDFLOSL 25
 DB 360 GFLLTLPLPYNFVPEFALIFIMGL 385

RESULT 12
 ID Q9F2A1 PRELIMINARY; PRT; 416 AA.
 AC Q9F2A1;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE DSRP.
 GN DSRP.
 OS Chromatium vinosum.
 OC Bacteria; Proteobacteria; gamma subdivision; Chromatiaceae;
 OC Allochromatium.
 OK NCBI_TaxID=1049;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D DSM 180;
 RA Pott-Sperling A.S., Dahl C.;
 RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: U84760; AAG33085.1; -.
 SQ SEQUENCE 416 AA; 45664 MW; B0B95AFFEC71DC21 CRC64;

Query Match 36.6%; Score 49; DB 2; Length 416;
 Best Local Similarity 58.8%; Pred. NO. 21;
 Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 GFLLQMDGFPPEHLV 19
 DB 103 GLVIVMDLGRPERLIV 119

RESULT 13
 ID Q9HFE5 PRELIMINARY; PRT; 426 AA.
 AC Q9HFE5;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE CLATHRIN-ASSOCIATED ADAPTOR MEDIUM CHAIN.
 GN SPBP16F5.07.
 OS Schizosaccharomyces pombe (Pislon yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972H-;
 RA Aert R., Robben J., Volckaert G., Wood V., Rajandream M.A.,
 RA Battelet B.G.;
 RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AL441603; CAC08546.1; -.
 DR InterPro: IPR001392; Adap_comp_sub.
 DR Pfam: PF00928; Adap_comp_sub; 1.
 DR PRINTS: PR00314; CLATHRINADPT.
 DR PROSITE: PS00990; CLAT_ADAPTOR_M.1; 1.
 SQ SEQUENCE 426 AA; 48955 MW; 911FEB137C63AED3 CRC64;

Query Match 36.6%; Score 49; DB 3; Length 426;
 Best Local Similarity 41.4%; Pred. NO. 22;
 Matches 12; Conservative 3; Mismatches 8; Indels 6; Gaps 1;

QY 1 RDGFLIQD-----MDGFPPEHLVDFLO 23
 DB 104 RDNFVLVELDEITMDGFPPTETKILQ 132

RESULT 14
 ID Q9KCE3 PRELIMINARY; PRT; 390 AA.
 AC Q9KCE3;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE CYSTATHIONINE BETA-LYASE.
 GN METC OR BH1628.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125 / JCM 9153;
 RC MEDLINE=20512582; PubMed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 RT *Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis.*;
 RL Nucleic Acids Res. 28:4317-4331(2000).
 DR EMBL: AP001512; BAB05347.1; -.
 DR HSRP: P00935; 1CS1.
 DR InterPro: IPR002277; Cys_Met_Meta_PP.
 DR InterPro: IPR002026; Urease_gamma.
 DR Pfam: PF01053; Cys_Met_Meta_PP; 1.
 DR PROSITE: PS00868; Cys_MET_METAB_PP; 1.
 KW Lyase; Complete proteome.
 SQ SEQUENCE 390 AA; 42918 MW; 73EACD4C9533425 CRC64;

Query Match 35.8%; Score 48; DB 16; Length 390;
 Best Local Similarity 47.6%; Pred. NO. 28;
 Matches 10; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 RDGFLIQDMDGFPPEHLVDF 21
 DB 356 RDGILRLSVGLERPELMADE 376

RESULT 15
 ID Q22715 PRELIMINARY; PRT; 428 AA.
 AC Q22715;
 DT 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE PUTATIVE CLATHRIN COAT ASSEMBLY PROTEIN.
 GN F8A5.29.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Federici J.L., Palm C.J., Conway A.B., Kurtz D.B., Conway A.R.,
 RA Au M., Araujo R., Brendel V., Buehler E., Dewar K., Feng J., Kim C.,
 RA Li Y., Oji O., Osborne B.I., Shlim P., Sun H., Toriumi M.,
 RA Vysotskaya V.S., Yu G., Becker J., Theologis A., Davis R.W.;
 RT *Genomic sequence of Arabidopsis.*;

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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:05:51 ; Search time 51.68 Seconds
(without alignments)
55.881 Million cell updates/sec

Title: US-09-943-334-1
Sequence: 1 RDGFLLQMDRGFPENHLVDFLQSL 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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19: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA1998.DAT:*
20: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA1999.DAT:*
21: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	134	100.0	26	17	AAW06128 Human cholesteryl
2	134	100.0	26	20	AAV13801 Rabbit CERP immuno
3	134	100.0	26	21	AAV91228 Human cholesteryl
4	134	100.0	46	21	AAV91232 Modified MVF Th ep
5	134	100.0	46	21	AAV91233 Modified MVF Th ep
6	134	100.0	476	17	AAW06127 Human cholesteryl
7	134	100.0	476	18	AAW46446 Human mature chole
8	134	100.0	476	20	AAV02466 Human cholesteryl
9	134	100.0	491	15	AAW60342 Partial human Lipo
10	134	100.0	493	20	AAV49556 Human cholesteryl
11	134	100.0	493	20	AAV49568 Human cholesteryl

12	134	100.0	493	22	AAW65636 Human cholesteryl
13	121	90.3	496	20	AAV02469 Humanised rabbit c
14	117	87.3	26	20	AAV13802 Rabbit CERP immuno
15	117	87.3	26	21	AAV91231 Human cholesteryl
16	117	87.3	46	21	AAV91240 Modified MVF Th ep
17	117	87.3	46	21	AAV91241 Modified MVF Th ep
18	117	87.3	477	20	AAV02468 Modified rabbit ch
19	117	87.3	496	17	AAW06133 Rabbit cholesteryl
20	117	87.3	496	18	AAW46445 Mature rabbit chol
21	117	87.3	496	20	AAV02467 Rabbit cholesteryl
22	111	82.8	22	20	AAV13815 Rabbit CERP immuno
23	111	82.8	22	20	AAV13821 Human CERP immuno
24	107	79.9	22	20	AAV13809 Rabbit CERP immuno
25	85	63.4	31	17	AAW06129 Anti-cholesteryl e
26	85	63.4	31	20	AAW02470 Fusion of a tetanu
27	83	61.9	16	21	AAV91229 Human cholesteryl
28	83	61.9	35	21	AAV91236 Modified HVSurfac
29	83	61.9	36	21	AAV91234 Modified MVF Th ep
30	83	61.9	36	21	AAV91235 Modified MVF Th ep
31	83	61.9	36	21	AAV91237 Modified MVF Th ep
32	83	61.9	50	17	AAW06131 Anti-cholesteryl e
33	79	59.0	16	21	AAV91230 Human cholesteryl
34	79	59.0	36	21	AAV91238 Modified MVF Th ep
35	79	59.0	36	21	AAV91239 Modified MVF Th ep
36	79	59.0	50	17	AAW06132 CERP B cell epitop
37	79	59.0	50	18	AAW46447 Streptococcus pneu
38	56	41.8	97	18	AAW44126 Streptococcus pneu
39	56	41.8	587	22	AAW31915 Streptococcus pneu
40	56	41.8	587	22	AAU37899 Human/Rabbit CERP
41	53	39.6	11	18	AAW24294 Enterococcus faeca
42	52	38.8	584	22	AAU3517 Enterococcus faeca
43	52	38.8	589	22	AAU35285 Maize mvo-Inositol
44	51.5	38.4	353	20	AAW97881 Wheat Inositol 1,3
45	50.5	37.7	67	21	AAV59432

ALIGNMENTS

RESULT 1
ID AAW06128 standard; Peptide: 26 AA.
XX
AC AAW06128;
XX
DT 07-FEB-1997 (first entry)
XX
DE Human cholesteryl ester transfer protein C-terminal B-cell epitope.
XX
KW Cholesteryl ester transfer protein; CERP; antigen; vaccine;
KM cardiovascular disease; atherosclerosis; B-cell epitope.
XX
OS Homo sapiens.
XX
PN WQ9634888-A1
XX
PD 07-NOV-1996.
XX
PF 01-MAY-1996; 96MO-US06147.
XX
PR 01-MAY-1995; 95US-0432483.
XX
PA (TCEL-) T CELL SCI INC.
XX
PI Rittershaus CW, Thomas Ltd.
XX
DR WPI, 1996-506103/50.
XX
PT Cholesteryl ester transfer protein B cell epitope linked to T cell
PT epitope - used to generate vaccine to regulate CERP activity for
PT decreasing the risk of developing a cardiovascular disease e.g.
XX atherosclerosis
XX

PS Claim 5; Page 41; 72pp; English.

XX
CC A B-cell epitope (AAW06128) comprising the C-terminal 26 amino acids
CC of human liver mature cholesterol ester transfer protein (CEP)
CC (see also AAW06127) is involved in a neutral lipid binding or a
CC transfer activity of CEP. It can be linked to a universal or
CC broad range immunogenic T-cell epitope, such as that found at amino
CC acids 830-843 of tetanus toxoid protein, to produce a synthetic
CC vaccine (see also AAW06129) that elicits an immune response against
CC endogenous CEP activity, thereby treating or preventing
CC cardiovascular disease, such as atherosclerosis. It may also be
CC incorporated into a multivalent vaccine (see also AAW06131)
CC including another CEP B-cell epitope.

XX
CC Sequence 26 AA;

SQ
Query Match 100.0%; Score 134; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.2e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY
1 RDGFLLQMDFGPPEHLVDFLOSLIS 26
|||||
1 rdgflilqmdfgfpehlvdfllqsls 26

Db
1 rdgflilqmdfgfpehlvdfllqsls 26

RESULT 2
AAV13801
ID AAV13801 standard; peptide; 26 AA.
XX
XX AAV13801;
AC
XX
XX 08-JUL-1999 (first entry)
DT
XX
XX Rabbit CEP immunogenic fragment.
DE
XX
XX CEP; cholesterol-ester transfer protein; recombinant DNA vaccine; HDL;
KM antibody production; cholesterol ester transfer; therapy;
KM high density lipoprotein; HDL cholesterol concentration;
KM pro-atherogenic dyslipoproteinemia.
XX
XX Oryctolagus sp.
OS
XX
XX WO915655-A1.
PN
XX
XX 01-APR-1999.
PD
XX
XX 17-SEP-1998; 98WO-US19366.
PF
XX
XX 19-SEP-1997; 97US-0934367.
PR
XX
XX (MONS) MONSANTO CO.
PA
XX
XX
XX Glenn K, Needleman P;
PI
XX
XX WPI; 1999-276984/23.
DR
XX
XX
XX New recombinant DNA vaccines
PT
XX
XX
XX Claim 15; Page 85; 99pp; English.

XX
CC This sequence represents an immunogenic fragment of the rabbit
CC cholesterol ester transferase protein (CEP).
CC The invention relates to recombinant DNA vaccines that contain DNA
CC encoding CEP, which can be used for producing antibodies to lessen the
CC transfer of cholesterol esters from high density lipoprotein (HDL). The
CC method can provide an autogenous immunological process for lessening the
CC transfer of cholesterol esters from HDL particles and for increasing the
CC HDL cholesterol concentration of a mammal whose blood also contains
CC CEP. The method may be useful in treating human pro-atherogenic
CC dyslipoproteinemias characterised by low HDL/LDL cholesterol ratios. The
CC method can have an effect that lasts for months as compared to the
CC short-term effects of the small molecule drugs now available.

XX
SQ Sequence 26 AA;

XX
CC Query Match 100.0%; Score 134; DB 20; Length 26;
CC Best Local Similarity 100.0%; Pred. No. 1.2e-13;
CC Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY
1 RDGFLLQMDFGPPEHLVDFLOSLIS 26
|||||
1 rdgflilqmdfgfpehlvdfllqsls 26

Db
1 rdgflilqmdfgfpehlvdfllqsls 26

RESULT 3
AAV91228
ID AAV91228 standard; peptide; 26 AA.
XX
XX AAV91228;
AC
XX
XX 22-MAY-2000 (first entry)
DT
XX
XX Human cholesterol transport protein (CEP) peptide, SEQ ID NO.106.
DE
XX
XX Promiscuous T-cell epitope; measles virus F protein; MVR;
KM hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KM interleukin B virus surface antigen; HBV; immunogenic; B-cell epitope;
KM somatostatin; growth promoting hormone; LHRH; contraceptive; anticancer;
KM foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KM Plasmodium falciparum; circumporozoite; antimalarial; CEP;
KM cholesterol ester transport protein; anti-arteriosclerotic.
XX
XX Homo sapiens.
OS
XX
XX WO966957-A2.
PN
XX
XX 29-DEC-1999.
PD
XX
XX 21-JUN-1999; 99WO-US13975.
PF
XX
XX 20-JUN-1998; 98US-0100412.
PR
XX
XX (UNBI-) UNITED BIOMEDICAL INC.
PA
XX
XX
XX Wang CY;
PI
XX
XX WPI; 2000-160564/14.
DR
XX
XX
XX New artificial T helper cell epitope and derived immunogens with target
XX antigenic site, for immunization against e.g. malaria, arteriosclerosis
XX or human immune deficiency virus
XX
XX
XX Claim 10; Page 49; 129pp; English.

XX
CC The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response,
CC specifically against Plasmodium falciparum, cholesterol ester transport
CC protein (CEP) or HIV epitopes, but more generally against any pathogen,
CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC peptide immunogens may be used for prevention and/or treatment of
CC infections (HIV, foot-and-mouth disease or malaria); for cancer
CC immunotherapy; for inhibition of the action of interleukin hormone
CC releasing hormone (LHRH) for contraception, treatment of hormone-
CC dependent cancer, prevention of boar taint in meat, and
CC immunosuppression; for promoting the growth of animals; or for
CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
CC Th (functional in genetically diverse subjects) into an immunogen
CC improves capacity to induce a strong T helper cell-mediated immune
CC response, resulting in production of antibodies against a target
CC antigen. Th can replace carrier proteins and pathogen-derived T helper
CC epitopes. Sequence AAV91121 represents a promiscuous T helper epitope
CC from the measles virus F (MVR) protein and sequences AAV91122-Y91142,

CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
CC MVE Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
CC from hepatitis B virus (HBV) surface antigen, and sequences
CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
CC comprising an IHRH sequence joined to a promiscuous Th epitope. AAY91197
CC is the IHRH target antigenic peptide used in these IHRH antigenic
CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
CC peptides comprising somatostatin and a Th epitope. Somatostatin
CC immunogens may be used to promote growth in livestock. AAY91208 is a
CC human CD4 CD82-1 like domain antigenic site, and AAY91209-Y90211 are MIV
CC epitope/CD4 CD82 antigenic peptides which may be used to prevent HIV
CC infection of T cells. AAY90212 is a modified version of a human IGE
CC (immunoglobulin E) C_{H3} domain, and AAY90213-Y90219 are Th epitope/IGE C_{H3}
CC antigenic peptides which may be used in the treatment of allergies.
CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVE Th
CC epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent
CC CEMP-derived peptides and AAY91232-Y91241 are immunogens comprising a
CC CEMP peptide and a Th epitope which may be used to prevent or treat
CC arteriosclerosis and cardiovascular disease. AAY91242 and AAY91252-Y91257
CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
CC AAY91258-Y91273 are antigenic peptides comprising MVE Th and HIV-1 B-cell
CC epitope which may be used as a component in an anti-HIV-1 vaccine.
CC AAY91198 and AAY91199 are respectively an immunostimulatory invasion
CC protein epitope from Yersinia species, and hinge spacer peptide, both of
CC which may optionally be used in the antigenic peptides of the invention.
CC Note: Sequence AAY91227 is also designated SEQ ID NO:106 in the
CC specification.

Query Match	100.0%;	Score 134;	DB 21;	Length 26;
Best Local Similarity	100.0%;	Pred. No. 1,2e-13;		
Matches 26; Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	

	Query Match	Similarity	Score	DB	Length
Best Local	Similarity	100.0%	Pred. NO.	1.2e-13	
Matches	26	Conservative	0	Mismatches	0
				Indels	0
				Gaps	0
QY	1	RDGFFLLQMDGFPPEHLVDFQSLVS	26		
DB	1	rdgffllqmdgfppehlvdfqslvs	26		

Query Match	100.0%	Score 134;	DB 21;	Length 26;
Best Local Similarity	100.0%	Pred. No. 1.2e-13;		
Matches 26; Conservative	0;	Mismatches	0;	Gaps 0;

Query Match	100.0%	Score 134;	DB 21;	Length 26;
Best Local Similarity	100.0%	Pred. No. 1.2e-13;		
Matches 26; Conservative	0;	Mismatches	0;	Gaps 0;

	Query Match	Similarity	Score	DB	Length
Best Local	Similarity	100.0%	Pred. NO.	1.2e-13	
Matches	26	Conservative	0	Mismatches	0
				Indels	0
				Gaps	0
QY	1	RDGFFLLQMDGFPPEHLVDFQSLVS	26		
DB	1	rdgffllqmdgfppehlvdfqslvs	26		

	Query Match	Similarity	Score	DB	Length
Best Local	Similarity	100.0%	Pred. NO.	1.2e-13	
Matches	26	Conservative	0	Mismatches	0
				Indels	0
				Gaps	0
QY	1	RDGFFLLQMDGFPPEHLVDFQSLVS	26		
DB	1	rdgffllqmdgfppehlvdfqslvs	26		

RESULT	4
AAAY91232	
ID	AAAY91232 standard; peptide: 46 AA.

RESULT	4
AAAY91232	
ID	AAAY91232 standard; peptide: 46 AA.

AY 91232, AC

DT 22-MAY-2000 (first entry)

DE Modified MVT Th epitope/CETP peptide, SEQ ID NO:110.

KM Promiostatin T-cell epitope; measles virus F protein; MVE;
KM hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KM interleukin hormone releasing hormone, LHRH; contraceptive; anticancer;
KM somatostatin; growth promotoin; CD4 receptor; HIV-T; antiviral; FMDV;
KM Foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KM Plasmodium falciparum; circumsporozoite; antimalarial; CEMP;
KM cholesteryl ester transport protein; anti-arteriosclerotic.

KM Promiostatin T-cell epitope; measles virus F protein; MVE;
KM hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KM interleukin hormone releasing hormone, LHRH; contraceptive; anticancer;
KM somatostatin; growth promotoin; CD4 receptor; HIV-T; antiviral; FMDV;
KM Foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KM Plasmodium falciparum; circumsporozoite; antimalarial; CEMP;
KM cholesteryl ester transport protein; anti-arteriosclerotic.

KM Promiostatin T-cell epitope; measles virus F protein; MVE;
KM hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KM interleukin hormone releasing hormone, LHRH; contraceptive; anticancer;
KM somatostatin; growth promotoin; CD4 receptor; HIV-T; antiviral; FMDV;
KM Foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KM Plasmodium falciparum; circumsporozoite; antimalarial; CEMP;
KM cholesteryl ester transport protein; anti-arteriosclerotic.

KM Promiostatin T-cell epitope; measles virus F protein; MVE;
KM hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KM interleukin hormone releasing hormone, LHRH; contraceptive; anticancer;
KM somatostatin; growth promotoin; CD4 receptor; HIV-T; antiviral; FMDV;
KM Foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KM Plasmodium falciparum; circumsporozoite; antimalarial; CEMP;
KM cholesteryl ester transport protein; anti-arteriosclerotic.

KM Promiostatin T-cell epitope; measles virus F protein; MVE;
KM hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KM interleukin hormone releasing hormone, LHRH; contraceptive; anticancer;
KM somatostatin; growth promotoin; CD4 receptor; HIV-T; antiviral; FMDV;
KM Foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KM Plasmodium falciparum; circumsporozoite; antimalarial; CEMP;
KM cholesteryl ester transport protein; anti-arteriosclerotic.

KM Promiomasin T-cell epitope; measles virus F protein; MVE;
KM hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KM interleukin hormone releasing hormone; LHRH; contraceptive; anticancer;
KM somatostatin; growth promotoin; CD4 receptor; HIV-T; antiviral; FMDV;
KM Foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KM Plasmodium falciparum; circumsporozoite; antimalarial; CDP;
KM cholesteryl ester transport protein; anti-arteriosclerotic.

KM Promiostatin T-cell epitope; measles virus F protein; MVE;
KM hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KM interleukin hormone releasing hormone, LHRH; contraceptive; anticancer;
KM somatostatin; growth promotoin; CD4 receptor; HIV-T; antiviral; FMDV;
KM Foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KM Plasmodium falciparum; circumsporozoite; antimalarial; CEMP;
KM cholesteryl ester transport protein; anti-arteriosclerotic.

OS Chimeric - Measles virus.
OS Chimeric - Homo sapiens.

OS Chimeric - Measles virus.
OS Chimeric - Homo sapiens.

PN W09966957-A2.

PD 29-DEC-1999.

PF 21-JUN-1999; 99WO-US13975.

PR 20-JUN-1998; 98US-0100412.

PA (UNBI-) UNITED BIOMEDICAL INC

Wang C
PI

DR WPI; 2000-160564/14.

PT New artificial T helper cell epitope and derived immunogens with target

AA Claim 11; Page 104; 129pp; English.
PS

The invention relates to novel promiscuous T helper cell epitopes (Th), and immunogenic peptides comprising the Th epitopes of the invention along with B cell epitopes. The Th epitopes and peptide immunogens containing them, are used to induce a T helper cell response, specifically against Plasmodium falciparum, cholesteryl ester transport protein (CEPT) or HIV epitopes, but more generally against any pathogen, immunoreactive self-antigen or tumour antigen. The Th epitopes and peptide immunogens may be used for prevention and/or treatment of infections (HIV, foot-and-mouth disease or malaria); for cancer immunotherapy; for inhibition of the action of luteinising hormone releasing hormone (LHRH) for contraception, treatment of hormone-dependent cancer, prevention of boar taint in meat, and immunocastration; for promoting the growth of animals; or for treating allergies or arteriosclerosis. Incorporation of a promiscuous Th (functional in genetically diverse subjects) into an immunogen improves capacity to induce a strong T helper cell-mediated immune response, resulting in production of antibodies against a target antigen. Th can replace carrier proteins and pathogen-derived T helper epitopes. Sequence AA91121 represents a promiscuous T helper epitope from the measles virus F (WVF) protein and sequences AA91122-Y91142, AA91126 and AA91245-Y91246 represent synthetic Th epitopes based on the WVF Th epitope. Sequence AA91143 represents a promiscuous Th epitope from hepatitis B virus (HBV) surface antigen, and sequences AA91144-Y91145 are synthetic epitopes derived from this HBV epitope. AA91156-Y91186, AA91227 and AA91242-Y91244 are antigenic peptides comprising an LHRH sequence joined to a promiscuous Th epitope. AA91197 is the LHRH target antigenic peptide used in these LHRH antigenic peptides. AA91200 is somatostatin, and AA91201-Y91207 are antigenic peptides comprising somatostatin and a Th epitope. Somatostatin immunogens may be used to promote growth in livestock. AA91208 is a human CD4 CDR2-like domain antigenic site, and AA91209-Y90211 are MVN Th epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV infection of T cells. AA90212 is a modified version of a human IGE (immunoglobulin E) CH3 domain, and AA90213-Y90219 are Th epitope/IgE CH3 antigenic peptides which may be used in the treatment of allergies. AA91220 is a peptide derived from foot and mouth disease virus (FMDV) VP1 capsid protein and AA91221-Y91222 comprise this peptide and a Th epitope. AA91223 is a Plasmodium falciparum circumsporozoite (CS) target antigen, and AA91224-Y91225 comprise the CS antigen and an MVE Th epitope, and AA91226-Y91228 represent immunogens comprising a CEMP-derived peptides and AA91232-Y91241 are immunogens comprising a CEMP peptide and a Th epitope which may be used to prevent or treat arteriosclerosis and cardiovascular disease. AA91247 and AA91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AA91248-Y91251 and AA91258-Y91273 are antigenic peptides comprising MVN Th and HIV-1 B-cell epitope, which may be used as a component in an anti-HIV-1 vaccine. AA91198 and AA91199 are respectively an immunostimulatory invasive protein epitope from yersinia species, and hinge spacer peptide, both of which may optionally be used in the antigenic peptides of the invention.

Sequence 46 AA;

Query Match	100.0%	Score 134	DB 21	length 46
Best Local Similarity	100.0%	Pred. No. 2.3e-13		
Matches 26; Conservative	0	Missmatches	0	Indels 0; Gaps 0

Query Match	100.0%	Score 134	DB 21	length 46
Best Local Similarity	100.0%	Pred. No. 2.3e-13		
Matches 26; Conservative	0	Missmatches	0	Gaps 0

Query Match	100.0%	Score 134	DB 21	length 46
Best Local Similarity	100.0%	Pred. No. 2.3e-13		
Matches 26; Conservative	0	Missmatches	0	Indels 0; Gaps 0

```
QY      1 RDGFLLLQMDFGFPEHLLVDFLQSL$ 26
         |||||
Db      21 rdgflilqmdfgfpehllvdfllqsl$ 46
```

```
QY      1 RDGFLLLQMDFGFPEHLLVDFLQSL$ 26
         |||||
Db      21 rdgflilqmdfgfpehllvdfllqsl$ 46
```

RESULT 5
AA91233
ID AAY91233 standard; peptide: 46 AA.
XX
AC AAY91233;
XX
DT 22-MAY-2000 (first entry)
XX
DE Modified MVF Th epitope/CETP peptide, SEQ ID NO:111.
XX
KM Promiscuous T-cell epitope; measles virus F protein; MVF;
KM hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KM luteinizing hormone releasing hormone; LHRH; contraceptive; anticancer;
KM somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
KM foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KM Plasmodium falciparum; circumsporozoite; antimalarial; CETP;
KM cholesterol ester transfer protein; anti-arteriosclerotic.
XX
OS Chimeric - Measles virus.
OS Chimeric - Homo sapiens.
PN WO966957-A2.
XX
PD 29-DEC-1999.
XX
PF 21-JUN-1999; 99WO-US13975.
XX
PR 20-JUN-1998; 98US-0100412.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI; 2000-160564/14.
XX
PT New artificial T helper cell epitope and derived immunogens with target
PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
XX or human immune deficiency virus
XX
PS Claim 11; Page 104-105; 123p; English.
XX
CC The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response.
CC Specifically against Plasmodium falciparum, cholesterol ester transport
CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC peptide immunogens may be used for prevention and/or treatment of
CC infections (HIV, foot-and-mouth disease or malaria); for cancer
CC immunotherapy; for inhibition of the action of luteinizing hormone
CC releasing hormone (LHRH) for contraception, treatment of hormone-
CC dependent cancer, prevention of boar taint in meat, and
CC immunocastration); for promoting the growth of animals; or for
CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
CC Th (functional in genetically diverse subjects) into an immunogen
CC improves capacity to induce a strong T helper cell-mediated immune
CC response, resulting in production of antibodies against a target
CC antigen. Th can replace carrier proteins and pathogen-derived T helper
CC epitopes. Sequence AAY91221 represents a promiscuous T helper epitope
CC from the measles virus F (MVF) protein and sequences AAY91122-Y91142,
CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
CC MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
CC from hepatitis B virus (HBV) surface antigen, and sequences
CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
CC is the LHRH target antigenic peptide used in these LHRH antigenic
CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
CC peptides comprising somatostatin and a Th epitope. Somatostatin
CC immunogens may be used to promote growth in livestock. AAY91208 is a

CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVF Th
CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
CC infection of T cells. AAY90212 is a modified version of a human IgE
CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IgE CH3
CC antigenic peptides which may be used in the treatment of allergies.
CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
CC epitope, and AAY91224-Y91225 comprise the CS antigen and an MVF Th
CC epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent
CC CETP-derived peptides and AAY91232-Y91241 are immunogens comprising a
CC CETP peptide and a Th epitope which may be used to prevent or treat
CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
CC AAY91258-Y91273 are antigenic peptides comprising MVF Th and HIV-1 B-cell
CC epitope which may be used as a component in an anti-HIV-1 vaccine.
CC AAY91198 and AAY91199 are respectively an immunostimulatory invasin
CC protein epitope from Yersinia species, and hinge spacer peptide, both of
CC which may optionally be used in the antigenic peptides of the
CC invention.
XX
SQ Sequence 46 AA:

Query Match 100.0%; Score 134; DB 21; Length 46;
Best local Similarity 100.0%; Pred. No. 2.3e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLOMDFGFPHLLVDFLOSLIS 26
Db 21 rdgflldmdfgfphllvdfldslis 46

RESULT 6
ID AAM06127 standard; Protein: 476 AA.
XX
AC AAM06127;
XX
DT 07-FEB-1997 (first entry)
XX
DE Human cholesterol ester transfer protein.
XX
KM Cholesterol ester transfer protein; CETP; antigen; vaccine;
KM cardiovascular disease; arteriosclerosis.
XX
OS Homo sapiens.
XX
FT Key Location/Qualifiers
FT Region 349..367
FT /label= B-cell epitope
FT Region 461..476
FT /label= B-cell epitope
FT /note= "C-terminal epitope involved in neutral
FT lipid binding or a transfer activity of
FT CETP (Claim 3)"
XX
PN WO9634888-A1.
XX
PD 07-NOV-1996.
XX
PF 01-MAY-1996; 96WO-US06147.
XX
PR 01-MAY-1995; 95US-0432483.
XX
PA (TCCEL-) T CELL SCI INC.
XX
PI Rittershaus CW, Thomas LJ;
XX
DR WPI; 1996-506103/50.
XX
PT Cholesterol ester transfer protein B cell epitope linked to T cell
PT epitope - used to generate vaccine to regulate CETP activity for

PT decreasing the risk of developing a cardiovascular disease e.g.
 PT atherosclerosis
 XX
 PS
 XX Claim 2: Page 44-47; 72pp: English.
 CC Human liver mature cholesteryl ester transfer protein (CETP) (AAW06127)
 CC plays a role in altering the relative profile of circulating
 CC lipoproteins to one associated with an increased risk of
 CC cardiovascular disease. B-cell epitopes (see also AAW06128) of CETP
 CC can be used in novel peptide vaccines (see also AAW06129, AAW06131)
 CC that elicit an immune response against endogenous CETP activity,
 CC thereby treating or preventing cardiovascular disease, such as
 CC atherosclerosis.
 CC
 XX
 SQ Sequence 476 AA:
 Query Match 100.0%; Score 134; DB 17; Length 476;
 Best Local Similarity 100.0%; Pred. No. 3e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RDGFLLLQMDGFPPEHLVDFLOSL 26
 Db 451 rdgflillqmdfgfpehlvdfllqsls 476
 RESULT 7
 AAW46446
 ID AAW46446 standard; Peptide; 476 AA.
 XX
 AC AAW46446;
 XX
 DT 18-MAY-1998 (first entry)
 XX
 DE Human mature cholesteryl ester transfer protein (CETP).
 XX
 KW Cholesteryl ester transfer protein; CETP; cholesteryl ester;
 KW high density lipoprotein; HDL; very low density lipoprotein; VLDL;
 KW low density lipoprotein; LDL; atherosclerosis; neutral lipid binding;
 KW transfer activity; Immunogenic; B cell epitope; antibody; TP2;
 KW DNA plasmid-based vaccine; broad range helper T cell epitope;
 KW treatment; cardiovascular disease.
 XX
 OS Homo sapiens.
 XX
 PN MO9741227-A1.
 XX
 PD 06-NOV-1997.
 XX
 PF 01-MAY-1997; 97WO-US07294.
 XX
 PR 21-FEB-1997; 97US-0802967.
 PR 01-MAY-1996; 96US-0640713.
 XX
 PA (TCEL-) T CELL SCI INC.
 XX
 PI Thomas LJ;
 PI
 DR WPI: 1997-549731/50.
 DR N-PSDB; AAV05127.
 XX
 PT DNA plasmid-based vaccine encodes CETP B cell and helper T cell
 PT epitope(s) - used for elevating high density lipoprotein levels, and
 PT for treating cardiovascular disease
 XX
 PS Claim 6: Pages 36-38; 67pp: English.
 XX
 CC The present sequence represents a human mature cholesteryl ester transfer
 CC protein (CETP). CETPs mediate the transfer of cholesteryl esters from
 CC high density lipoprotein (HDL) to very low density lipoprotein (VLDL) and
 CC low density lipoprotein (LDL). An increased CETP activity
 CC produces an atherogenic lipoprotein profile and induces atherosclerosis.
 CC A 13 amino acid stretch in the human CETP (Phe463 to Leu475), and also

CC possibly Asp460, are particularly important for neutral lipid binding and
 CC transfer activity. This region has been shown to be immunogenic as a B
 CC cell epitope of CETP, and a monoclonal antibody (TP2) directed at this
 CC region has been shown to inhibit neutral lipid transfer. A second B cell
 CC epitope is defined by Arg349 to Ile367. Antibodies to this second epitope
 CC would allow the formation of immune complexes involving CETP, and promote
 CC the removal of the complexed CETP. This peptide region was selected for
 CC its potential antigenicity and high possibility for surface expression
 CC on native CETP. Sequences encoding these 2 epitopes can be used in a DNA
 CC plasmid-based vaccine which comprises sequences encoding at least 1 B
 CC cell epitope of CETP linked in frame with at least one segment encoding
 CC a broad range helper T cell epitope. The vaccines can be used to elevate
 CC the ratio of circulating HDL to circulating LDL, VLDL or total
 CC cholesterol in a human. It can also be used for decreasing the level of
 CC endogenous CETP activity in a human. The vaccine can be used to produce
 CC anti-CETP antibodies in vivo and for treating cardiovascular disease.
 CC
 XX
 SQ Sequence 476 AA:
 Query Match 100.0%; Score 134; DB 18; Length 476;
 Best Local Similarity 100.0%; Pred. No. 3e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RDGFLLLQMDGFPPEHLVDFLOSL 26
 Db 451 rdgflillqmdfgfpehlvdfllqsls 476
 RESULT 8
 AAY02466
 ID AAY02466 standard; protein; 476 AA.
 XX
 AC AAY02466;
 XX
 DT 14-JUL-1999 (first entry)
 XX
 DE Human cholesteryl ester transfer protein (CETP).
 XX
 KW Vaccine; antibody; endogenous; cholesteryl ester transfer protein; CETP;
 KW high-density lipoprotein-associated cholesterol; metabolism;
 KW low-density lipoprotein-associated cholesterol; atherosclerotic lesion;
 KW cholesterol; atherosclerosis; heart disease.
 XX
 OS Homo sapiens.
 XX
 PN MO9920302-A1.
 XX
 PD 29-APR-1999.
 XX
 PF 20-OCT-1998; 98WO-US22145.
 XX
 PR 20-OCT-1997; 97US-0954643.
 XX
 PA (AVAN-) AVANT IMMUNOTHERAPEUTICS INC.
 XX
 PI Rittershaus CW, Thomas LJ;
 PI
 DR WPI: 1999-302645/25.
 DR N-PSDB; AAX35807.
 XX
 PT Vaccine against cholesteryl ester transfer protein
 PT disclosure; Page 44-46; 61pp: English.
 XX
 PS
 CC The specification describes a vaccine that promotes the production of
 CC antibodies that bind endogenous cholesteryl ester transfer protein
 CC (CETP). The vaccines (and equivalent plasmid-based vaccines) are
 CC used to increase the ratio of circulating high-density lipoprotein
 CC (HDL)-associated cholesterol to low-density lipoprotein (LDL)-associated
 CC cholesterol; to decrease the level of endogenous CETP activity in humans
 CC or other animals; to alter metabolism of LDL-associated cholesterol; for
 CC inhibiting development of atherosclerotic lesions; to lower circulating

CC levels of LDL and total cholesterol; and to treat or prevent
 CC atherosclerosis (or more generally heart disease). The present sequence
 CC represents human CERP.
 XX

SO Sequence 476 AA;

Query Match 100.0%; Score 134; DB 20; Length 476;
 Best Local Similarity 100.0%; Pred. No. 3e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RDGFLLLQMDFGPPEHLVDFLOSLS 26
 Db 451 rdgfilllqmdfgfpehlvdflosls 476

RESULT 9
 AAR60342
 ID AAR60342 standard; protein; 491 AA.

AC AAR60342;
 DT 01-MAR-1995 (first entry)
 DE Partial human lipid transfer protein.
 XX
 KW lipid transfer protein; LTP; monoclonal antibody; immunoassay;
 KW antigen determining group.
 XX
 OS Homo sapiens.

FT Key Location/Qualifiers
 FT Peptide 16..43
 FT /label= peptide 1
 FT /note= "claim 1; antigen determining group"
 FT 209..221
 FT /label= peptide 2
 FT /note= "claim 1; antigen determining group"
 FT 275..288
 FT /label= peptide 3
 FT /note= "claim 1; antigen determining group"
 FT 303..322
 FT /label= peptide 4
 FT /note= "claim 1; antigen determining group"
 FT 360..370
 FT /label= peptide 5
 FT /note= "claim 1; antigen determining group"

FT Peptide
 FT JP06169793-A.
 XX 21-JUN-1994.
 PD
 XX
 PF 02-DEC-1992; 92JP-0349842.
 XX
 PR 02-DEC-1992; 92JP-0349842.
 XX
 PA (EIKE) EIKEN KAGAKU KK.
 XX
 DR WPI; 1994-237601/29.

PT A monoclonal antibody recognising human lipid transfer protein -
 PT useful for immunoassay

PS Disclosure: Fig 1; 14pp; Japanese.

CC This sequence shows a partial human lipid transfer protein,
 CC containing specific peptide groups that are antigen determining. The
 CC monoclonal antibody of the invention recognises any of these
 CC peptides. The MAb can be used in an immunoassay for LTP.
 CC
 XX Sequence 491 AA;

Query Match 100.0%; Score 134; DB 15; Length 491;
 Best Local Similarity 100.0%; Pred. No. 3.1e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDFGPPEHLVDFLOSLS 26
 Db 466 rdgfilllqmdfgfpehlvdflosls 491

RESULT 10
 AAY49556
 ID AAY49556 standard; protein; 493 AA.

AC AAY49556;
 DT 13-JAN-2000 (first entry)
 DE Human cholesterol ester transfer protein sequence.
 DE
 XX
 KW Human; coding sequence polymorphism; vascular pathology gene;
 KW polymorphic site; phenotype correlation; forensic; paternity testing;
 KW medicine; genetic analysis; vascular disease.
 XX

OS Homo sapiens.
 XX
 PN WO9950454-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 26-MAR-1999; 99WO-US06473.
 XX
 PR 01-APR-1998; 98US-0054272.
 XX

PA (WHED) WHITEHEAD INST BIOMEDICAL RES.

PI Lander ES, Daley GO, Cargill M, Ireland JS, Rozen SG;
 DR WPI; 1999-620066/53.
 DR N-PSDB; AA232165.

PT Determination of polymorphisms in genes, especially those identifying
 PT predisposition to vascular disease -
 PS Disclosure: Fig 9; 134pp; English.

CC AA232159 to AA232194 represent reference alleles for specifically
 CC claimed nucleic acid sequences from the present invention which comprise
 CC polymorphic sites as given in a table in the specification, selected
 CC from 92 single nucleotide polymorphisms in which the nucleotide at the
 CC polymorphic site is different from a nucleotide at the same site in a
 CC reference allele. The nucleic acids, and primers and probes, are used to
 CC identify polymorphisms, which may predispose an individual to disease,
 CC especially a vascular disease. They can also be used in phenotype
 CC correlations, forensics, paternity testing, medicine or genetic
 CC analysis. AAY49550 to AAY49573 represent the proteins which correspond
 CC to some of the reference alleles.
 CC
 XX Sequence 493 AA;

Query Match 100.0%; Score 134; DB 20; Length 493;
 Best Local Similarity 100.0%; Pred. No. 3.2e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDFGPPEHLVDFLOSLS 26
 Db 468 rdgfilllqmdfgfpehlvdflosls 493

RESULT 11
 AAY49568
 ID AAY49568 standard; protein; 493 AA.

AC	AAV49568	
XX		
DT	13-JAN-2000	(first entry)
XX		
DE	Human cholesterol[ester transfer protein sequence.	
XX		
KW	Human; coding sequence polymorphism; vascular pathology gene;	
KM	polymorphic site; phenotype correlation; forensic; paternity testing;	
KW	medicine; genetic analysis; vascular disease.	
XX		
OS	Homo sapiens.	
XX		
PN	MO9950454-A2.	
XX		
PD	07-OCT-1999.	
XX		
PF	26-MAR-1999; 99WO-US06473.	
XX		
PR	01-APR-1998; 98US-0054272.	
XX		
PA	(WHED) WHITEHEAD INST BIOMEDICAL RES.	
XX		
PI	Lander ES, Daley GO, Cargill M, Ireland JS, Rozen SG;	
XX		
DR	WPI; 1999-620066/53.	
DR	N-PSDB; AAV32188.	
PT	Determination of polymorphisms in genes, especially those identifying	
PT	predisposition to vascular disease -	
XX		
PS	Disclosure: Fig 32; 134pp: English.	
XX		
CC	AAV32159 to AAV32194 represent reference alleles for specifically	
CC	claimed nucleic acid sequences from the present invention which comprise	
CC	polymorphic sites as given in a table in the specification, selected	
CC	from 92 single nucleotide polymorphisms in which the nucleotide at the	
CC	polymorphic site is different from a nucleotide at the same site in a	
CC	reference allele. The nucleic acids, and primers and probes, are used to	
CC	identify polymorphisms, which may predispose an individual to disease,	
CC	especially a vascular disease. They can also be used in phenotype	
CC	correlations, forensics, paternity testing, medicine or genetic	
CC	analysts. AAV49550 to AAV49573 represent the proteins which correspond	
CC	to some of the reference alleles.	
XX		
SO	Sequence 493 AA;	
Query Match	100.0%; Score 134; DB 20; Length 493;	
Best Local Similarity	100.0%; Pred. No. 3,2e-12;	
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0		
OY	1 RDGFTLLQMDGFPEHLLVDPLQSUS 26	
Db	468 rdgfillqmdfgfpehllyvdfqsis 493	
RESULT 12		
AAG65636		
ID	AAG65636 standard; Protein; 493 AA.	
XX		
AC	AAG65636;	
XX		
DT	07-JAN-2002 (first entry)	
XX		
DE	Human cholesterol ester transfer protein (CETP).	
XX		
KM	CETP; arteriosclerosis; cholesterol ester transfer protein; HDL;	
KW	high density lipoprotein; human.	
XX		
OS	Homo sapiens.	
XX		
FH	Key Location/Qualifiers	
FT	Peptide 1..17	

FT	/note= "signal peptide"
FT	18..493
FT	/note= "mature protein indicated as Seq Id No. 2"
XX	
XX	WO200171032-A1.
PD	27-SEP-2001.
XX	
PE	23-MAR-2001; 2001WO-JP02327.
XX	
PR	24-MAR-2000; 2000JP-0084264.
XX	
PA	(BMLB-) BML INC.
PI	Nagano M, Ito M, Sagehashi Y, Hattori H, Egashira T, Yamashita S;
PI	Matsuzawa Y;
DR	WP1; 2001-611516/70.
DR	N-PDB; AA166654.
XX	
PT	Determining a risk factor for arteriosclerosis comprises detecting
PT	mutations in genes for cholesterol ester transfer protein.
PS	Disclosure: Page 43-47; 58pp; Japanese.
XX	
CC	The invention relates to detecting the risk factor for arteriosclerosis
CC	in a subject that involves detecting mutations in the gene for
CC	cholesterol ester transfer protein (CETP) related to the degree of risk
CC	of arteriosclerosis. The mutant proteins alter the level of HDL in the
CC	blood. The high frequency mutations can be detected for prevention and
CC	treatment of arteriosclerosis. The present sequence represents a
CC	human CETP.
SQ	
SQ	Sequence 493 AA:
OY	
Query Match	100.0%; Score 134; DB 22; Length 493;
Best Local Similarity	100.0%; Pred. NO. 3.2e-12;
Matches 26; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
1 RDGFLQLMDFGFPEHLVDFLOSTLS 26	
Db 468 rdgfillqmdfgfpehllydflosts 493	
RESULT 13	
AAY02469	
ID AAY02469 standard; protein; 496 AA.	
AC AAY02469;	
DT 14-JUL-1999 (first entry)	
DE Humanised rabbit cholesteryl ester transfer protein (CETP).	
XX	
KW Vaccine: antibody; endogenous; cholesteryl ester transfer protein; CETP;	
KW high-density lipoprotein-associated cholesterol; metabolism;	
KW low-density lipoprotein-associated cholesterol; atherosclerotic lesion;	
KW cholesterol; atherosclerosis; heart disease.	
OS Synthetic.	
OS Oryctolagus sp.	
PN WO9920302-A1.	
PD 29-APR-1999.	
PF 20-OCT-1998; 98WO-US22145.	
PR 20-OCT-1997; 97US-0954643.	
PA (AVAN-) AVANT IMMUNOTHERAPEUTICS INC.	

transfer of cholesteryl esters from high density lipoprotein (HDL). The method can provide an autogenic immunological process for lessening the

dependent cancer, prevention of boar taint in meat, and immunocastration); for promoting the growth of animals; or for treating ailments (e.g., mastitis). Transmonitors can be used to

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:05:51 ; Search time 205.61 Seconds
(without alignments)
44.509 Million cell updates/sec

Title: US-09-943-334-1
Perfect score: 134
Sequence: 1 RDGFLLQMDGFPENHLYDFLOSLIS 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues
Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	134	100.0	26 1 PCT-US99-13975B-106	Sequence 106, App
2	134	100.0	26 8 US-08-432-483-1	Sequence 1, Appl1
3	134	100.0	26 8 US-08-432-483A-1	Sequence 1, Appl1
4	134	100.0	26 11 US-08-785-997-29	Sequence 29, Appl1
5	134	100.0	26 11 US-08-788-882-29	Sequence 29, Appl1
6	134	100.0	26 13 US-08-934-367-29	Sequence 29, Appl1
7	134	100.0	26 13 US-08-945-289-1	Sequence 1, Appl1

8	134	100.0	26 17 US-09-386-591-29	Sequence 29, Appl1
9	134	100.0	26 17 US-09-387-340-29	Sequence 29, Appl1
10	134	100.0	26 21 US-09-701-588-106	Sequence 106, Appl
11	134	100.0	26 23 US-09-943-334-1	Sequence 1, Appl1
12	134	100.0	26 23 US-09-943-548-1	Sequence 1, Appl1
13	134	100.0	26 1 PCT-US99-13975B-110	Sequence 110, App
14	134	100.0	46 1 PCT-US99-13975B-111	Sequence 111, App
15	134	100.0	46 21 US-09-701-588-110	Sequence 110, App
16	134	100.0	46 21 US-09-701-588-111	Sequence 111, App
17	134	100.0	470 19 US-09-518-598-14	Sequence 14, Appl
18	134	100.0	470 22 US-09-872-128-14	Sequence 14, Appl
19	134	100.0	476 10 US-08-640-713-4	Sequence 4, Appl1
20	134	100.0	476 11 US-08-785-997-28	Sequence 28, Appl1
21	134	100.0	476 11 US-08-788-882-28	Sequence 28, Appl1
22	134	100.0	476 12 US-08-802-967A-4	Sequence 4, Appl1
23	134	100.0	476 13 US-08-934-367-28	Sequence 28, Appl
24	134	100.0	476 13 US-08-945-289-4	Sequence 4, Appl1
25	134	100.0	476 13 US-08-954-643-1	Sequence 1, Appl1
26	134	100.0	476 17 US-09-386-591-28	Sequence 28, Appl
27	134	100.0	476 17 US-09-387-340-28	Sequence 28, Appl
28	134	100.0	476 19 US-09-529-762-1	Sequence 1, Appl1
29	134	100.0	476 23 US-09-943-334-4	Sequence 4, Appl1
30	134	100.0	476 23 US-09-943-548-4	Sequence 4, Appl1
31	134	100.0	493 11 US-08-783-997-30	Sequence 30, Appl
32	134	100.0	493 11 US-08-788-882-30	Sequence 30, Appl
33	134	100.0	493 11 US-08-934-367-30	Sequence 30, Appl
34	134	100.0	493 14 US-09-054-772-14	Sequence 14, Appl
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36	134	100.0	493 17 US-09-386-591-30	Sequence 30, Appl
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38	134	100.0	493 22 US-09-802-640-12	Sequence 12, Appl
39	121	90.3	496 13 US-08-954-643-6	Sequence 6, Appl1
40	121	90.3	496 19 US-09-529-762-6	Sequence 19, App
41	117	87.3	26 1 PCT-US99-13975B-109	Sequence 109, App
42	117	87.3	26 11 US-08-785-997-50	Sequence 50, Appl
43	117	87.3	26 11 US-08-788-882-50	Sequence 50, Appl
44	117	87.3	26 13 US-08-934-367-50	Sequence 50, Appl
45	117	87.3	26 17 US-09-386-591-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1
PCT-US99-13975B-106
Sequence 106, Application PC/TUS9913975B
GENERAL INFORMATION: UNITED BIO MEDICAL INC., ET AL.
APPLICANT: UNITED BIO MEDICAL INC., ET AL.
TITLE OF INVENTION: ARTIFICIAL T HELPER CELL
TITLE OF INVENTION: EPITOPES AS IMMUNE STIMULATORS FOR SYNTHETIC
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESSES:
ADDRESSER: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/13975B
FILING DATE: 21-JUNE-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,412
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin

```

;
;   REGISTRATION NUMBER: 29,323
;   REFERENCE/DOCKET NUMBER: 1151-4158PC1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 212-758-4800
;   TELEFAX: 212-751-6849
;   INFORMATION FOR SEQ ID NO: 106:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 26 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   PCT-US99-13975B-106

Query Match      100.0%; Score 134; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1,5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLDMDGFGPEPHLLVDFLOSLS 26
Db 1 RDGFLLDMDGFGPEPHLLVDFLOSLS 26

RESULT 2
US-08-432-483-1
; Sequence 1, Application US/08432483
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles, W.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
; TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: Ten South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-7407
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/432,483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; ATTORNEY/AGENT INFORMATION:
; NAME: Leon R. Yankwich
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: 95,179(TCS-95179)
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 26 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   HYPOTHETICAL:
;   ANTI-SENSE:
;   FEATURE:
; NAME/KEY: Carboxyl terminal 26 amino acids of
; NAME/KEY: human CETP
; LOCATION:
; PUBLICATION INFORMATION:
; AUTHORS: Drayna, Dennis, et al.
; TITLE: Cloning and sequencing of human
; TITLE: cholesteryl ester transfer CDNA
; JOURNAL: Nature
; VOLUME: 327
; ISSUE:
; PAGES: 632-634
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;   DATE: 18-JUN-1987
;   RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 26
US-08-432-483-1

Query Match      100.0%; Score 134; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 1,5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLDMDGFGPEPHLLVDFLOSLS 26
Db 1 RDGFLLDMDGFGPEPHLLVDFLOSLS 26

RESULT 3
US-08-432-483A-1
; Sequence 1, Application US/08432483A
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
; TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Wilcoff, Ltd.
; STREET: Ten South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-7407
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/432,483A
; FILING DATE: 1-May-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Leon R. Yankwich
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: 95,179(TCS-95179)
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 26 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   HYPOTHETICAL:
;   ANTI-SENSE:
;   FEATURE:
; NAME/KEY: Carboxyl terminal 26 amino acids of
; NAME/KEY: human CETP
; LOCATION:
; PUBLICATION INFORMATION:
; AUTHORS: Drayna, Dennis, et al.
; TITLE: Cloning and sequencing of human
; TITLE: cholesteryl ester transfer CDNA
; JOURNAL: Nature
; VOLUME: 327
; ISSUE:
; PAGES: 632-634
; DATE: 18-JUN-1987
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 26
US-08-432-483A-1

Query Match      100.0%; Score 134; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 1,5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 RDGFLQMDGFPPEHLVDFLOSLS 26
 Db 1 RDGFLQMDGFPPEHLVDFLOSLS 26

RESULT 4

US-08-785-997-29

Sequence 29, Application US/08785997

GENERAL INFORMATION:

APPLICANT: Needleman, Philip

APPLICANT: Glenn, Kevin

TITLE OF INVENTION: An Immunological Process for Increasing

TITLE OF INVENTION: the HDL Cholesterol Concentration

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: Welsh & Katz, Ltd.

STREET: 120 South Riverside Plaza, 22nd Floor

CITY: Chicago

STATE: IL

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/785,997

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Gamson Ph.D., Edward P.

REGISTRATION NUMBER: 29,381

REFERENCE/DOCKET NUMBER: MON-101.0 6018/68346

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312)655-1501

TELEFAX: (312)655-1501

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

PUBLICATION INFORMATION:

AUTHORS: Swenson, T. L.

AUTHORS: et al.,

JOURNAL: J. Biol. Chem.

VOLUME: 264

PAGES: 14318-14326

DATE: 1989

US-08-785-997-29

Query Match 100.0%; Score 134; DB 11; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.5e-12;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLQMDGFPPEHLVDFLOSLS 26

Db 1 RDGFLQMDGFPPEHLVDFLOSLS 26

RESULT 5

US-08-788-882-29

Sequence 29, Application US/08788882

GENERAL INFORMATION:

APPLICANT: Needleman, Philip

APPLICANT: Glenn, Kevin

APPLICANT: Krul, Elaine

APPLICANT: Gamson, Edward P.

TITLE OF INVENTION: An Immunological Process and Constructs

TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: Welsh & Katz, Ltd.

STREET: 120 South Riverside Plaza, 22nd Floor

CITY: Chicago

STATE: IL

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/788,882

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Gamson, Edward P.

REGISTRATION NUMBER: 29,381

REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312)655-1501

TELEFAX: (312)655-1501

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

PUBLICATION INFORMATION:

AUTHORS: Swenson, T. L.

AUTHORS: et al.,

JOURNAL: J. Biol. Chem.

VOLUME: 264

PAGES: 14318-14326

DATE: 1989

US-08-788-882-29.

OY 1 RDGFLQMDGFPPEHLVDFLOSLS 26

Db 1 RDGFLQMDGFPPEHLVDFLOSLS 26

RESULT 6

US-08-934-367-29

Sequence 29, Application US/08934367

GENERAL INFORMATION:

APPLICANT: Needleman, Philip

APPLICANT: Glenn, Kevin

TITLE OF INVENTION: An Immunological Process and Constructs

TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration by DNA

TITLE OF INVENTION: Vaccination

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: Welsh & Katz, Ltd.

STREET: 120 South Riverside Plaza, 22nd Floor

CITY: Chicago

STATE: IL

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

Query Match 100.0%; Score 134; DB 11; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.5e-12;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/934,367
;; FILING DATE:
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Gamsen Ph.D., Edward P.
;; REGISTRATION NUMBER: 29,381
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312)655-1500
;; TELEFAX: (312)655-1501
;; INFORMATION FOR SEQ ID NO: 29:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 26 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; PUBLICATION INFORMATION:
;; AUTHORS: Swenson, T. L.
;; JOURNAL: J. Biol. Chem.
;; VOLUME: 264
;; PAGES: 14318-14326
;; DATE: 1989
US-08-934-367-29

Query Match 100.0%; Score 134; DB 13; Length 26;
Best Local Similarity 100.0%; Pred. No. 1,5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLQMDFGFPEHLVDFLOSLS 26
DB 1 RDGFLLQMDFGFPEHLVDFLOSLS 26

RESULT 7
US-08-945-289-1
;; Sequence 1, Application US/08945289
;; GENERAL INFORMATION:
;; APPLICANT: Riltershaus, Charles, W.
;; APPLICANT: Thomas, Lawrence J.
;; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
;; TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
;; NUMBER OF SEQUENCES: 9
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Yankwich & Associates
;; STREET: 130 Bishop Allen Drive
;; CITY: Cambridge
;; STATE: Massachusetts
;; COUNTRY: USA
;; ZIP: 02139
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: Windows 95
;; SOFTWARE: Word 97
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/945,289
;; FILING DATE: October 17, 1997
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/432,483
;; FILING DATE: May 1, 1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Leon R. Yankwich
;; REGISTRATION NUMBER: 30,237
;; REFERENCE/DOCKET NUMBER: TCS-411.1P US
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 26 amino acids
;; TYPE: amino acid

;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL:
;; ANTI-SENSE:
;; FEATURE:
;; NAME/KEY: Carboxyl terminal 26 amino
;; NAME/KEY: acids of human CETP
;; LOCATION:
;; PUBLICATION INFORMATION:
;; AUTHORS: Drayna, Dennis, et al.
;; TITLE: Cloning and sequencing of human cholesterol ester transfer CDNA
;; JOURNAL: Nature
;; VOLUME: 327
;; ISSUE:
;; PAGES: 632-634
;; DATE: 18 JUN-1987
;; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 26
US-08-945-289-1

Query Match 100.0%; Score 134; DB 13; Length 26;
Best Local Similarity 100.0%; Pred. No. 1,5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLQMDFGFPEHLVDFLOSLS 26
DB 1 RDGFLLQMDFGFPEHLVDFLOSLS 26

RESULT 8
US-09-386-591-29
;; Sequence 29, Application US/09386591
;; GENERAL INFORMATION:
;; APPLICANT: Needleman, Philip
;; APPLICANT: Glenn, Kevin
;; TITLE OF INVENTION: An Immunological Process and Constructs
;; TITLE OF INVENTION: for increasing the HDL Cholesterol Concentration by DNA
;; NUMBER OF SEQUENCES: 52
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Welsh & Katz, Ltd.
;; STREET: 120 South Riverside Plaza, 22nd Floor
;; CITY: Chicago
;; STATE: IL
;; COUNTRY: USA
;; ZIP: 60606
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentln Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/386,591
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Gamsen Ph.D., Edward P.
;; REGISTRATION NUMBER: 29,381
;; REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312)655-1500
;; TELEFAX: (312)655-1501
;; INFORMATION FOR SEQ ID NO: 29:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 26 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; PUBLICATION INFORMATION:
;; AUTHORS: Swenson, T. L.
;; JOURNAL: J. Biol. Chem.

VOLUME: 264
PAGES: 14318-14326
DATE: 1989
US-09-386-591-29

Query Match 100.0%; Score 134; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDGFPPEHLVDFLOSLS 26
DB 1 RDGFLLLQMDGFPPEHLVDFLOSLS 26

RESULT 9
US-09-387-340-29
; Sequence 29, Application US/09387340
; GENERAL INFORMATION:
; APPLICANT: Needleman, Philip
; APPLICANT: Glenn, Kevin
; APPLICANT: Krul, Elaine
; APPLICANT: Gamsom, Edward P.
; TITLE OF INVENTION: An Immunological Process and Constructs
; TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 120 South Riverside Plaza, 22nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/387,340
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamsom, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)655-1500
; TELEFAX: (312)655-1501
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PUBLICATION INFORMATION:
; AUTHORS: Swenson, T. L.
; JOURNAL: J. Biol. Chem.
; VOLUME: 264
; PAGES: 14318-14326
; DATE: 1989
US-09-387-340-29

Query Match 100.0%; Score 134; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDGFPPEHLVDFLOSLS 26
DB 1 RDGFLLLQMDGFPPEHLVDFLOSLS 26

RESULT 10
US-09-701-588-106

; Sequence 106, Application US/09701588
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang YI
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 122
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/701,588
; FILING DATE: 29-NOV-2000
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-158051

TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849

INFORMATION FOR SEQ ID NO: 106
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 106

US-09-701-588-106

Query Match 100.0%; Score 134; DB 21; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDGFPPEHLVDFLOSLS 26
DB 1 RDGFLLLQMDGFPPEHLVDFLOSLS 26

RESULT 11
US-09-943-334-1

; Sequence 1, Application US/09943334
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; APPLICANT: Thomas, Lawrence J.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVI
; FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
; CURRENT APPLICATION NUMBER: US/09/943,334
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 08/432,483
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: PCT/US96/06147
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/945,289
; PRIOR FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.1

SEQ ID NO 1
LENGTH: 26
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: C - terminal 26 amino acids of Human CTP
US-09-943-334-1

Query Match 100.0%; Score 134; DB 23; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDGFPFPHLLVDFLQSL 26
DB 1 RDGFLLLQMDGFPFPHLLVDFLQSL 26

RESULT 12
US-09-943-548-1
Sequence 1, Application US/09943548
GENERAL INFORMATION:
APPLICANT: Riltershaus, Charles W.
APPLICANT: Thomas, Lawrence J.
TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CTP) ACTIVITY
FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
CURRENT APPLICATION NUMBER: US/09/943,548
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: 08/432,483
PRIOR FILING DATE: 1995-05-01
PRIOR APPLICATION NUMBER: PCT/US96/06147
PRIOR FILING DATE: 1996-05-01
PRIOR APPLICATION NUMBER: 08/945,289
PRIOR FILING DATE: 1997-10-17
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 26
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: C - terminal 26 amino acids of Human CTP
US-09-943-548-1

Query Match 100.0%; Score 134; DB 23; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDGFPFPHLLVDFLQSL 26
DB 1 RDGFLLLQMDGFPFPHLLVDFLQSL 26

RESULT 13
PCT-US99-13975B-110
Sequence 110, Application PC/TUS9913975B
GENERAL INFORMATION:
APPLICANT: UNITED BIOMEDICAL INC., ET AL.
TITLE OF INVENTION: ARTIFICIAL T HELPER CELL
TITLE OF INVENTION: EPITOPES AS IMMUNE STIMULATORS FOR SYNTHETIC
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/13975B
FILING DATE: 21-JUNE-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,412
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4158PC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-751-6849
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US99-13975B-110

Query Match 100.0%; Score 134; DB 1; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.8e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDGFPFPHLLVDFLQSL 26
DB 21 RDGFLLLQMDGFPFPHLLVDFLQSL 46

RESULT 14
PCT-US99-13975B-111
Sequence 111, Application PC/TUS9913975B
GENERAL INFORMATION:
APPLICANT: UNITED BIOMEDICAL INC., ET AL.
TITLE OF INVENTION: ARTIFICIAL T HELPER CELL
TITLE OF INVENTION: EPITOPES AS IMMUNE STIMULATORS FOR SYNTHETIC
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/13975B
FILING DATE: 21-JUNE-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,412
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4158PC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-751-6849
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-0599-139758-111

Query Match 100.0%; Score 134; DB 1; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.8e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDFGPEHLVDFIQSL 26
DB 21 RDGFLLLQMDFGPEHLVDFIQSL 46

RESULT 15
US-09-701-588-110
; Sequence 110, Application US/09701588
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Y
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; IMMUNOGENS
; NUMBER OF SEQUENCES: 122
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/701,588
; FILING DATE: 29-Nov-2000
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-158US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 110
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 110
US-09-701-588-110

Query Match 100.0%; Score 134; DB 21; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.8e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDFGPEHLVDFIQSL 26
DB 21 RDGFLLLQMDFGPEHLVDFIQSL 46

Search completed: June 18, 2002, 08:11:59
Job time: 368 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:05:51 ; Search time 26.26 Seconds

(Without alignments)
83.832 Million cell updates/sec

Title:

US-09-943-334-1

Perfect score:

1 RDGFLLQMDGFPEHLLVDFLOSLLS 26

Sequence:

BIOSUM62
Gapop 10.0 , Gapext 0.5

Scoring table:

257105 seqs, 84670655 residues

Total number of hits satisfying chosen parameters: 257.05

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/1/paa/PCF_NEW_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	134	100.0	470	5	US-09-446-415B-6 Sequence 6, Appl1
2	53	39.6	11	5	US-09-523-033A-3 Sequence 3, Appl1
3	50	37.3	80	5	US-09-935-625-631 Sequence 631, Appl
4	50	37.3	80	5	US-09-935-625-19787 Sequence 19787, A
5	50	37.3	180	5	US-09-935-625-1494 Sequence 1494, Ap
6	50	37.3	180	5	US-09-935-625-21627 Sequence 21627, A
7	50	37.3	183	5	US-09-935-625-592 Sequence 592, Appl
8	50	37.3	183	5	US-09-935-625-19733 Sequence 19733, A
9	50	37.3	628	6	US-10-041-007-22 Sequence 22, Appl1
10	48	35.8	348	7	US-60-360-039-850 Sequence 850, Appl
11	48	35.8	390	7	US-60-360-039-17233 Sequence 17233, A
12	47.5	35.4	434	7	US-60-360-039-13240 Sequence 13240, A
13	46	34.3	428	5	US-09-573-655B-240 Sequence 240, Appl
14	46	34.3	428	5	US-09-573-655B-787 Sequence 787, Appl
15	46	34.3	754	5	US-09-935-625-557 Sequence 557, Appl
16	46	34.3	826	5	US-09-935-625-556 Sequence 556, Appl
17	46	34.3	849	5	US-09-935-625-555 Sequence 555, Appl
18	45	33.6	442	6	US-10-106-698-6383 Sequence 6383, Ap
19	44	32.8	324	5	US-09-935-625-5733 Sequence 5733, Ap
20	44	32.8	324	5	US-09-935-625-9347 Sequence 9347, Ap
21	44	32.8	352	5	US-09-935-625-5732 Sequence 5732, Ap
22	44	32.8	352	5	US-09-935-625-9346 Sequence 9346, Ap
23	44	32.8	371	5	US-09-935-625-5731 Sequence 5731, Ap
24	44	32.8	371	5	US-09-935-625-9345 Sequence 9345, Ap
25	44	32.8	401	5	US-09-935-625-5737 Sequence 5737, Ap
26	44	32.8	401	5	US-09-935-625-9351 Sequence 9351, Ap

27	44	32.8	435	7	US-60-360-039-17062 Sequence 17062, A
28	44	32.8	444	5	US-09-935-625-5228 Sequence 5228, Ap
29	44	32.8	444	5	US-09-935-625-5736 Sequence 5736, Ap
30	44	32.8	444	5	US-09-935-625-7740 Sequence 7740, Ap
31	44	32.8	444	5	US-09-935-625-9350 Sequence 9350, Ap
32	44	32.8	472	5	US-09-935-625-5227 Sequence 5227, Ap
33	44	32.8	472	5	US-09-935-625-5735 Sequence 5735, Ap
34	44	32.8	472	5	US-09-935-625-7739 Sequence 7739, Ap
35	44	32.8	472	5	US-09-935-625-9349 Sequence 9349, Ap
36	44	32.8	492	5	US-09-935-625-5226 Sequence 5226, Ap
37	44	32.8	492	5	US-09-935-625-7738 Sequence 7738, Ap
38	43.5	32.5	216	7	US-60-360-039-9644 Sequence 9644, Appl
39	43.5	32.5	430	6	US-10-145-415-8 Sequence 8, Appl1
40	43.5	32.5	430	6	US-10-145-415-12 Sequence 12, Appl
41	43.5	32.5	430	6	US-10-145-415-20 Sequence 20, Appl
42	43.5	32.5	430	6	US-10-145-415-30 Sequence 30, Appl
43	43	32.1	80	5	US-09-620-393B-4183 Sequence 4183, Ap
44	43	32.1	80	5	US-09-620-393B-8965 Sequence 8965, Ap
45	43	32.1	99	5	US-09-620-393B-4182 Sequence 4182, Ap

ALIGNMENTS

RESULT 1
US-09-446-415B-6
Sequence 6, Application US/09446415B
GENERAL INFORMATION:
APPLICANT: Beamet, Lesa J.
APPLICANT: Eisenberg, David
TITLE OF INVENTION: BACTERICIDAL/PERMEABILITY-INCREASING PROTEIN:
TITLE OF INVENTION: CRYSTALLIZATION, X-RAY DIFFRACTION, THREE-DIMENSIONAL
TITLE OF INVENTION: STRUCTURE DETERMINATION, RATIONAL DRUG DESIGN AND
FILE REFERENCE: 11034US02
CURRENT APPLICATION NUMBER: US/09/446, 415B
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 08/879, 565
PRIOR FILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 470
TYPE: PRT
ORGANISM: Human
FEATURE:
OTHER INFORMATION: cholesteryl ester transfer protein (CETP) (Figure
OTHER INFORMATION: 5)
US-09-446-415B-6
Query Match 100.0% Score 134; DB 5; Length 470;
Best Local Similarity 100.0% Pred. No. 4.3e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RDGFLLQMDGFPEHLLVDFLOSLLS 26
DB 445 RDGFLLQMDGFPEHLLVDFLOSLLS 470
RESULT 2
US-09-523-033A-3
Sequence 3, Application US/09523033A
GENERAL INFORMATION:
APPLICANT: Kwosh, Deborah Y.
APPLICANT: Brostoff, Steven W.
APPLICANT: Carlio, Dennis J.
TITLE OF INVENTION: METHOD FOR INCREASING HDL CHOLESTEROL LEVEL
FILE REFERENCE: TCS-428.0 US-1
CURRENT APPLICATION NUMBER: US/09/523, 033A
CURRENT FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: US 08/482, 454

;; PRIOR FILING DATE: 1995-06-06
;; NUMBER OF SEQ ID NOS: 3
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 3
;; LENGTH: 11
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-523-033A-3

Query Match 39.6%; Score 53; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 16 HLIVDFLOSLS 26
Db 1 HLIVDFLOSLS 11

RESULT 3
US-09-935-625-631
; Sequence 631, Application US/09935625
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE
; FILE REFERENCE: 2750-1481P
; CURRENT APPLICATION NUMBER: US/09/935,625
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 33136
; SEQ ID NO 631
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: 1..80
; OTHER INFORMATION: Ceres Seq. ID no. 1977520
US-09-935-625-631

Query Match 37.3%; Score 50; DB 5; Length 80;
Best Local Similarity 32.0%; Pred. No. 1.7;
Matches 8; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Oy 1 RDGFLLLQMDGFPPEHLVDFLOSL 25
Db 17 KEGVLFPAKKDFNLPOHPLIESV PNL 41

RESULT 4
US-09-935-625-19787
; Sequence 19787, Application US/09935625
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE
; FILE REFERENCE: 2750-1481P
; CURRENT APPLICATION NUMBER: US/09/935,625
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 33136
; SEQ ID NO 19787
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: 1..80
; OTHER INFORMATION: Ceres Seq. ID no. 1977520
US-09-935-625-19787

Query Match 37.3%; Score 50; DB 5; Length 80;

Best Local Similarity 32.0%; Pred. No. 1.7;
Matches 8; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Oy 1 RDGFLLLQMDGFPPEHLVDFLOSL 25
Db 17 KEGVLFPAKKDFNLPOHPLIESV PNL 41

RESULT 5
US-09-935-625-1494
; Sequence 1494, Application US/09935625
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA
; FILE REFERENCE: 2750-1481P
; CURRENT APPLICATION NUMBER: US/09/935,625
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 33136
; SEQ ID NO 1494
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: 1..180
; OTHER INFORMATION: Ceres Seq. ID no. 3058194
US-09-935-625-1494

Query Match 37.3%; Score 50; DB 5; Length 180;
Best Local Similarity 32.0%; Pred. No. 4.1;
Matches 8; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Oy 1 RDGFLLLQMDGFPPEHLVDFLOSL 25
Db 17 KEGVLFPAKKDFNLPOHPLIESV PNL 41

RESULT 6
US-09-935-625-21627
; Sequence 21627, Application US/09935625
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA
; FILE REFERENCE: 2750-1481P
; CURRENT APPLICATION NUMBER: US/09/935,625
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 33136
; SEQ ID NO 21627
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: 1..180
; OTHER INFORMATION: Ceres Seq. ID no. 3058194
US-09-935-625-21627

Query Match 37.3%; Score 50; DB 5; Length 180;
Best Local Similarity 32.0%; Pred. No. 4.1;
Matches 8; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Oy 1 RDGFLLLQMDGFPPEHLVDFLOSL 25
Db 17 KEGVLFPAKKDFNLPOHPLIESV PNL 41

RESULT 7
US-09-935-625-592
; Sequence 592, Application US/09935625

```
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE
; FILE REFERENCE: 2750-1481P
; CURRENT APPLICATION NUMBER: US/09/935,625
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 33136
; SEQ ID NO 592
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: 1..183
; OTHER INFORMATION: Ceres Seq. ID no. 1976020
US-09-935-625-592

Query Match          37.3%; Score 50; DB 5; Length 183;
Best Local Similarity 32.0%; Pred. No. 4.2;
Matches 8; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

OY      1 RDGFLQMDFGPEHLVDPLQSL 25
       :| | :| | :| | :| | :| |
Db      17 KEGVLEFAKKDFNLPOHPLIESV 41

RESULT 8
US-09-935-625-19733
; Sequence 19733, Application US/09935625
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE
; FILE REFERENCE: 2750-1481P
; CURRENT APPLICATION NUMBER: US/09/935,625
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 33136
; SEQ ID NO 19733
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: 1..183
; OTHER INFORMATION: Ceres Seq. ID no. 1976020
US-09-935-625-19733

Query Match          37.3%; Score 50; DB 5; Length 183;
Best Local Similarity 32.0%; Pred. No. 4.2;
Matches 8; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

OY      1 RDGFLQMDFGPEHLVDPLQSL 25
       :| | :| | :| | :| | :| |
Db      17 KEGVLEFAKKDFNLPOHPLIESV 41

RESULT 9
US-10-041-007-22
; Sequence 22, Application US/10041007
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seichi P.T.
; APPLICANT: Schepmann, Hala G
; TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase
; FILE REFERENCE: P02081US1
; CURRENT APPLICATION NUMBER: US/10/041,007
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259,881
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 22
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Adles grandis
US-10-041-007-22

Query Match          37.3%; Score 50; DB 6; Length 628;
Best Local Similarity 47.8%; Pred. No. 15;
Matches 11; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

OY      6 LQMDGFEHL--VDPLQSL 26
       :| | ||| :| | :| | :| |
Db      490 ILTMDIPFDHLKEVDPSKIN 512

RESULT 10
US-60-360-039-850
; Sequence 850, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 850
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Escherichia coli
US-60-360-039-850

Query Match          35.8%; Score 48; DB 7; Length 348;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY      10 DFGPEHLVDF 21
       :| ||||| :| |
Db      254 EFDLPEHLVDF 265

RESULT 11
US-60-360-039-17233
; Sequence 17233, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 17233
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Bacillus halodurans
US-60-360-039-17233

Query Match          35.8%; Score 48; DB 7; Length 390;
Best Local Similarity 47.6%; Pred. No. 18;
Matches 10; Conservative 2; Mismatches 9; Indels 0; Gaps 0;
```

```
OY      1  RDGFLLLQMDGFPEHLVDF 21
      ||| | | : ||| | | : ||
      356  RDGRLRLSVGLERPELMADE 376

RESULT 12
US-60-360-039-13240
; Sequence 13240, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 4/374
; SEQ ID NO 13240
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Aspergillus nidulans
US-60-360-039-13240

Query Match      35.4%; Score 47.5; DB 7; Length 434;
Best Local Similarity 52.4%; Pred. No. 24;
Matches 11; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

OY      7  LQMDGFPE-HLVDFLOSLS 26
      ||| | | | | : ||| | | : |
      272  LQLDIGAPELHNVDALKGLT 292

RESULT 13
US-09-573-655B-240
; Sequence 240, Application US/09573655B
; GENERAL INFORMATION:
; APPLICANT: SOLOVYEV, Victor and TROUKHAN, Maxim
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-0876P
; CURRENT APPLICATION NUMBER: US/09/573,655B
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 3281
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 240
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-573-655B-240

Query Match      34.3%; Score 46; DB 5; Length 428;
Best Local Similarity 29.4%; Pred. No. 40;
Matches 10; Conservative 10; Mismatches 4; Indels 10; Gaps 2;

OY      1  RDGFLLL-----QMDGFPE---HLVDFLOS 24
      ||| | | : ||| | | : | : | : |
      107  RDNFVYVELDEMDRGYPOFTEARILSEFT 140

RESULT 14
US-09-573-655B-787
; Sequence 787, Application US/09573655B
; GENERAL INFORMATION:
; APPLICANT: SOLOVYEV, Victor and TROUKHAN, Maxim
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-0876P
; CURRENT APPLICATION NUMBER: US/09/573,655B
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; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 3281
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 787
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-573-655B-787

Query Match      34.3%; Score 46; DB 5; Length 428;
Best Local Similarity 29.4%; Pred. No. 40;
Matches 10; Conservative 10; Mismatches 4; Indels 10; Gaps 2;

OY      1  RDGFLLL-----QMDGFPE---HLVDFLOS 24
      ||| | | : ||| | | : | : | : |
      107  RDNFVYVELDEMDRGYPOFTEARILSEFT 140

RESULT 15
US-09-935-625-557
; Sequence 557, Application US/09935625
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA
; FILE REFERENCE: 2750-1481P
; CURRENT APPLICATION NUMBER: US/09/935,625
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 33136
; SEQ ID NO 557
; LENGTH: 754
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: 1..754
; OTHER INFORMATION: Ceres Seq. ID no. 1825655
US-09-935-625-557

Query Match      34.3%; Score 46; DB 5; Length 754;
Best Local Similarity 52.2%; Pred. No. 72;
Matches 12; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

OY      2  DGFLLQLM-----DGFPEHLVND 20
      | | | | : | | | | | | | |
      260  DFLRLKSVKLPDREPEHNLVD 282
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Search completed: June 18, 2002, 08:07:29
Job time: 98 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:05:51 ; Search time 21.83 Seconds
(without alignments)
29.091 Million cell updates/sec

Title: US-09-943-334-1
Perfect score: 134
Sequence: 1 RDGFLQLQMDGFPFHLVDFLOSLS 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA:*
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfilltest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	134	100.0	476	US-08-879-565-14	Sequence 14, Appl
2	134	100.0	476	US-09-171-869-4	Sequence 4, Appl
3	117	87.3	456	US-09-171-869-2	Sequence 2, Appl
4	79	59.0	50	US-09-171-869-7	Sequence 7, Appl
5	56	41.8	97	US-08-844-280-4	Sequence 4, Appl
6	56	41.8	97	US-09-006-726-4	Sequence 4, Appl
7	56	41.8	587	US-08-844-280-2	Sequence 2, Appl
8	56	41.8	587	US-09-006-726-2	Sequence 2, Appl
9	51.5	38.4	353	US-09-118-442-6	Sequence 6, Appl
10	51.5	38.4	353	US-09-677-064-6	Sequence 6, Appl
11	44.5	33.2	428	US-08-050-132A-2	Sequence 2, Appl
12	44.5	33.2	428	US-08-750-222A-2	Sequence 2, Appl
13	44.5	33.2	428	US-08-815-652B-2	Sequence 2, Appl
14	44.5	33.2	428	US-08-254-353A-2	Sequence 2, Appl
15	44.5	33.2	428	PCT-US92-05374A-2	Sequence 2, Appl
16	44.5	33.2	428	PCT-US95-07084-2	Sequence 2, Appl
17	44	32.8	472	US-08-622-166A-2	Sequence 2, Appl
18	44	32.8	472	US-08-622-166A-2	Sequence 2, Appl
19	44	32.1	422	US-08-403-852D-17	Sequence 17, Appl
20	43	32.1	422	US-08-510-646B-18	Sequence 18, Appl
21	43	32.1	422	US-09-231-818-17	Sequence 17, Appl
22	42	31.3	387	US-08-968-563-37	Sequence 37, Appl
23	42	31.3	387	US-08-969-683A-37	Sequence 37, Appl
24	41	30.6	418	US-08-795-430-13	Sequence 13, Appl
25	41	30.6	564	US-09-211-704A-8	Sequence 8, Appl
26	41	30.6	669	US-08-704-711A-3	Sequence 3, Appl
27	40.5	30.2	462	US-09-036-987A-18	Sequence 18, Appl

28	40.5	30.2	462	US-09-370-700-18	Sequence 18, Appl
29	40	29.9	433	US-08-919-624-1	Sequence 1, Appl
30	40	29.9	578	US-08-766-014-4	Sequence 4, Appl
31	40	29.9	608	US-08-766-014-3	Sequence 3, Appl
32	40	29.9	872	US-08-766-014-2	Sequence 2, Appl
33	40	29.9	906	US-08-608-230A-9	Sequence 9, Appl
34	40	29.9	907	US-08-990-140-4	Sequence 4, Appl
35	40	29.9	907	US-09-546-238-4	Sequence 4, Appl
36	40	29.9	940	US-08-810-712-7	Sequence 7, Appl
37	39.5	29.5	1174	US-08-446-345-36	Sequence 36, Appl
38	39	29.1	268	US-08-652-877-4	Sequence 4, Appl
39	39	29.1	268	US-08-476-515A-4	Sequence 4, Appl
40	39	29.1	363	US-08-484-105-20	Sequence 20, Appl
41	39	29.1	363	US-08-484-106-20	Sequence 20, Appl
42	39	29.1	582	US-08-899-244-2	Sequence 2, Appl
43	39	29.1	582	US-09-224-772-2	Sequence 2, Appl
44	39	29.1	582	US-09-227-804-2	Sequence 2, Appl
45	39	29.1	607	US-09-211-704A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-879-565-14
Sequence 14, Application US/08879565A
Patent No. 6093573
GENERAL INFORMATION:
APPLICANT: Beamer, Lisa J.
APPLICANT: Carroll, Stephen F.
TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF
FILE REFERENCE: 1103/11034US01
CURRENT FILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 470
TYPE: PRT
ORGANISM: Human
FEATURE:
OTHER INFORMATION: cholesterol ester transfer protein (CETP) (Figure
US-08-879-565-14

Query Match 100.0% Score 134; DB 3; Length 470;
Best Local Similarity 100.0% Pred. No. 8.7e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RDGFLQLQMDGFPFHLVDFLOSLS 26
Db 445 RDGFLQLQMDGFPFHLVDFLOSLS 470

RESULT 2
US-09-171-869-4
Sequence 4, Application US/09171969
Patent No. 6284533
GENERAL INFORMATION:
APPLICANT: Thomas, Lawrence J.
TITLE OF INVENTION: PLASMID-BASED VACCINE FOR TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Wilcoff, Ltd.
STREET: 75 State Street, Suite 2300
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1807
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,969
FILING DATE: 01 May 1997 (01.05.97)
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/640,713
FILING DATE: 01 May 1996 (01.05.96)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/802,967
FILING DATE: 21 February 1997 (21.02.97)
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: TCS 414.1 PCT (05872)
INFORMATION FOR SEQ. ID NO.: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL:
ANTI-SENSE:
FEATURE:
NAME/KEY: Amino acid sequence of mature human
NAME/KEY: CERP
LOCATION:
PUBLICATION INFORMATION:
AUTHORS: Drayna, Dennis, et al.
TITLE: Cloning and sequencing of human
TITLE: cholesterol ester transfer cDNA
JOURNAL: Nature
VOLUME: 327
ISSUE:
PAGES: 632 - 634
DATE: 18-JUN-1987
RELEVANT RESIDUES IN SEQ ID NO: 4: FROM 1 TO 476
US-09-171-969-4

Query Match 100.0%; Score 134; DB 4; Length 476;
Best Local Similarity 100.0%; Pred. No. 8.8e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RDGFLIQMDGFGFPHLLVDFLOSLS 26
DB 451 RDGFLIQMDGFGFPHLLVDFLOSLS 476

RESULT 3
US-09-171-969-2
Sequence 2, Application US/09171969
Patent No. 6284533
GENERAL INFORMATION:
APPLICANT: Thomas, Lawrence J.
TITLE OF INVENTION: PLASMID-BASED VACCINE FOR TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 75 State Street, Suite 2300
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1807
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,969
FILING DATE: 01 May 1997 (01.05.97)
CLASSIFICATION: 514

APPLICATION NUMBER: US/09/171,969
FILING DATE: 01 May 1997 (01.05.97)
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/640,713
FILING DATE: 01 May 1996 (01.05.96)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/802,967
FILING DATE: 21 February 1997 (21.02.97)
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: TCS 414.1 PCT (05872)
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL:
ANTI-SENSE:
FEATURE:
NAME/KEY: Amino acid sequence for mature
NAME/KEY: rabbit CERP protein.
LOCATION:
PUBLICATION INFORMATION:
AUTHORS: Nagashima, Mariko, et al.
TITLE: Cloning and mRNA tissue
TITLE: distribution of rabbit
TITLE: cholesterol ester transfer
JOURNAL: J. Lipid Res.
VOLUME: 29
ISSUE:
PAGES: 1643 - 1649
DATE: 1988
RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 496
US-09-171-969-2

Query Match 87.3%; Score 117; DB 4; Length 496;
Best Local Similarity 92.0%; Pred. No. 5.1e-11;
Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 DGFLLIQMDGFGFPHLLVDFLOSLS 26
DB 472 DGFLLIQMDGFGFPHLLVDFLOSLS 496

RESULT 4
US-09-171-969-7
Sequence 7, Application US/09171969
Patent No. 6284533
GENERAL INFORMATION:
APPLICANT: Thomas, Lawrence J.
TITLE OF INVENTION: PLASMID-BASED VACCINE FOR TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 75 State Street, Suite 2300
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1807
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,969
FILING DATE: 01 May 1997 (01.05.97)
CLASSIFICATION: 514

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/640,713
; FILING DATE: 01 May 1996 (01.05.96)
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/802,967
; FILING DATE: 21 February 1997 (21.02.97)
; ATTORNEY/AGENT INFORMATION:
; NAME: Leon R. Yankwich
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: TCS 414.1 PCT (05872)
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL:
; ANTI-SENSE:
; FEATURE: amino acid sequence of peptide encoded
; FEATURE: by bases 10 to 159 of SEQ ID NO:5
; NAME/KEY:
; LOCATION:
; US-09-171-969-7

Query Match          59.0%; Score 79; DB 4; Length 50;
Best Local Similarity 93.8%; Pred. No. 4.6e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 FGPEHLVDPLQSL 26
DB 35 FGPEHLVDPLQSL 50

RESULT 5
; US-08-844-280-4
; Sequence 4, Application US/08844280
; Patent No. 5747315
; GENERAL INFORMATION:
; APPLICANT: Lawlor, Elizabeth
; TITLE OF INVENTION: No. 5747315el Compounds
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,280
; FILING DATE: 18-APR-1997
; CLASSIFICATION: ?
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9607993.4
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimm1, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P31457-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97 amino acids
; TYPE: amino acid
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```

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-844-280-4

Query Match          41.8%; Score 56; DB 1; Length 97;
Best Local Similarity 71.4%; Pred. No. 0.051;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 GFLLQMDYGFPPH 16
DB 33 GFLLQMDYGFPPH 46

RESULT 6
; US-09-006-726-4
; Sequence 4, Application US/09006726
; Patent No. 6210940
; GENERAL INFORMATION:
; APPLICANT: Lawlor, Elizabeth J.
; TITLE OF INVENTION: No. 6210940el Compounds
; FILE REFERENCE: P31457-2-D1
; CURRENT APPLICATION NUMBER: US/09/006,726
; EARLIER FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 08/844,280
; EARLIER FILING DATE: 1997-04-18
; EARLIER APPLICATION NUMBER: UK9607993.4
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; US-09-006-726-4

Query Match          41.8%; Score 56; DB 4; Length 97;
Best Local Similarity 71.4%; Pred. No. 0.051;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 GFLLQMDYGFPPH 16
DB 33 GFLLQMDYGFPPH 46

RESULT 7
; US-08-844-280-2
; Sequence 2, Application US/08844280
; Patent No. 5747315
; GENERAL INFORMATION:
; APPLICANT: Lawlor, Elizabeth
; TITLE OF INVENTION: No. 5747315el Compounds
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,280
; FILING DATE: 18-APR-1997
; CLASSIFICATION: ?
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9607993.4
```

```
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmil, Edward R.
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P31457-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 587 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-844-280-2
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```
Query Match          41.8%; Score 56; DB 1; Length 587;
Best Local Similarity 71.4%; Pred. No. 0.43;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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```
QY 3 GFLLLQMDFGFPEH 16
    |||  ||: |||  |
DB 510 GFLLEAMDYGFPFH 523
```

```
RESULT 8
US-09-006-726-2
; Sequence 2, Application US/09006726
; Patent No. 6210940
; GENERAL INFORMATION:
; APPLICANT: Lawlor, Elizabeth J.
; TITLE OF INVENTION: No. 6210940el compounds
; FILE REFERENCE: P31457-2-D1
; CURRENT APPLICATION NUMBER: US/09/006,726
; EARLIER FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 08/844,280
; EARLIER FILING DATE: 1997-04-18
; EARLIER APPLICATION NUMBER: UK9607993.4
; EARLIER FILING DATE: 1996-04-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 587
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; US-09-006-726-2
```

```
Query Match          41.8%; Score 56; DB 4; Length 587;
Best Local Similarity 71.4%; Pred. No. 0.43;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 3 GFLLLQMDFGFPEH 16
    |||  ||: |||  |
DB 510 GFLLEAMDYGFPFH 523
```

```
RESULT 9
US-09-118-442-6
; Sequence 6, Application US/09118442B
; Patent No. 6197561
; GENERAL INFORMATION:
; APPLICANT: Martino-Catt, Susan J.
; APPLICANT: Wang, Hongyu
; APPLICANT: Beach, Larry R.
; APPLICANT: Wang, Xun
; APPLICANT: Bowen, Benjamin A.
; TITLE OF INVENTION: Genes Controlling Phytate Metabolism in
; TYPE OF INVENTION: Plants and Uses Thereof
; FILE REFERENCE: 0706
```

```
; CURRENT APPLICATION NUMBER: US/09/118,442B
; CURRENT FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 60/055,446
; EARLIER FILING DATE: 1997-08-11
; EARLIER APPLICATION NUMBER: 60/055,526
; EARLIER FILING DATE: 1997-08-08
; EARLIER APPLICATION NUMBER: 60/053,944
; EARLIER FILING DATE: 1997-07-28
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Zea mays
; US-09-118-442-6
```

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Query Match          38.4%; Score 51.5; DB 4; Length 353;
Best Local Similarity 38.2%; Pred. No. 1.3;
Matches 13; Conservative 6; Mismatches 6; Indels 9; Gaps 2;
```

```
QY 1 RDGFLLLQMDFGFP-----EHLVDYFIQSLS 26
    || | : | : | | | : |||  ||:
DB 303 RDRFYVIDMNY-FPGYGRMPGVEHVFDFLLSLA 335
```

```
RESULT 10
US-09-677-064-6
; Sequence 6, Application US/09677064
; Patent No. 6291224
; GENERAL INFORMATION:
; APPLICANT: Martino-Catt, Susan J.
; APPLICANT: Wang, Hongyu
; APPLICANT: Beach, Larry R.
; TITLE OF INVENTION: Genes Controlling Phytate Metabolism in
; FILE REFERENCE: 0706D
; CURRENT APPLICATION NUMBER: US/09/677,064
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/055,446
; PRIOR FILING DATE: 1997-08-11
; PRIOR APPLICATION NUMBER: 60/055,526
; PRIOR FILING DATE: 1997-08-08
; PRIOR APPLICATION NUMBER: 60/053,944
; PRIOR FILING DATE: 1997-07-28
; PRIOR APPLICATION NUMBER: 09/118,442
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Zea mays
; US-09-677-064-6
```

```
Query Match          38.4%; Score 51.5; DB 4; Length 353;
Best Local Similarity 38.2%; Pred. No. 1.3;
Matches 13; Conservative 6; Mismatches 6; Indels 9; Gaps 2;
```

```
QY 1 RDGFLLLQMDFGFP-----EHLVDYFIQSLS 26
    || | : | : | | | : |||  ||:
DB 303 RDRFYVIDMNY-FPGYGRMPGVEHVFDFLLSLA 335
```

```
RESULT 11
US-08-050-132A-2
; Sequence 2, Application US/08050132A
; Patent No. 5661007
; GENERAL INFORMATION:
; APPLICANT: Wozney, John M.
; APPLICANT: Celeste, Anthony
; TITLE OF INVENTION: BMP-9 COMPOSITIONS
```



```

;
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: Legal Affairs - 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: US
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,132A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplanos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: GI 5186A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 428 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-050-132A-2

Query Match          33.2%; Score 44.5; DB 1; Length 428;
Best Local Similarity 48.0%; Pred. No. 21;
Matches 12; Conservative 5; Mismatches 5; Indels 3; Gaps 1;

OY      2 DGFLLQNDGFPEHLVDPLQSL 26
       : | | | | | : : | | | | | :
Db      49 EGVFDLQD---FLENMKVDPLRSLN 70

RESULT 12
US-08-750-222A-2
; Sequence 2, Application US/08750222A
; Patent No. 6034061
; GENERAL INFORMATION:
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wozney, John M.
; APPLICANT: Celeste, Anthony J.
; APPLICANT: Song, Jeffrey
; APPLICANT: Thies, Scott
; TITLE OF INVENTION: BMP-9 COMPOSITIONS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: Legal Affairs - 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: US
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,222A
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/254,353
; FILING DATE:

```

```

;
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplanos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: GI 5186B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 428 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-750-222A-2

Query Match          33.2%; Score 44.5; DB 3; Length 428;
Best Local Similarity 48.0%; Pred. No. 21;
Matches 12; Conservative 5; Mismatches 5; Indels 3; Gaps 1;

OY      2 DGFLLQNDGFPEHLVDPLQSL 26
       : | | | | | : : | | | | | :
Db      49 EGVFDLQD---FLENMKVDPLRSLN 70

```

```

RESULT 13
US-08-815-652B-2
; Sequence 2, Application US/08815652B
; Patent No. 6034062
; GENERAL INFORMATION:
; APPLICANT: Wozney, John M.
; APPLICANT: Celeste, Anthony
; APPLICANT: Song, Jeffrey
; APPLICANT: Thies, R. Scott
; TITLE OF INVENTION: BMP-9 COMPOSITIONS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: Legal Affairs - 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: US
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,652B
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplanos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: GI 5186D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 428 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-815-652B-2

Query Match          33.2%; Score 44.5; DB 3; Length 428;
Best Local Similarity 48.0%; Pred. No. 21;
Matches 12; Conservative 5; Mismatches 5; Indels 3; Gaps 1;

OY      2 DGFLLQNDGFPEHLVDPLQSL 26

```

DB 49 EGVFDLQW--FLENMKVDFLRSLN 70

RESULT 14

US-08-254-353A-2
Sequence 2, Application US/08254353A
Patent No. 6287816
GENERAL INFORMATION:
APPLICANT: Rosen, Vicki A.
APPLICANT: Wozney, John M.
APPLICANT: Celeste, Anthony J.
APPLICANT: Song, Jeffrey
APPLICANT: Ties, Scott
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: US
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/254,353A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 5186B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-254-353A-2

Query Match 33.2%; Score 44.5; DB 4; Length 428;

Best Local Similarity 48.0%; Pred. No. 21;
Matches 12; Conservative 5; Mismatches 5; Indels 3; Gaps 1;

QY 2 DGFLLQMDFGPPEHLVDFIQSLS 26
DB 49 EGVFDLQW--FLENMKVDFLRSLN 70

RESULT 15

PCT-US92-05374A-2
Sequence 2, Application PC/TUS9205374A
GENERAL INFORMATION:
APPLICANT: Wozney, John M.
APPLICANT: Celeste, Anthony
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: US
ZIP: 02140
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05374A
FILING DATE: 19920625
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 5186A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-05374A-2

Query Match 33.2%; Score 44.5; DB 5; Length 428;
Best Local Similarity 48.0%; Pred. No. 21;
Matches 12; Conservative 5; Mismatches 5; Indels 3; Gaps 1;

QY 2 DGFLLQMDFGPPEHLVDFIQSLS 26
DB 49 EGVFDLQW--FLENMKVDFLRSLN 70

Search completed: June 18, 2002, 08:06:56
Job time: 65 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:06:29 ; Search time 26.94 Seconds
(without alignments)
110.571 Million cell updates/sec

Title: US-09-943-334-2

Perfect score: 162

Sequence: 1 CQYKANSKFIGTREFGPEHLVDVFLQSLS 31

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing First 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	52.5	493	2 A53176	cholesteryl ester
2	85	52.5	493	2 A26841	cholesteryl ester
3	82	50.6	289	2 A38700	cholesteryl ester
4	81	50.0	497	2 I46692	cholesteryl ester
5	70	43.2	1315	1 BTCLTN	lentoxylisin (EC 3
6	56.5	34.9	458	2 T32634	hypothetical prote
7	54	33.3	310	2 D82199	conserved hypothet
8	52.5	32.4	1071	2 T51224	related to small s
9	52	32.1	348	2 AD0294	2-dehydro-3-deoxyp
10	52	32.1	386	2 T28176	hypothetical prote
11	51	31.5	215	2 H97154	sporulation factor
12	51	31.5	274	2 C83497	conserved hypothet
13	51	31.5	289	2 S74959	lipic acid synthet
14	51	31.5	348	1 ADECH	2-dehydro-3-deoxyp
15	51	31.5	348	2 C90930	hypothetical prote
16	51	31.5	348	2 G85778	hypothetical prote
17	51	31.5	348	2 AD0704	3-deoxy-D-arabinon
18	51	31.5	899	2 T42976	hypothetical prote
19	50	30.9	212	2 B71161	hypothetical prote
20	50	30.9	311	1 C64884	ydao protein - Esc
21	50	30.9	311	2 A85749	hypothetical prote
22	50	30.9	311	2 H90869	hypothetical prote
23	49.5	30.6	406	2 A71109	probable phosphate
24	49	30.2	233	2 C75002	chea histidine kin
25	49	30.2	233	2 T01867	hypothetical prote
26	49	30.2	252	2 T03873	photosystem II oxy
27	49	30.2	254	2 T02873	probable photosyst
28	48.5	29.9	810	2 JC4837	hypoxia-inducible
29	48.5	29.9	813	2 JC5809	hypoxia-inducible

30	48.5	29.9	826	2 I38972	hypoxia-inducible
31	48	29.6	213	2 AD2533	hypothetical prote
32	48	29.6	478	2 H90445	hypothetical prote
33	48	29.6	564	2 I64134	D-lactate dehydrog
34	47.5	29.3	252	2 C75007	competence-damage
35	47.5	29.3	395	2 T44512	hypothetical prote
36	47.5	29.3	1298	2 T18360	Os-1p - Neurospora
37	47	29.0	229	1 G64371	conserved hypothet
38	47	29.0	269	2 T15635	hypothetical prote
39	47	29.0	311	2 AC0653	conserved hypothet
40	47	29.0	348	2 I40070	2-dehydro-3-deoxyp
41	47	29.0	442	2 A71314	trigger factor lig
42	47	29.0	512	2 JC7599	cisplatin(CDDP) re
43	47	29.0	611	2 T28171	hypothetical prote
44	47	29.0	758	2 E81140	5-methyltetrahydro
45	47	29.0	1034	2 A95262	probable formate d

ALIGNMENTS

RESULT 1
A53176
cholesteryl ester transfer protein - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 07-May-1999
C:Accession: A53176
R:Pape, M.E.; Rehberg, E.F.; Marotti, K.R.; Melchior, G.W.
Arterioscler. Thromb. 11, 1759-1771, 1991
A:Title: Molecular cloning, sequence, and expression of cynomolgus monkey cholesteryl
asma high density lipoprotein levels.
A:Reference number: A53176; MUID:92031355
A:Accession: A53176
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-493 <PAP>
A:Cross-References: GB:M86343

Query Match 52.5%; Score 85; DB 2; Length 493;

Best Local Similarity 94.1%; Pred. No. 8.7e-05;

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 EFGFPEHLVDVFLQSLS 31

DB 477 DFGFPEHLVDVFLQSLS 493

RESULT 2

A26941
cholesteryl ester transfer protein precursor - human

C:Species: Homo sapiens (man)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 21-Jul-2000

C:Accession: A26941

R:Prayna, D.; Jarnagin, A.S.; McLean, J.; Henzel, W.; Kohr, W.; Fielding, C.; Lavin, R.

Nature 327, 632-634, 1987

A:Title: Cloning and sequencing of human cholesteryl ester transfer protein cDNA.

A:Reference number: A26941; MUID:87258172

A:Accession: A26941

A:Molecule type: mRNA

A:Residues: 1-493 <DRA>

A:Cross-References: EMBL:M30185; NID:g180259; PIDN:AAA51977.1; PID:g180260

C:Gene: GDB:CEPT

A:Gene: GDB:CEPT

A:Cross-References: GDB:119773; OMIM:118470

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-493/Product: cholesteryl ester transfer protein #status predicted <MAT>

Query Match 52.5%; Score 85; DB 2; Length 493;

Best Local Similarity 94.1%; Pred. No. 8.7e-05;

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 EFGFPHLVLDFLOSL 31
:|||||
Db 477 DFGFPHLVLDFLOSL 493

RESULT 3
A38700
cholesteryl ester transfer protein - golden hamster (fragment)
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 28-Feb-1992 #sequence_revision 10-Apr-1992 #text_change 05-Nov-1999
C:Accession: A38700
R:Jiang, X.C.; Moulin, P.; Quinet, E.; Goldberg, I.J.; Yacoub, L.R.; Agellon, L.B.; Comp
J. Biol. Chem. 266, 4631-4639, 1991
A>Title: Mammalian adipose tissue and muscle are major sources of lipid transfer protein
A:Reference number: A38700; MUID:91154277
A:Accession: A38700
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-289 <I>A>
A:Cross-references: GB:M63992; NID:g191342; PIDN:AAA37066.1; PID:g191343
A>Note: the authors translated the codon CTG for residue 68 as Gly, GCG for residue 69 as
as Ser, and TTC for residue 267 as Ser

Query Match 50.6%; Score 82; DB 2; Length 289;
Best Local Similarity 88.2%; Pred. No. 0.00014;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 15 EFGFPHLVLDFLOSL 31
:|||||
Db 273 DFGFPHLVLDFLOSL 289

RESULT 4
I46692
cholesteryl ester transfer protein - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 05-Nov-1999
C:Accession: I46692
R:Nagashima, M.; McLean, J.W.; Lawn, R.M.
J. Lipid Res. 29, 1643-1649, 1988
A>Title: Cloning and mRNA tissue distribution of rabbit cholesteryl ester transfer prote
A:Reference number: I46692; MUID:89215620
A:Accession: I46692
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-497 <NAG>
A:Cross-references: GB:M27486; NID:g530906; PIDN:AAA31199.1; PID:g530907
C:Genetics:
A:Gene: CETP

Query Match 50.0%; Score 81; DB 2; Length 497;
Best Local Similarity 88.2%; Pred. No. 0.00035;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 15 EFGFPHLVLDFLOSL 31
:|||||
Db 481 DFGFPHLVLDFLOSL 497

RESULT 5
BCTTN
tentoxylisin (EC 3.4.24.68) precursor - Clostridium tetani
M:Alternate names: tetanus neurotoxin
C:Species: Clostridium tetani
C>Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 18-Jun-1999
C:Accession: A25689; A25757; A25194; B25194; A60759; S69348; S09364
R:Eisel, U.; Jarausch, M.; Goretzki, K.; Henschen, A.; Engels, J.; Weller, U.; Hudel, M.
EMBO J. 5, 2495-2502, 1986
A>Title: Tetanus toxin: primary structure, expression in E. coli, and homology with both
A:Reference number: A25689; MUID:87053814

A:Accession: A25689
A:Molecule type: DNA
A:Residues: 1-1315 <EIS>
A:Cross-references: GB:X04436; NID:g40769; PIDN:CAA28033.1; PID:g40770
R:Fairweather, N.F.; Lyness, V.A.
Nucleic Acids Res. 14, 7809-7812, 1986
A>Title: The complete nucleotide sequence of tetanus toxin.
A:Reference number: A25757; MUID:87040747
A:Accession: A25757

A:Molecule type: DNA
A:Residues: 1-1315 <FA1>
A:Cross-references: GB:X06214; NID:g40773; PIDN:CAA29564.1; PID:g40774
A:Experimental source: strain CN3911
R:Fairweather, N.F.; Lyness, V.A.; Pickard, D.J.; Allen, G.; Thomson, R.O.
J. Bacteriol. 165, 21-27, 1986

A>Title: Cloning, nucleotide sequencing, and expression of tetanus toxin fragment C 1
A:Reference number: A25194; MUID:86085672
A:Accession: A25194

A:Molecule type: DNA
A:Residues: 743-1315 <FA2>
A:Cross-references: GB:M12739; NID:g144920; PIDN:AAA23282.1; PID:g144921

A:Molecule type: protein
A:Residues: 865-894 <FA3>
R:Matsuda, M.; Lei, D.L.; Sugimoto, N.; Ozutsumi, K.; Okabe, T.
Infect. Immun. 57, 3588-3593, 1989

A>Title: Isolation, purification, and characterization of fragment B, the NH-2-termin
A:Reference number: A60759; MUID:96035436
A:Accession: A60759

A:Molecule type: protein
A:Residues: 461-475 <MAT>
R:Demotz, S.; Lanzavecchia, L.; Eisel, U.; Niemann, H.; Widmann, C.; Corradin, G.
J. Immunol. 142, 394-402, 1989

A>Title: Delineation of several DR-restricted tetanus toxin T cell epitopes.
A:Reference number: JS0098; MUID:89093918
A:Accession: JS0098

A:Contents: annotation; epitope region
R:Schiavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; Dasgupta,
Nature 359, 832-835, 1992
A>Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteo
A:Reference number: S27125; MUID:93063293

A:Contents: annotation
R:de Filipis, V.; Vangelista, L.; Schiavo, G.; Tonello, F.; Montecucco, C.
Eur. J. Biochem. 229, 61-69, 1995

A>Title: Structural studies on the zinc-endopeptidase light chain of tetanus neurotox
A:Reference number: S69348; MUID:95262688
A:Accession: S69348

A:Molecule type: protein
A:Residues: 2-31 <DEF>

C:Comment: The source of this protein was an extrachromosomal plasmid.

C:Comment: The precursor is cleaved by endogenous proteinase activity to form light (dual chains are not toxic when separated). The amino end of the heavy chain (fragment C) forms ion channels in a lipid bilayer. Fragment C binds to ganglionic presynaptic neurons. It inhibits neurotransmitter release by proteolytic cleavage of

A:Description: blocks neuroexocytosis via hydrolysis of a Gln-Phe peptide bond in syn

C:Superfamily: tetanus toxin
C:Keywords: hydrolase; metalloproteinase; neurotoxin; transmembrane protein; zinc

F:2-457/Product: tentoxylisin light chain (fragment A) #status predicted <TRL>
F:461-1315/Product: tentoxylisin heavy chain (fragment B) #status experimental <TTH

F:461-864/Domain: channel forming (fragment B) #status predicted <TXB>
F:865-1315/Domain: ganglioside binding (fragment C) #status predicted <TXC>
F:233,237/Binding site: zinc (His) #status predicted
F:234/Active site: Glu #status predicted

Query Match 43.2%; Score 70; DB 1; Length 1315;
Best Local Similarity 100.0%; Pred. No. 0.047;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYIKANSKFIGITE 15
:|||||
Db 830 QYIKANSKFIGITE 843

A:Experimental source: isolate Tuscon
C:Genetics:
A:Note: MSV015

Query Match 32.1%; Score 52; DB 2; Length 386;
Best Local Similarity 55.0%; Pred. No. 6.5;
Matches 11; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

4 IKANSKFIGTFCGPEHL 23
|||:|:|:|:|:|:|:|:
Db 232 IKLNCFCGIDTFKEDLV 251

RESULT 11

H97154
sporulation factor spoIIM, uncharacterized membrane protein [Imported] - Clostridium ac
C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: H97154
R:Moiling, J.; Breton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: H97154
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-215 <KOR>
A:Cross-references: GB:AE001437; PIDN:AAK80027.1; PID:g15025055; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC2068

Query Match 31.5%; Score 51; DB 2; Length 215;
Best Local Similarity 40.9%; Pred. No. 4.8;
Matches 9; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

10 FIGITFCGPEHLVDFLOSL 31
|:|:|:|:|:|:|:|:|:
Db 87 FIGITMGIVLITLIDLKGS 108

RESULT 12

conserved hypothetical protein PA1192 [Imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: C83497
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapidig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A62950; MUID:20437337
A:Accession: C83497
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-274 <STO>
A:Cross-references: GB:AE004549; GB:AE004091; NID:g9947110; PIDN:AAQ04581.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA1192
C:superfamily: conserved hypothetical protein MJ1157

Query Match 31.5%; Score 51; DB 2; Length 274;
Best Local Similarity 57.1%; Pred. No. 6.3;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

17 GPEHLLVDFLOSL 30
|:|:|:|:|:|:|:|:|:

Db 76 GPEHVLPEYLKSI 89

RESULT 13

S74959
lipote acid synthetase (EC 2.8.1.-) 1 - Synechocystis sp. (strain PCC 6803)
N:Alternate names: protein slr1598
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S74959
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
s.
A:Reference number: S74322; MUID:97061201
A:Accession: S74959
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-289 <KAN>
A:Cross-references: EMBL:D90902; GB:AB001339; NID:g1652027; PIDN:BAAL6999.1; PID:g165
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
A:Pathway: lipote acid synthesis
C:Superfamily: lipote acid synthase
C:Keywords: lipote biosynthesis; sulfurtransferase

Query Match 31.5%; Score 51; DB 2; Length 289;
Best Local Similarity 31.6%; Pred. No. 6.7;
Matches 12; Conservative 7; Mismatches 11; Indels 8; Gaps 1;

2 QYIKANSKFIGTFCGPEHL-----LVDFLOSL 31
|:|:|:|:|:|:|:|:|:
Db 230 QYIOPSOHGLGKEFVPEQDFWRIYGESIGFLQVVS 267

RESULT 14

ADECH
2-dehydro-3-deoxyphosphohexonate aldolase (EC 4.1.2.15) (Trp-sensitive) - Escherich
N:Alternate names: 3-deoxy-D-arabino-hepulosonate-7-phosphate synthase; phospho-2-de
C:Species: Escherichia coli
C>Date: 22-May-1981 #sequence_revision 31-Oct-1997 #text_change 18-Jun-1999
C:Accession: H64928; J01131; A31384; A01107
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.T.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: H64928
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-348 <BIAT>
A:Cross-references: GB:AE000265; GB:U00096; NID:g2367122; PIDN:AACT4774.1; PID:g17879
A:Experimental source: strain K-12, substrain MG1655
R:Hudson, G.S.; Rellos, P.; Davidson, B.E.
Gene 102, 87-91, 1991
A:Title: Two promoters control the aroH gene of Escherichia coli.
A:Reference number: J01131; MUID:91323737
A:Accession: J01131
A:Molecule type: DNA
A:Residues: 1-332, 'S', '334-348 <HUD>
A:Cross-references: GB:M38266; NID:g145376; PIDN:AAA2497.1; PID:g145378
R:Ray, J.M.; Yanofsky, C.; Bauerle, R.
J. Bacteriol. 170, 5500-5506, 1988
A:Title: Mutational analysis of the catalytic and feedback sites of the tryptophan-se
A:Reference number: A31384; MUID:85053867
A:Accession: A31384

A:Molecule type: DNA
 A:Residues: 1-132,'A',124-202;204,'Q',206-332,'RQ',335-348 <RAY>
 A:Cross-references: GB:J04221
 R:Zurawski, G.; Gunsalus, R.P.; Brown, K.D.; Yanofsky, C.
 J. Mol. Biol. 145, 47-73, 1981
 A:title: Structure and regulation of *aroH*, the structural gene for the tryptophan-repress
 A:Reference number: A01107; MUID:81267314
 A:Accession: A01107
 A:Molecule type: DNA
 A:Residues: 1-36:231-332,'RQ',335-348 <ZUR>
 A:Cross-references: GB:J01592; GB:J01593
 C:Genetics:
 A:Gene: *aroH*
 A:Map position: 37 min
 C:Function:
 A:Description: aldehyde-lyase; carbon-carbon lyase; this is one of the DAHP synthases th
 ic acid-7-phosphate
 A:Pathway: aromatic amino acid biosynthesis; shikimate pathway
 A:Note: the first reaction in aromatic amino acid biosynthesis
 A:Note: feedback-inhibited by tryptophan; the other two DAHP synthases are tyrosine- and
 C:superfamily: phospho-2-dehydro-3-deoxyheptone aldolase
 C:Keywords: aldehyde-lyase; aromatic amino acid biosynthesis; carbon-carbon lyase; shik

Query Match 31.5%; Score 51; DB 1; Length 348;
 Best Local Similarity 75.0%; Pred. No. 8.2;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 15 EFGFPEHLVDF 26
 11 ||||:111
 Db 254 EFDLPPEHLVDF 265

RESULT 15
 C90930
 hypothetical protein Ecs2411 [Imported] - Escherichia coli (strain O157:H7, substrain RT
 C:Species: Escherichia coli
 C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
 C:Accession: C90930
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shida, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A:title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
 A:Reference number: A59629; MUID:21156231; PMID:11258796
 A:Accession: C90930
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-348 <HAY>
 A:Cross-references: GB:BA000007; PIDN:BA935834.1; PTD:q1361878; GSPDB:GN00154
 A:Experimental source: strain O157:H7, substrain RMD 0509952
 C:Genetics:
 A:Gene: Ecs2411
 C:Superfamily: phospho-2-dehydro-3-deoxyheptone aldolase

Query Match 31.5%; Score 51; DB 2; Length 348;
 Best Local Similarity 75.0%; Pred. No. 8.2;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 15 EFGFPEHLVDF 26
 11 ||||:111
 Db 254 EFDLPPEHLVDF 265

Search completed: June 18, 2002, 08:06:30
 Job time: 39 sec

10

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:13:08 ; Search time 13.5 Seconds
(without alignments)
88.912 Million cell updates/sec

Title: US-09-943-334-2
Sequence: 1 COYIKANSKFGITGFEFGPEHLVDPLQSLIS 31

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the total score distribution,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	52.5	493	1	CERP_HUMAN
2	85	52.5	493	1	CERP_MACRA
3	82	50.6	289	1	CERP_MESAU
4	81	50.0	497	1	CERP_RABIT
5	70	43.2	1314	1	TERX_CLOTE
6	52	32.1	313	1	YDAO_HAEIN
7	51	31.5	289	1	LIRL_SYNY3
8	51	31.5	348	1	AROH_ECOLI
9	50	30.9	311	1	YDAO_ECOLI
10	49.5	30.6	406	1	Y640_PYRHO
11	49	30.2	935	1	AD22_XENLA
12	48.5	29.9	822	1	HIFA_MOUSE
13	48.5	29.9	826	1	HIFA_HUMAN
14	48	29.6	204	1	PRRC_SERMA
15	48	29.6	564	1	LDHD_HAEIN
16	48	29.6	626	1	MP44_FOPV
17	48	29.6	911	1	MAN1_HUMAN
18	47.5	29.3	252	1	YD05_PYRAB
19	47	29.0	229	1	V575_METUA
20	47	29.0	348	1	AROH_BUCAP
21	47	29.0	442	1	TIG_TREPA
22	47	29.0	757	1	METE_PASMO
23	47	29.0	758	1	METE_NEIMB
24	46.5	28.7	394	1	GATR_MOUSE
25	46.5	28.7	591	1	MP44_VACCA
26	46.5	28.7	591	1	MP44_VACCC
27	46.5	28.7	591	1	MP44_VACCV
28	46.5	28.7	591	1	MP44_VARV
29	46.5	28.7	816	1	SUS3_ORYSA
30	46	28.4	314	1	HEMZ_CHLTR
31	46	28.4	516	1	LEP9_NPVAC
32	46	28.4	644	1	HM38_CAEEL
33	46	28.4	899	1	V120_HSVSA

34	45	27.8	348	1	AROH_BUCAI	P57224	buchnera ap
35	45	27.8	429	1	GDF2_HUMAN	Q9UK05	homo sapien
36	45	27.8	590	1	MP44_YLDV	G9dhr2	yaba-like d
37	45	27.8	648	1	KAPC_DICDI	P34099	dictyostell
38	45	27.8	756	1	METE_HAEIN	P45331	haemophilus
39	45	27.8	886	1	LEUR_YEAST	P08638	saccharomyc
40	44.5	27.5	376	1	V550_BUCAI	P57615	buchnera ap
41	44.5	27.5	640	1	UL35_HCMVA	P16766	human cytom
42	44	27.2	70	1	ESM6_DROME	O97179	drosoophila
43	44	27.2	478	1	Y4RH_RHISN	P55641	rhizobium s
44	44	27.2	870	1	PAS1_HUMAN	Q99814	homo sapien
45	44	27.2	874	1	PAS1_MOUSE	P97481	mus musculu

ALIGNMENTS

RESULT 1
ID CERP_HUMAN STANDARD: PRT: 493 AA.
AC P11597; 013987; 013988;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cholesteryl ester transfer protein precursor (Lipid transfer protein
DE I).
GN CERP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=87258172; PubMed=3600759.
RA Drayna D., Jarnequin A.S., McLean J., Henzel W., Kohr W., Fielding C.,
RA Lawn R.;
RT "Cloning and sequencing of human cholesteryl ester transfer protein
RT cDNA.";
RL Nature 327:632-634(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90241928; PubMed=2334701;
RA Agellon L.B., Quinet E.M., Gillette T.G., Drayna D.T., Brown M.L.,
RA Tall A.R.;
RT "Organization of the human cholesteryl ester transfer protein gene.";
RL Biochemistry 29:1372-1376(1990).
RN [3]
RP SEQUENCE OF 1-15 FROM N.A.
RX MEDLINE=97112972; PubMed=8943225;
RA Oliveira C.F.O., Chouinard R.A., Agellon L.B., Bruce C., Ma L.,
RA Walsh A., Breslow J.L., Tall A.R.;
RT "Human cholesteryl ester transfer protein gene proximal promoter
RT contains dietary cholesterol positive response elements and mediates
RT expression in small intestine and periphery while predominant liver
RT and spleen expression is controlled by 5'-distal sequences. Cis-acting
RT sequences mapped in transgenic mice.";
RL J. Biol. Chem. 271:31831-31838(1996).
RN [4]
RP SEQUENCE OF 1-27 FROM N.A.
RX MEDLINE=97473500; PubMed=9332354;
RA Williams S., Hayes L., Eisenboss L., Williams A., Andre C.,
RA Abramson R., Thompson J.F., Milos P.M.;
RT "Sequencing of the cholesteryl ester transfer protein 5' regulatory
RT region using artificial transposons.";
RL Gene 197:101-107(1997).
RN [5]
RP SEQUENCE OF 9-493 FROM N.A.
RX TISSUE=Liver;
RC Dinchuk J.E., Hart J.T., Mirak D.O.;
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
RN [6]
RP VARIANT GLY-459.
RX MEDLINE=94013514; PubMed=8408659;

RA Takahashi K., Jiang X.-C., Sakai N., Yamashita S., Hirano K., Bujo H.,
 RA Yamazaki H., Kusunoki J., Miura T., Kussie P., Matsuzawa Y., Saito Y.,
 RA Tani A.;
 RT "A missense mutation in the cholesterol ester transfer protein gene
 RT with possible dominant effects on plasma high density lipoproteins.",
 RL J. Clin. Invest. 92:2060-2064(1993).
 CC -1- FUNCTION: CETP IS AN EXTREMELY HYDROPHOBIC PROTEIN INVOLVED IN THE
 CC TRANSFER OF INSOLUBLE CHOLESTERYL ESTERS IN THE REVERSE TRANSPORT
 CC OF CHOLESTEROL.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED MAINLY IN THE LIVER.
 CC -1- DISEASE: PROBABLY INVOLVED IN THE DEVELOPMENT OF ATHEROSCLEROSIS.
 CC -1- SIMILARITY: BELONGS TO THE BPI/CETP/LBP/PLTP FAMILY.
 CC -----
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 CC -----
 DR EMBL: M30185; AAA51977.1; -;
 DR EMBL: M32998; AAA51978.1; -;
 DR EMBL: M32992; AAA51978.1; JOINED.
 DR EMBL: M32993; AAA51978.1; JOINED.
 DR EMBL: M32994; AAA51978.1; JOINED.
 DR EMBL: M32995; AAA51978.1; JOINED.
 DR EMBL: M32996; AAA51978.1; JOINED.
 DR EMBL: M32997; AAA51978.1; JOINED.
 DR EMBL: U71187; AAD14876.1; -;
 DR EMBL: AF027656; AAB8604.1; -;
 DR EMBL: M83573; AAB59388.1; -;
 DR PIR: A26941; A26941.
 DR MIM: 118470; -;
 DR InterPro: IPR001124; LBP_BPI_CETP.
 DR Pfam: PF01273; LBP_BPI_CETP.1.
 DR SMART: SM00328; BPI1.1.
 DR SMART: SM00329; BPI2.1.
 DR PROSITE: PS00400; LBP_BPI_CETP.1.
 DR Lipid transport; Cholesterol metabolism; glycoprotein; signal;
 KM Atherosclerosis; Disease mutation.
 FT SIGNAL 1 17
 FT CHAIN 18 493 CHOLESTERYL ESTER TRANSFER PROTEIN.
 FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 358 358 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 413 413 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 459 459 D -> G (IN CETP DEFICIENCY).
 FT CONFLICT 251 310 /FTID=VAR_004172.
 FT CONFLICT 422 422 MISSING (IN REF. 5).
 FT CONFLICT 422 422 I -> V (IN REF. 2).
 SQ SEQUENCE 493 AA; 54770 MW; 16DA7ACDC9B063C CRC64;
 OY 15 EFGFPEHLVDPLQSL 31
 Db 477 DFGFPEHLVDPLQSL 493
 Query Match 52.5%; Score 85; DB 1; Length 493;
 Best Local Similarity 94.1%; Pred. No. 2.9e-05;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
 CETP_MACFA
 ID CETP_MACFA STANDARD; PRT; 493 AA.
 AC P47896;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Cholesteryl ester transfer protein precursor (Lipid transfer protein

DE I).
 GN CETP.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92031355; PubMed=1931878;
 RA Pape M.E., Rehberg E.F., Marotti K.R., Melchior G.W.;
 RT "Molecular cloning, sequence, and expression of cynomolgus monkey
 RT cholesteryl ester transfer protein. Inverse correlation between
 RT hepatic cholesteryl ester transfer protein mRNA levels and plasma
 RT high density lipoprotein levels.";
 RL Arterioscler. Thromb. 11:1759-1771(1991).
 CC -1- FUNCTION: CETP IS AN EXTREMELY HYDROPHOBIC PROTEIN INVOLVED IN THE
 CC TRANSFER OF INSOLUBLE CHOLESTERYL ESTERS IN THE REVERSE TRANSPORT
 CC OF CHOLESTEROL.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED MAINLY IN THE LIVER.
 CC -1- SIMILARITY: BELONGS TO THE BPI/CETP/LBP/PLTP FAMILY.
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 CC -----
 DR EMBL: M86343; AAA36840.1; -;
 DR InterPro: IPR001124; LBP_BPI_CETP.
 DR Pfam: PF01273; LBP_BPI_CETP.1.
 DR SMART: SM00328; BPI1.1.
 DR SMART: SM00329; BPI2.1.
 DR PROSITE: PS00400; LBP_BPI_CETP.1.
 DR Lipid transport; Cholesterol metabolism; glycoprotein; signal;
 KM Lipid transport; Cholesterol metabolism; glycoprotein; signal;
 FT SIGNAL 1 17
 FT CHAIN 18 493 CHOLESTERYL ESTER TRANSFER PROTEIN.
 FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 358 358 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 413 413 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SEQUENCE 493 AA; 54743 MW; 7B82BE3C2A8FAEDD CRC64;

Query Match 52.5%; Score 85; DB 1; Length 493;
 Best Local Similarity 94.1%; Pred. No. 2.9e-05;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 15 EFGFPEHLVDPLQSL 31
 Db 477 DFGFPEHLVDPLQSL 493
 Query Match 52.5%; Score 85; DB 1; Length 493;
 Best Local Similarity 94.1%; Pred. No. 2.9e-05;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 RESULT 3
 CETP_MESAU
 ID CETP_MESAU STANDARD; PRT; 289 AA.
 AC P25914;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Cholesteryl ester transfer protein (Lipid transfer protein I)
 DE (Fragment).
 GN CETP.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus
 OX NCBI_TaxID=10036;

```
RM [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91154277; PubMed=1999438;
RA Jiang X.C., Moulin P., Guinet E., Goldberg I.J., Yacoub L.K.,
RA Agellon L.B., Compton D., Schmitzer-Polokoff R., Tall A.R.;
RT "Mammalian adipose tissue and muscle are major sources of lipid
RT transfer protein mRNA."
RL J. Biol. Chem. 266:4631-4639(1991).
CC -1- FUNCTION: CETP IS AN EXTREMELY HYDROPHOBIC PROTEIN INVOLVED IN THE
CC TRANSFER OF INSOLUBLE CHOLESTERYL ESTERS IN THE REVERSE TRANSPORT
CC OF CHOLESTEROL.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- SIMILARITY: BELONGS TO THE BPI/CETP/LBP/PLTP FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: M63992; AAA37066.1; -.
CC PIR: A38700; A38700.
CC InterPro: IPR001124; LBP_BPI_CETP.
CC Pfam: PF01273; LBP_BPI_CETP; 1.
CC SMART: SM00329; BPI2; 1.
CC PROSITE: PS00400; LBP_BPI_CETP; PARTIAL.
CC Lipid transport; Cholesterol metabolism; Glycoprotein.
CC NON_TER 1 1
CC CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 269 AA; 32330 MW; CA91A06D83927747 CRC64;
SO

Query Match 50.6%; Score 82; DB 1; Length 389;
Best Local Similarity 88.2%; Pred. No. 4.7e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 15 EFGPEHLVDFLOSLS 31
DB 273 DFGPEHLVDFLOSLS 289

RESULT 4
CETP_RABIT STANDARD; PRT; 497 AA.
AC P22687;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cholesteryl ester transfer protein precursor (lipid transfer protein
DE I) (fragment).
GN CETP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89215620; PubMed=3244015;
RA Nagashima M., McLean J.W., Lavin R.M.;
RT "Cloning and mRNA tissue distribution of rabbit cholesteryl ester
RT transfer protein."
RL J. Lipid Res. 29:1643-1649(1988).
CC -1- FUNCTION: CETP IS AN EXTREMELY HYDROPHOBIC PROTEIN INVOLVED IN THE
CC TRANSFER OF INSOLUBLE CHOLESTERYL ESTERS IN THE REVERSE TRANSPORT
CC OF CHOLESTEROL.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED MAINLY IN THE LIVER.
CC -1- SIMILARITY: BELONGS TO THE BPI/CETP/LBP/PLTP FAMILY.
CC -----
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CC -----
CC EMBL: M27486; AAA31199.1; -.
CC InterPro: IPR001124; LBP_BPI_CETP.
CC Pfam: PF01273; LBP_BPI_CETP; 1.
CC SMART: SM00328; BPI1; 1.
CC SMART: SM00329; BPI2; 1.
CC PROSITE: PS00400; LBP_BPI_CETP; 1.
CC Lipid transport; Cholesterol metabolism; Glycoprotein; Signal.
CC NON_TER 1 1
CC SIGNAL <1 1
CC CHAIN 2 497
CC CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 417 417 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 497 AA; 54513 MW; E82944E1821D0332 CRC64;
SO

Query Match 50.0%; Score 81; DB 1; Length 497;
Best Local Similarity 88.2%; Pred. No. 0.00012;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 15 EFGPEHLVDFLOSLS 31
DB 481 DFGPEHLVDFLOSLS 497

RESULT 5
TETX_CLOTE STANDARD; PRT; 1314 AA.
AC P04958;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Tetanus toxin precursor (EC 3.4.24.68) (Tentoxylisin).
DE Clostridium tetani.
OS Clostridium.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1513;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87053814; PubMed=3536478;
RA Eisel U., Jarasch W., Goretzki K., Henschen A., Engels J.,
RA Weller U., Hudel M., Habermann E., Niemann H.;
RT "Tetanus toxin: primary structure, expression in E. coli, and
RT homology with botulinum toxins."
RL EMBO J. 5:2495-2502(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CN3911;
RX MEDLINE=87040747; PubMed=3774547;
RA Fairweather N.F., Lyness V.A.;
RT "The complete nucleotide sequence of tetanus toxin."
RL Nucleic Acids Res. 14:7809-7812(1986).
RN [3]
RP SEQUENCE OF 742-1314 FROM N.A.
RX MEDLINE=8608672; PubMed=3510187;
RA Fairweather N.F., Lyness V.A., Pickard D.J., Allen G., Thomson R.O.;
RT "Cloning, nucleotide sequencing, and expression of tetanus toxin
RT fragment C in Escherichia coli."
RL J. Bacteriol. 165:21-27(1986).
RN [4]
```

RP PARTIAL SEQUENCE, AND DISULFIDE BONDS.
 RX MEDLINE=90201034; PubMed=2108021;
 RA Kriegstein K., Henschen A., Weller U., Habermann E.;
 RT "Arrangement of disulfide bridges and positions of sulfhydryl groups
 in tetanus toxin.";
 RL Eur. J. Biochem. 188:39-45(1990).
 RN (5)
 RP PARTIAL SEQUENCE.
 RX MEDLINE=92037649; PubMed=1935979;
 RA Kriegstein K.G., Henschen A.H., Weller U., Habermann E.;
 RT "Limited proteolysis of tetanus toxin. Relation to activity and
 identification of cleavage sites.";
 RL Eur. J. Biochem. 202:41-51(1991).
 RN (6)
 RP IDENTIFICATION AS ZINC-PROTEASE.
 RX MEDLINE=93010948; PubMed=1396558;
 RA Schiavo G., Poulain B., Rossetto O., Benfenati F., Tauc L.,
 RT Montecucco C.;
 RT "Tetanus toxin is a zinc protein and its inhibition of
 neurotransmitter release and protease activity depend on zinc.";
 RL EMBO J. 11:3577-3583(1992).
 RN (7)
 RP IDENTIFICATION OF SUBSTRATE.
 RX MEDLINE=93063293; PubMed=1331807;
 RA Schiavo G., Benfenati F., Poulain B., Rossetto O., de Laureto P.P.,
 RT Dasgupta B.R., Montecucco C.;
 RT "Tetanus and botulinum-B neurotoxins block neurotransmitter release
 by proteolytic cleavage of synaptobrevin.";
 RL Nature 359:832-835(1992).
 RN (8)
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 874-1314.
 RX MEDLINE=97475217; PubMed=9334741;
 RA Umland T.C., Wingerl L.M., Swaminathan S., Furey W.F., Schmidt J.J.,
 RA Sax M.;
 RT "Structure of the receptor binding fragment HC of tetanus
 neurotoxin.";
 RL Nat. Struct. Biol. 4:788-792(1997).
 CC -1- FUNCTION: TETANUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
 RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
 AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
 WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
 INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
 ENDOPEPTIDASE THAT CATALYZES THE HYDROLYSIS OF THE 76-GLN-1-PHE-77
 BOND OF SYNAPTOBREVIN-2.
 CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF 76-GLN-1-PHE-77 BOND IN
 SYNAPTOBREVIN.
 CC -1- SUBUNIT: THE PRECURSOR POLYPEPTIDE IS SUBSEQUENTLY CLEAVED TO
 YIELD SUBUNITS L AND H. THESE REMAIN LINKED BY A DISULFIDE BRIDGE
 AND ARE NON-TOXIC AFTER SEPARATION.
 CC -1- MISCELLANEOUS: THE C-TERMINAL OF THE HEAVY CHAIN BINDS TO
 GANGLIOSIDE RECEPTORS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27.
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 CC -----
 DR EMBL: X04436; CAA28033.1; -
 DR EMBL: M12739; AAA23282.1; -
 DR EMBL: X06214; CAA29564.1; -
 DR PIR: A25689; B7CLTN.
 DR PDB: 1AE9; 29-APR-98.
 DR PDB: 1ABD; 14-OCT-98.
 DR MEROPS: M27.001; -
 DR InterPro: IPR000395; Bontoxilysin.
 DR InterPro: IPR000130; Zn_MTPeptide.
 DR Pfam: PF01142; Peptidase_M27; 1.
 DR PRINTS: PR00760; BONTOXILYSIN.
 DR ProDom: PD001963; Bontoxilysin; 1.

DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 KW Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc; Plasmid;
 KM 3D-structure.
 FT INIT_MET 0 0
 FT CHAIN 1 456 TETANUS TOXIN LIGHT CHAIN.
 FT METAL 457 1314 TETANUS TOXIN HEAVY CHAIN.
 FT METAL 232 232 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT_SITE 233 233 BY SIMILARITY.
 FT METAL 236 236 ZINC (CATALYTIC) (BY SIMILARITY).
 FT TRANSMEM 226 246 POTENTIAL.
 FT TRANSMEM 669 689 POTENTIAL.
 FT DISULFID 438 466 INTERCHAIN.
 FT DISULFID 1076 1092
 SQ SEQUENCE 1314 AA; 150550 MW; 134C3657133EF81D CRC64;
 QY Query Match 43.2%; Score 70; DB 1; Length 1314;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 829 OYKANSKFIGITE 842
 OY 2 OYKANSKFIGITE 15
 DB |||||||||||||
 RESULT 6
 YDAA_HAEIN
 ID YDAA_HAEIN STANDARD; PRT: 313 AA.
 AC Q57184; Q05059;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein H1371.1.
 GN H1371.1.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 CC Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RD / KW20 / ATCC 51907.
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischiemann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Uutterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus
 influenzae Rd.";
 RL Science 269:496-512(1995).
 RN [2]
 RP REVISIONS.
 RA White O., Clayton R.A., Kerlavage A.R., Fleischiemann R.D.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: STRONG, TO E.COLI YDAA.
 CC -----
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 CC -----
 DR EMBL: U32817; AAC23019.1; -
 DR TIGR: H1371.1; -
 DR InterPro: IPR000541; UPF0021.
 DR Pfam: PF01171; UPF0021; 1.
 KW Hypothetical protein; Complete proteome.

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DR EMBL; M38266; AAA23497.1; -
 DR EMBL; J04221; AAA23493.1; -
 DR EMBL; AE000265; AAC74774.1; -
 DR EMBL; D90813; BAA15473.1; -
 DR EMBL; V00261; CAA23510.1; -
 DR EMBL; X04373; CAA27956.1; -
 DR PIR; J01131; ADECH.
 DR HSSP; P00886; IQR7.
 DR EcoGene; EG10080; arOH.
 DR InterPro; IPR001785; DAHP_synth_1.
 DR Pfam; PF00793; DAHP_synth_1; 1.
 DR ProDom; PD005060; DAHP_synth_1; 1.
 KW Aromatic amino acid biosynthesis; Lyase; Complete proteome.
 FT CONFLICT 123 123 E -> G (IN REF. 2).
 FT CONFLICT 203 205 RAS -> AQ (IN REF. 2).
 FT CONFLICT 333 333 S -> T (IN REF. 3 AND 4).
 FT CONFLICT 333 334 SE -> RO (IN REF. 2 AND 5).
 SQ SEQUENCE 348 AA; 38721 MW; F293C482447226E6 CRC64;

Query Match 31.5%; Score 51; DB 1; Length 348;
 Best Local Similarity 75.0%; Pred. No. 2.9;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 15 EFGPEHLVDF 26
 II IIII:II
 DB 254 EFDLPEHLVDF 265

RESULT 9
 YDAO_ECOLI STANDARD; PRT; 311 AA.
 AC P76055; Q47558;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein ydao.
 GN YDAO OR B1344.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE-97426617; PubMed-9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12."
 RL Science 277:1453-1474(1997).
 RN 12
 RP SEQUENCE OF 1-40 FROM N.A.
 RC STRAIN-K12 / W3110;
 RX MEDLINE-94162733; PubMed-7764507;
 RA Yamada M., Yanai S., Talkader A.;
 RT "Analysis of products of the Escherichia coli genomic genes and
 RT regulation of their expressions: an applicable procedure for genomic
 RT analysis of other microorganisms."
 RL Biosci. Biotechnol. Biochem. 58:117-120(1994).
 CC -1- SIMILARITY: STRONG, TO H.INFLUENZAE H1171.1.
 CC -----
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DR EMBL; AE000232; AAC74426.1; -
 DR EMBL; D21139; BAA04675.1; -
 DR EcoGene; EG13357; ydao.
 DR InterPro; IPR000541; uPF0021.
 DR Pfam; PF01171; uPF0021; 1.
 KW Hypothetical protein; Complete proteome.
 FT CONFLICT 11 11 E -> A (IN REF. 2).
 SQ SEQUENCE 311 AA; 35561 MW; D696057B/C092D79 CRC64;

Query Match 30.9%; Score 50; DB 1; Length 311;
 Best Local Similarity 57.1%; Pred. No. 3.7;
 Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 17 GPEHLVDFLOSL 30
 IIII:II ::I
 DB 83 GPEHLVDFLEKL 96

RESULT 10
 Y640_PYRHO STANDARD; PRT; 406 AA.
 AC O58374;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Putative phosphate permease PH0640.
 GN PH0640.
 OS Pyrococcus horikoshii.
 OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
 OX NCBI_TaxID=53953;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-OT3;
 RX MEDLINE-98344137; PubMed-9679194;
 RA Kawarabayashi Y., Sawada M., Horikawa H., Haino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamaya M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushiida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-
 RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3."
 RL DNA Res. 5:55-76(1998).
 CC -1- FUNCTION: POTENTIAL TRANSPORTER FOR PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: BELONGS TO THE PHO-4 FAMILY OF TRANSPORTERS.
 CC -----
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DR EMBL; AP000003; BAA29731.1; -
 DR InterPro; IPR001204; PHO4.
 DR Pfam; PF01384; PHO4; 1.
 KW Hypothetical protein; Phosphate transport; Transport; Transmembrane;
 CC Complete proteome.
 FT TRANSMEM 2 22 POTENTIAL.
 FT TRANSMEM 45 65 POTENTIAL.
 FT TRANSMEM 83 103 POTENTIAL.
 FT TRANSMEM 114 134 POTENTIAL.
 FT TRANSMEM 140 160 POTENTIAL.
 FT TRANSMEM 182 202 POTENTIAL.
 FT TRANSMEM 207 227 POTENTIAL.
 FT TRANSMEM 265 285 POTENTIAL.

FT	TRANSMEM	288	308	POTENTIAL.
FT <td>TRANSMEM</td> <td>330</td> <td>350</td> <td>POTENTIAL.</td>	TRANSMEM	330	350	POTENTIAL.
FT <td>TRANSMEM</td> <td>385</td> <td>405</td> <td>POTENTIAL.</td>	TRANSMEM	385	405	POTENTIAL.
SD <td>SEQUENCE</td> <td>406 AA;</td> <td>42928 MW;</td> <td>6F413000DDF83FC6 CRC64</td>	SEQUENCE	406 AA;	42928 MW;	6F413000DDF83FC6 CRC64

	Query Match	30.6%	Score 49.5;	DB 1;	Length 406;
	Best Local Similarity	35.5%	Pred. No. 5.8;		
Matches	11; Conservative	8;	Mismatches	9;	Gaps 1
Qy	3 YIK---ANSKFGITGFCEPHHLADFDQSL 30				
	: : : :				
Db	196 YIKVLGSSLYLISILNKGITGITFIITSM 226				

RESULT	11
ID	AD22_XENLA
STANDARD:	PRT: 935 MA.
AC	0425256:
DT	16-OCT-2001 (rel. 40, Created)
DT	16-OCT-2001 (rel. 40, Last sequence update)
DT	16-OCT-2001 (rel. 40, Last annotation update)
DT	ADAM 22 precursor (A disintegrin and metalloproteinase domain 22)
DE	(Metalloproteinase-disintegrin MDC11b).
OS	ADAM22 OR MDC11b.
OS	Xenopus laevis (African clawed frog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; P.pidae;
OC	Xenopodinae; Xenopus.
OX	NCBI_TaxID=8355;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Testis;
RC	MEDLINE=99102794; PubMed=9882486;
RX	Cal H., Kretzschmar J., Alfandari D., Hunnicutt G., Biobel C.P.;
RA	"Neutral creet-specific and general expression of distinct
RT	metalloproteinase-disintegrins in early Xenopus laevis development.";
RT	Dev. Biol. 204:508-524(1998).
RL	[2]
RN	SEQUENCE OF 464-511 FROM N.A.
RC	TISSUE=Testis;
RX	MEDLINE=97349132; PubMed=9205136;
RA	Shilling F.M., Kretzschmar J., Cal H., Weiskamp G., Gayko U.,
RA	Laibow J., Myles D.G., Nuccitelli R., Biobel C.P.;
RT	"Identification of metalloproteinase/disintegrins in Xenopus laevis
RT	testis with a potential role in fertilization.";
RT	Dev. Biol. 186:155-164(1997).
CC	-1- FUNCTION: PROBABLE LIGAND FOR INTEGRIN IN THE BRAIN. THIS IS A NON
CC	CATALYTIC METALLOPROTEASE-LIKE PROTEIN (BY SIMILARITY).
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.
CC	-1- TISSUE SPECIFICITY: LOW LEVELS IN ADULT TISSUES. NOT DETECTED IN
CC	DEVELOPING EMBRYOS.
CC	-1- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
CC	SIMILARITY).
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
CC	-1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC	-1- SIMILARITY: CONTAINS 1 DISINTEGRIN DOMAIN.
CC	-----
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CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; AF032383; AAC61847.1; -
DR	HSSP; 078188; AAB87148.1; -
DR	Interpro: IPR001762; Disintegrin.
DR	Interpro: IPR000561; EGF-like.
DR	Interpro: IPR002870; Pep_M12B-Propep.
DR	Interpro: IPR001530; RepPolysin.

DR	InterPro:	IPR000130; Zn_MPeptidse.
DR	pfam:	PF00200; disintegrin_1.
DR	pfam:	PF01562; pep_M12B-propep_1.
DR	pfam:	PF01421; Reprolysin_1.
DR	PRINTS:	PR00289; DISINTEGRIN.
DR	ProDom:	PDO00664; Disintegrin_1.
DR	SMART:	SMO0050; DIsInt_1.
DR	SMART:	SMO0181; EGF_1.
DR	PROSITE:	PS50215; ADAM_MEPRO; 1.
DR	PROSITE:	PS00427; DISINTEGRIN_1; 1.
DR	PROSITE:	PS50214; DISINTEGRIN_2; 1.
DR	PROSITE:	PS00022; EGF_1; 1.
DR	PROSITE:	PS01186; EGF_2; FALSE_NEG.
DR	PROSITE:	PS00142; ZINC_PROTEASE; FALSE_NEG.
KM	Signal:	Glycoprotein; Transmembrane; EGF-like domain. POTENTIAL. 24 BY SIMILARITY.
FT	PROPEP	1 25 227
FT	CHAIN	228 935
FT	DOMAIN	228 736
FT	TRANSMEM	737 757
FT	DOMAIN	758 935
FT	DOMAIN	228 440
FT	DOMAIN	446 533
FT	DOMAIN	536 670
FT	DOMAIN	677 713
FT	DISULFID	351 435
FT	DISULFID	505 518
FT	DISULFID	681 695
FT	DISULFID	689 701
FT	DISULFID	703 712
FT	CARBOHYD	167 167
FT	CARBOHYD	210 210
FT	CARBOHYD	521 521
FT	CARBOHYD	609 609
FT	CARBOHYD	636 636
FT	CARBOHYD	677 677
QO	SEQUENCE	935 AA; 104161 MW; 77B7AFDC5C77C90 CRC64;

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Query Match          30.2%; Score 49; DB 1; Length 935;
Best Local Similarity 35.5%; Pred. NO. 17;
Matches    11; Conservative      5; Mismatches   11; Indels     4; Gaps     1.

OY      1 CQYKANSKFTCTTGFPGFPHLLVDFDLSLS 31
           | :| :||| |:| :| ||| :
DB      351 CSLKCG---GVNEFGKPDMVAVTLAQSLA 377

RESULT 12
HIFA_MOUSE STANDARD: PRT: 822 AA.
ID HIFA_MOUSE AC O61623: O61665; O61664; O08993; O08741;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (ARNT interacting protein).
DE
DE
GN HIFA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;

RM [1]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6; TISSUE=Hepatocytes;
RC MEDLINE=96355491; PubMed=8702901;
RX L.I.H., Ko H.P., Whitlock J.P., Jr.;
RA "Induction of phosphoglycerate kinase 1 gene expression by hypoxia.
RT Roles of Arnt and Hiralpha."
RL J Biol. Chem. 271:21262-21267(1996).
RN [2]
SEQUENCE FROM N.A.
RP STRAIN=129/SVJ;
RC
```

RX MEDLINE=98034461; PubMed=9368100;
 RA Luo G., Gu Y.-Z., Jain S., Chan W.K., Carr K.M., Hogenesch J.B.,
 RA Bradford C.A.;
 RT "Molecular characterization of the murine Hif-1 alpha locus.";
 RL Gene Expr. 6:287-299(1997).
 RM [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE=97354184; PubMed=9210478;
 RA Wenger R.H., Rolfs A., Kvietikova I., Spielmann P., Zimmermann D.R.,
 RA Gassmann M.;
 RT "The mouse gene for hypoxia-inducible factor-1alpha. Genomic
 RT organization, expression and characterization of an alternative first
 RT exon and 5' flanking sequence.";
 RL Eur. J. Biochem. 246:155-165(1997).
 RM [4]
 RP SEQUENCE OF 13-822 FROM N.A.
 RC TISSUE=Hepatocytes;
 RX MEDLINE=96254028; PubMed=8660378;
 RA Wenger R.H., Rolfs A., Marti H.H., Guenet J.-L., Gassmann M.;
 RT "Nucleotide sequence, chromosomal assignment and mRNA expression of
 RT mouse hypoxia-inducible factor-1 alpha.";
 RL Biochem. Biophys. Res. Commun. 223:54-59(1996).
 RM [5]
 RP SEQUENCE OF 22-85 FROM N.A.
 RC TISSUE=Hepatocytes;
 RA O'Rourke J.F.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1 FUNCTION: INVOLVED IN THE INDUCTION OF OXYGEN REGULATED GENES.
 CC SPECIFICALLY RECOGNIZES AN 8 BP HYPOXIA RESPONSE ELEMENT (HRE).
 CC -1 SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
 CC BHLH PROTEIN. HETERODIMER OF AN ALPHA AND A BETA (ARNT) SUBUNITS.
 CC THE ALPHA SUBUNIT IS UNIQUE TO HIF-1 WHEREAS HIF-1 BETA (ARNT) CAN
 CC DIMERIZE WITH OTHER BHLH-PAS PROTEINS. INTERACTS WITH HSP90 (BY
 CC SIMILARITY).
 CC -1 SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -1 TISSUE SPECIFICITY: Ubiquitous.
 CC -1 DOMAIN: BOTH HYPOXIA RESPONSIVENESS AND TRANSACTIVATION CAPABILITY
 CC RESIDE WITHIN THE C-TERMINAL PART.
 CC -1 PTM: REQUIRES PHOSPHORYLATION FOR DNA-BINDING.
 CC -1 SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
 CC TRANSCRIPTION FACTORS.
 CC -1 SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
 CC -1 SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
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 CC -----
 DR EMBL: U59496; AAC52730.1; -
 DR EMBL: AF003695; AAC53455.1; -
 DR EMBL: Y09085; CAAT0306.1; -
 DR EMBL: Y13656; CAAT0306.1; JOINED.
 DR EMBL: Y09085; CAAT0305.1; -
 DR EMBL: AF004155; AAC53461.1; -
 DR EMBL: AF004141; AAC53461.1; JOINED.
 DR EMBL: AF004142; AAC53461.1; JOINED.
 DR EMBL: AF004143; AAC53461.1; JOINED.
 DR EMBL: AF004144; AAC53461.1; JOINED.
 DR EMBL: AF004145; AAC53461.1; JOINED.
 DR EMBL: AF004146; AAC53461.1; JOINED.
 DR EMBL: AF004147; AAC53461.1; JOINED.
 DR EMBL: AF004148; AAC53461.1; JOINED.
 DR EMBL: AF004149; AAC53461.1; JOINED.
 DR EMBL: AF004150; AAC53461.1; JOINED.
 DR EMBL: AF004151; AAC53461.1; JOINED.
 DR EMBL: AF004152; AAC53461.1; JOINED.
 DR EMBL: AF004153; AAC53461.1; JOINED.
 DR EMBL: AF004154; AAC53461.1; JOINED.

DR EMBL: X95580; CAA64833.1; -
 DR EMBL: X95002; CAA64458.1; -
 DR MGd; MGd:106918; Hlfla.
 DR InterPro: IPR003015; HLH_MyC.
 DR InterPro: IPR001092; HLH_dlm.
 DR InterPro: IPR001321; HypoxIndf1a.
 DR InterPro: IPR001610; PAC.
 DR InterPro: IPR000014; PAS.
 DR Pfam: PF00785; PAC; 1.
 DR Pfam: PF00989; PAS; 2.
 DR PRINTS: PRO1080; HYPOXIAFLA.
 DR SMART: SM00353; HLH; 1.
 DR SMART: SM00086; PAC; 1.
 DR SMART: SM00091; PAS; 2.
 DR PROSITE: PS00038; HELIX_LOOP_HELIX; 1.
 DR PROSITE: PS0112; PAS; 2.
 KW Repeat; DNA-binding; Nuclear protein; Transcription regulation;
 KW Activator; Phosphorylation.
 FT DNA_BIND 17
 FT DOMAIN 31 71
 FT DOMAIN 80 155
 FT DOMAIN 228 298
 FT DOMAIN 302 345
 FT CONFLICT 31 31
 FT CONFLICT 128 128
 FT CONFLICT 351 351
 FT CONFLICT 511 511
 FT CONFLICT 686 686
 FT CONFLICT 785 785
 SQ SEQUENCE 822 AA; 91858 MW; E717ADCE4CA9D795 CRC64;
 Query Match 29.9%; Score 48.5; DB 1; Length 822;
 Best Local Similarity 40.0%; Pred. No. 17;
 Matches 10; Conservative 6; Mismatches 8; Indels 1; Gaps 1;
 Oy 3 YKAN-SKFIGITFGFPHLVDF 26
 Db 111 YISDNVNMGLTQPELAGHSVDF 135
 RESULT 13
 Hlfla_HUMAN
 ID Hlfla_HUMAN STANDARD; PRT; 826 AA.
 AC Q1665;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (ARNT interacting
 DE protein) (Member of PAS protein 1) (MOB1) (Hlfl alpha).
 GN Hlfla.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 166-170; 259-289 AND 771-781.
 RX MEDLINE=95296340; PubMed=7539918;
 RA Wang G.-L., Jiang B.-H., Rue R.A., Semenza G.L.;
 RT "Hypoxia-inducible factor 1 is a basic-helix-loop-helix-PAS
 RT heterodimer regulated by cellular O2 tension.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:5510-5514(1995).
 RM [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hepatoma;
 RX Hogenesch J.B., Chan W.K., Jackiw V.H., Brown R.C., Gu Y.-Z.,
 RA Pray-Grant M., Perdev G.H., Bradford C.A.;
 RT "Characterization of a subset of the basic-helix-loop-helix-PAS
 RT superfamily that interacts with components of the dioxin signaling
 RT pathway.";
 RL J. Biol. Chem. 272:8581-8593(1997).
 RM [3]

RP SEQUENCE FROM N.A.
 RA Roper J.L., Hochachka P.W.;
 RT "H1f1a sequence in the Quechua, a high altitude population.";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INVOLVED IN THE INDUCTION OF OXYGEN REGULATED GENES.
 CC -1- SPECIFICALLY RECOGNIZES AN 8 BP HYPOXIA RESPONSE ELEMENT (HRE).
 CC -1- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
 CC BHLH PROTEIN. HETEROIMER OF AN ALPHA AND A BETA (ARNT) SUBUNITS.
 CC THE ALPHA SUBUNIT IS UNIQUE TO HIF-1 WHEREAS HIF-1 BETA (ARNT) CAN
 CC DIMERIZE WITH OTHER BHLH-PAS PROTEINS. INTERACTS WITH HSP90.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. HIGHEST LEVELS IN
 CC KIDNEY AND HEART.
 CC -1- INDUCTION: UNDER REDUCED OXYGEN TENSION.
 CC -1- DOMAIN: BOTH HYPOXIA RESPONSIVENESS AND TRANSACTIVATION CAPABILITY
 CC RESIDE WITHIN THE C-TERMINAL PART.
 CC -1- PFM: REQUIRES PHOSPHORYLATION FOR DNA-BINDING.
 CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
 CC TRANSCRIPTION FACTORS.
 CC -1- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
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 CC -----
 CC EMBL: U22431; AAC50152.1; -
 CC EMBL: U29165; AAC51210.1; -
 CC EMBL: AF207602; AAF20139.1; -
 CC EMBL: AF207602; AAF20140.1; -
 CC EMBL: AF208487; AAF20149.1; -
 CC TRANSFAC: T01610; -
 CC MIM: 603348; -
 CC InterPro: IPR003015; HLH_Myc.
 CC InterPro: IPR001092; HLH_dlm.
 CC InterPro: IPR001321; HypoxIndefLA.
 CC InterPro: IPR001610; PAC.
 CC InterPro: IPR000014; PAS.
 CC Pfam: PF00785; PAC; 1.
 CC Pfam: PF00988; PAS; 2.
 CC PRINTS: PR01080; HYPOXIAFLA.
 CC SMART: SM00353; HLH; 1.
 CC SMART: SM00086; PAC; 1.
 CC SMART: SM00091; PAS; 2.
 CC PROSITE: PS00038; HELIX_LOOP_HELIX; 1.
 CC PROSITE: PS50113; PAS; 2.
 CC Repeat: DNA-binding; Nuclear protein; Transcription regulation;
 CC Activator; Phosphorylation.
 CC FT DNABIND 17 30 BASIC DOMAIN.
 CC FT DOMAIN 31 71 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
 CC FT DOMAIN 85 158 PAS 1.
 CC FT DOMAIN 228 298 PAS 2.
 CC FT DOMAIN 302 345 PAC.
 CC FT DOMAIN 615 621 POLY-THR.
 CC SEQUENCE 826 AA; 92670 MW; ABD4F7DA135BE2D CRC64;

Query Match 29.9%; Score 48.5; DB 1; Length 826;
 Best Local Similarity 40.0%; Pred. No. 17;
 Matches 10; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

OY 3 YIKAN-SKFIGITGEPFPHLLVP 26
 DB 111 YISDNVKNYKGLTQPELTGHSVDF 135

RESULT 14
 PYRC_SERMA STANDARD: PRT; 204 AA.

AC Q953SI;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Dihydroorotase (EC 3.5.2.3) (DHOase) (Fragment).
 GN PYRC.
 OS Serratia marcescens.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Serratia.
 CC NCBI_TaxID=615;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN=SM6;
 CC Berken M., Benedik M.J.;
 CC "DnaI inhibits transcription of Serratia marcescens nuclease.";
 CC Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: (S)-dihydroorotate + H(2)O = N-carbamoyl-L-
 CC aspartate.
 CC -1- COPACITOR: THIS ENZYME TIGHTLY BINDS ONE ZINC ATOM PER CHAIN WHICH
 CC IS REQUIRED FOR THE CATALYTIC MECHANISM. IT ALSO BINDS WEAKLY TO
 CC TWO OTHERS ZINCS WHICH ARE NOT ESSENTIAL FOR ACTIVITY (BY
 CC SIMILARITY).
 CC -1- PATHWAY: THIRD STEP IN PYRIMIDINE BIOSYNTHESIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE DHOASE FAMILY. SUBFAMILY 1.
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 CC -----
 CC EMBL: AF175466; AAD50307.1; ALT_INT.
 CC InterPro: IPR002195; Dihydroorotase.
 CC PROSITE: PS00482; DIHYDROOROTASE_1; PARTIAL.
 CC PROSITE: PS00483; DIHYDROOROTASE_2; 1.
 CC Pyrimidine biosynthesis; Hydrolyase; Zinc.
 CC FT NON_TER 1 1
 CC SEQUENCE 204 AA; 22899 MW; 9DB0B6C9B34B310 CRC64;

Query Match 29.6%; Score 48; DB 1; Length 204;
 Best Local Similarity 40.9%; Pred. No. 4.7;
 Matches 9; Conservative 7; Mismatches 4; Indels 2; Gaps 1;

OY 2 OYKANSKFIGITGEPFPHLL 23
 DB 42 OYVQNGNRFGLATI--TPQHLM 61

RESULT 15
 LQHD_HAEIN STANDARD: PRT; 564 AA.
 ID LQHD_HAEIN
 AC P45295;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE D-lactate dehydrogenase (EC 1.1.1.28).
 GN DLD OR H1649.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 CC NCBI_TaxID=727;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN=RD / KW20 / ATCC 51907;
 CC MEDLINE=95350630; PubMed=7542800;
 CC Fleischmann A.R., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 CC Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 CC McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 CC Scott J.D., Shirley R., Liu L.-I., Glodex A., Kelley J.M.,

```

RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudex D.M., Brandon R.C.,
RA Fine L.D., Pritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
RT influenzae Rd."
RL Science 269:496-512(1995).
CC -I- FUNCTION: FIRST COMPONENT OF THE MEMBRANE-BOUND D-LACTATE OXIDASE,
CC WHICH IS BELIEVED TO PLAY AN IMPORTANT ROLE IN THE ENERGIZATION OF
CC THE ACTIVE TRANSPORT OF A VARIETY OF SUGARS AND AMINO ACIDS
CC (BY SIMILARITY).
CC -I- CATALYTIC ACTIVITY: (R)-lactate + NAD(+) = pyruvate + NADH.
CC -I- COFACTOR: FAD.
CC -I- SUBCELLULAR LOCATION: MEMBRANE BOUND LOCATED AT THE INNER FACE OF
CC THE CYTOPLASMIC MEMBRANE (BY SIMILARITY).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U32838; AAC23296.1; -.
DR HSSP: P06149; IFOX.
DR TIGR: H1649; -.
DR InterPro: IPR001575; Oxid_FAD_bind.
DR Pfam: PF01565; FAD_binding_4; 1.
DR Oxidoreductase; NAD; Flavoprotein; FAD; Membrane; Complete proteome.
KW OXIDOREDUCTASE; NAD; FLAVOPROTEIN; FAD; MEMBRANE; COMPLETE PROTEOME.
SQ
SEQUENCE 564 AA; 64126 MW; D1211B2D3D5C6418 CRC64;

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Query Match          29.6%; Score 48; DB 1; Length 564;
Best Local Similarity 39.3%; Pred. No. 14;
Matches 11; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

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```

QY 4 IKANSKFIGITEGFEPEHLVDLFQSL 31
   :|:| | | | | | | | | | | | |
Db 337 LKSNVDRIQKRRFFLPQHLSDKFMOTVS 364

```

Search completed: June 18, 2002, 08:13:10
Job time: 369 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2002, 08:12:49 ; Search time 41.35 Seconds
(without alignments)
129,569 Million cell updates/sec

Title: US-09-943-334-2

Perfect score: 162
Sequence: 1 COYIKANSKEFGTEFGFPHLVDFLOSL 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	78	48.1	485	6	Q9BG59	Q9BG59 tupaia glis
2	70	43.2	1310	2	Q93N27	Q93N27 clostridium
3	56.5	34.9	458	5	O44506	O44506 caenorhabdit
4	56.5	34.9	609	3	O12601	O12601 candida vic
5	56	34.6	314	16	Q9CN39	Q9CN39 pasteurella
6	54	33.3	310	16	Q9KS29	Q9KS29 vibrio chol
7	54	33.3	469	11	Q910P5	Q910P5 melon yello
8	52.5	32.4	108	11	Q9Q294	Q9Q294 cavia porce
9	52.5	32.4	1071	3	Q9P388	Q9P388 neurospora
10	52	32.1	386	12	Q9Y777	Q9Y777 melanoplus
11	51	31.5	215	16	Q97HE3	Q97HE3 clostridium
12	51	31.5	274	16	Q914E6	Q914E6 pseudomonas
13	51	31.5	469	12	Q9WBS2	Q9WBS2 physalis se
14	51	31.5	899	12	Q9YTK4	Q9YTK4 atreline her
15	50.5	31.2	771	2	Q9S309	Q9S309 porphyromon
16	50	30.9	212	17	O58223	O58223 pyrococcus

17	50	30.9	493	4	Q9NX26	Q9NX26 homo sapien
18	50	30.9	493	4	Q9NND9	Q9NND9 homo sapien
19	49	30.2	165	5	O15887	O15887 trypanosoma
20	49	30.2	198	10	Q940L5	Q940L5 arabidopsis
21	49	30.2	212	17	Q9UYF5	Q9UYF5 pyrococcus
22	49	30.2	233	10	O81513	O81513 arabidopsis
23	49	30.2	252	10	Q40701	Q40701 oryza sativ
24	49	30.2	254	10	O65103	O65103 oryza sativ
25	49	30.2	513	3	Q9C1X4	Q9C1X4 schistosom
26	48.5	29.9	103	6	Q9N110	Q9N110 oris arles
27	48.5	29.9	106	11	Q9DA88	Q9DA88 mus musculu
28	48.5	29.9	258	11	Q9CYA8	Q9CYA8 mus musculu
29	48.5	29.9	735	4	Q96PY9	Q96PY9 homo sapien
30	48.5	29.9	823	6	Q9XTA5	Q9XTA5 bos taurus
31	48.5	29.9	823	11	Q9WYU9	Q9WYU9 ratus norv
32	48.5	29.9	825	11	O35800	O35800 ratus norv
33	48.5	29.9	826	4	Q9UPB1	Q9UPB1 homo sapien
34	48	29.6	440	16	Q9CNI1	Q9CNI1 pasteurella
35	48	29.6	478	17	Q97VC2	Q97VC2 sulfolobus
36	48	29.6	832	16	Q98GU5	Q98GU5 rhizobium
37	48	29.6	1173	5	Q9V7J8	Q9V7J8 drosophila
38	47.5	29.3	374	16	Q9CKE4	Q9CKE4 pasteurella
39	47.5	29.3	390	2	Q9F739	Q9F739 shigella so
40	47.5	29.3	395	2	Q9S0T2	Q9S0T2 plesiomonas
41	47.5	29.3	403	2	O55045	O55045 shigella so
42	47.5	29.3	1079	5	Q9VN30	Q9VN30 drosophila
43	47.5	29.3	1298	3	O01318	O01318 neurospora
44	47.5	29.3	1307	3	O9C1U1	O9C1U1 magnaporthe
45	47	29.0	189	5	Q95R25	Q95R25 babesia ros

ALIGNMENTS

RESULT 1
Q9BG59 PRELIMINARY; PRT; 485 AA.
AC Q9BG59;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CHOLESTERYL ESTER TRANSFER PROTEIN (FRAGMENT).
OS Tupaia glis (Tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupia.
OX NCBI_TaxID=9395;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Zeng W.W., Chen B.S., Zhang J.;
RT "Cloning and sequencing of tree shrew cholesterol ester transfer
RT protein (CETP) cDNA.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF344033; AAK08086.1;
DR InterPro; IPR001124; LBP_BPI_CETP.
DR Pfam; PF02886; LBP_BPI_CETP.1.
DR SMART; SM00328; BPI1.1.
DR SMART; SM00329; BPI2.1.
DR PROSITE; PS00400; LBP_BPI_CETP.1.
FT NON_TER
SQ SEQUENCE 485 AA; 53993 MM; 2605E76D263C367 CRC64;

Query Match 48.1%; Score 78; DB 6; Length 485;
Best Local Similarity 88.2%; Pred. No. 0.0026;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 15 ERGPEHLVDFLOSL 31
DB 469 DGFPEHLVDFLOSL 485

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RESULT 2
ID 093N27 PRELIMINARY; PRT; 1310 AA.
AC 093N27;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE TETANUS TOXIN (FRAGMENT).
OS Clostridium tetani.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1513;
RN [1]
RP SEQUENCE FROM N.A.
RA Shumin Z., Dianliang L.;
RT "Cloning and sequence analysis of tetanus toxin gene.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF389424; AAK72964.2; -.
FT NON_TER 1 1
FT 1310 1310
SQ SEQUENCE 1310 AA; 150316 MW; 9EADDC914418E450 CRC64;

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Query Match 43.2%; Score 70; DB 2; Length 1310;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 2 OYIKANSKFIGITE 15
DB 831 OYIKANSKFIGITE 844

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RESULT 3
ID 044506 PRELIMINARY; PRT; 458 AA.
AC 044506;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE HYPOTHETICAL 51.1 KDA PROTEIN.
GN FA2G8.9.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2016(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Gattung S., Holmes A.;
RT "The sequence of C. elegans cosmid FA2G8.";
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE038618; AAB92068.1; -.
KW Hypothetical protein.
SQ SEQUENCE 458 AA; 51070 MW; 9F4DF23D8CDABED5 CRC64;

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Query Match 34.9%; Score 56.5; DB 5; Length 458;
Best Local Similarity 40.0%; Pred. No. 4;
Matches 12; Conservative 6; Mismatches 9; Indels 3; Gaps 1;

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OY 1 COYIKANSKFIGITFGPEHLLVDFLOSL 30
DB 232 CMYIKNNKYLKSSGTHQ---LDFIOKL 258

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RESULT 4
ID 012601 PRELIMINARY; PRT; 609 AA.
AC 012601;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE BETA-GLUCOSIDASE PRECURSOR (EC 3.2.1.21).
GN BGLB
OS Candida wickerhamii.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=35521;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CAPRIOTTI;
RX MEDLINE=96031564; PubMed=7574590;
RA Skory C.D., Freer S.N.;
RT "Cloning and characterization of a gene encoding a cell-bound,
extracellular beta-glucosidase in the yeast Candida wickerhamii.";
RL Appl. Environ. Microbiol. 61:518-525(1995).
DR EMBL; U13672; AAC49036.1; -.
DR HSP; P26205; ICRG.
DR InterPro; IPR001360; Glyco_hydro_1.
DR Pfam; PF00232; Glyco_hydro_1; 3.
KW signal; Hydrolase; Glycosidase.
FT SIGNAL 1 21
FT CHAIN 22 609
FT 609 609
SQ SEQUENCE 609 AA; 68034 MW; 9C5624E3B3F1734E CRC64;

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Query Match 34.9%; Score 56.5; DB 3; Length 609;
Best Local Similarity 60.0%; Pred. No. 5.5;
Matches 15; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

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OY 11 IGITFGFP-----EHLVDFLOSL 30
DB 510 IFITFGFPFMRGKLVQVQDL 534

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RESULT 5
ID 09CN39 PRELIMINARY; PRT; 314 AA.
AC 09CN39;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE HYPOTHETICAL PROTEIN PM0606.
GN PM0606.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PM70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang O., Li L.L., Pautian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
DR EMBL; AE006096; AAK02690.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 314 AA; 36080 MW; 3C0EA33486CF62ED CRC64;

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```

Query Match 34.6%; Score 56; DB 16; Length 314;
Best Local Similarity 64.3%; Pred. No. 3.1;

```


QY 1 CQYTKA---NSKFIGTEFGPEHLVDL 27
 DB 659 CPMKQEDHNSLLTHKSGFPEHSDIDFI 688

RESULT 10

Q9YW77 PRELIMINARY; PRT; 386 AA.
 AC Q9YW77;
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, last annotation update)
 DE ORF MSV015 LEUCINE RICH REPEAT GENE FAMILY PROTEIN, SIMILAR TO AMSACTA MOOREI ENTOMOPOXVIRUS Q3 ORF SW:P28854.
 GN MSV015.
 OS Melanoplus sanguinipes entomopoxvirus (MSEPV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
 OC Entomopoxvirus B.
 OX NCBI_TaxID=83191;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TUCSON;
 RX MEDLINE=99102612; PubMed=9847359;
 RA Atonso C.L., Tullman E.R., Lu Z., Oma E., Kutish G.F., Rock D.L.;
 RT "The genome of Melanoplus sanguinipes entomopoxvirus.";
 RL J. Virol. 73:533-552(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TUCSON;
 RA Atonso C.L., Tullman E.R., Lu Z., Oma E., Kutish G.F., Rock D.L.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF063866; AAC97854.1; -
 SQ SEQUENCE 386 AA; 45125 MW; 401A84C7A755F200 CRC64;

Query Match 32.1%; Score 52; DB 12; Length 386;
 Best Local Similarity 55.0%; Pred. No. 15;
 Matches 11; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 4 IKANSKFIGTEFGPEHL 23
 DB 232 IKNCERCGITDFKFLDLY 251

RESULT 11

Q97HE3 PRELIMINARY; PRT; 215 AA.
 AC Q97HE3;
 DT 01-OCT-2001 (TREMblrel. 18, Created)
 DT 01-OCT-2001 (TREMblrel. 18, last sequence update)
 DT 01-OCT-2001 (TREMblrel. 18, last annotation update)
 DE SPORULATION FACTOR SPOIIM, UNCHARACTERIZED MEMBRANE PROTEIN.
 GN CAC2068.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RA Noelling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Oiu D., Hitti J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";
 RL J. Bacteriol. 183:4823-4838(2001).
 DR EMBL: AE007709; AAK80027.1; -
 KW Complete proteome.
 SQ SEQUENCE 215 AA; 24212 MW; ED6B010D6AD3C895 CRC64;

Query Match 31.5%; Score 51; DB 16; Length 215;
 Best Local Similarity 40.9%; Pred. No. 11;
 Matches 9; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 10 FIGITEFGPEHLVDLQSL 31
 DB 87 FLGLTMIGIPVILIDLLKGF 108

RESULT 12

Q91AE6 PRELIMINARY; PRT; 274 AA.
 AC Q91AE6;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, last sequence update)
 DT 01-OCT-2001 (TREMblrel. 18, last annotation update)
 DE HYPOTHEICAL PROTEIN PA1192.
 GN PA1192.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Huftagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Ladig K., Lam R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Relzer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.";
 RL Nature 406:959-964(2000).
 DR EMBL: AE004548; AAG04581.1; -
 DR InterPro: IPR000541; UPP0021.
 DR Pfam: PF01171; UPP0021; 1.
 KW Hypothetical protein: Complete proteome.
 SQ SEQUENCE 274 AA; 31260 MW; 4C042PA0198FA46 CRC64;

Query Match 31.5%; Score 51; DB 16; Length 274;
 Best Local Similarity 57.1%; Pred. No. 15;
 Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 17 GPEHLVDLQSL 30
 DB 76 GPEHLVDLQSL 89

RESULT 13

Q9WBS2 PRELIMINARY; PRT; 469 AA.
 AC Q9WBS2;
 DT 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
 DE NONSTRUCTURAL PROTEIN.
 GN NSS.
 OS Physalis severe mottle virus.
 OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Tospovirus.
 OX NCBI_TaxID=77028;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21213458; PubMed=11315637;
 RA Cortes I., Sailer J., Wongjkaew K.S., Pereira A.-M., Goldbach R.,
 RA Peters D., Kormelink R.;
 RT "Identification and characterization of a novel tospovirus species using a new RT-PCR approach.";
 RL Arch. Virol. 146:265-278(2001).
 DR EMBL: AF067151; AAD34200.1; -

SO SEQUENCE 469 AA: 53204 MW: 732435E83C3FC27D CRC64;

Query Match

Best Local Similarity 31.5%; Score 51; DB 12; Length 469;
Matches 11; Conservative 7; Mismatches 4; Indels 8; Gaps 1;

OY 5 KANSKFIGIT-----EFGFPEHLVDF 26
DB 413 KSNSSFWYLSKTWSPWKEPFEQHLVDY 442

RESULT 14

O9YTK4 PRELIMINARY; PRT: 899 AA.
AC O9YTK4; 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ORF 63.
OS Ateline herpesvirus 3
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=85618;
RN {1}
RP SEQUENCE FROM N.A.
RC STRAIN=73;
RX MEDLINE=20091363; PubMed=10623770;
RA Albrecht J.C.;
RT "Primary structure of the Herpesvirus Atelles genome.";
RL J. Virol. 74:1033-1037(2000).
RN {2}
RP SROUENCE FROM N.A.
RC STRAIN=73;
RA Albrecht J.-C., Fleckenstein B.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF083424; AAC95587.1; -
SQ SEQUENCE 899 AA: 103389 MW: 19440A7944DE2531 CRC64;

Query Match

Best Local Similarity 31.5%; Score 51; DB 12; Length 899;
Matches 11; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

OY 2 QYIKANSKFIGITTEFGFPEHLVDF 26
DB 124 QYITSNSTFGOTEPYVNNVILTF 148

RESULT 15

O9S309 PRELIMINARY; PRT: 771 AA.
AC O9S309; 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE IMMUNOREACTIVE 87KD ANTIGEN PG92.
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; CRB group; Bacteroidetes; Bacteroidales; Porphyromonadaceae;
OC Porphyromonas.
OX NCBI_TaxID=837;
RN {1}
RP SEQUENCE FROM N.A.
RC STRAIN=450;
RA Rose B.C., Barr I., Patterson M., Agius C., Rothel L., Margetts M.,
RT "Porphyromonas gingivalis polypeptides and nucleic acids.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF175724; AAD51077.1; -
SQ SEQUENCE 771 AA: 86667 MW: 75016BF66848C9B9 CRC64;

Query Match 31.2%; Score 50.5; DB 2; Length 771;

Best Local Similarity 50.0%; Pred. No. 56;
Matches 11; Conservative 5; Mismatches 3; Indels 3; Gaps 1;

OY 13 ITEFGFPE---HLVDFPLQSLIS 31
DB 162 ITEFAFPEGCHILNLGLQALS 183

Search completed: June 18, 2002, 08:12:52
Job time: 376 sec

XX 01-MAY-1995; 95US-0432483.
 XX (TCCL-) T CELL SCI INC.
 XX
 XX Rittershaus CW, Thomas LJ;
 XX WPI; 1996-506103/50.
 XX
 XX Cholesteryl ester transfer protein B cell epitope linked to T cell
 PT epitope - used to generate vaccine to regulate CERP activity for
 PT decreasing the risk of developing a cardiovascular disease e.g.
 PT atherosclerosis
 XX
 XX Claim 8; Page 41-42; 72pp; English.
 XX
 XX A synthetic peptide vaccine comprises an immunogenic helper T-cell
 CC epitope of tetanus toxoid protein covalently linked to the
 CC C-terminal B-cell epitope of human cholesteryl ester transfer
 CC protein (CERP) (see also AAW06127) that is involved in a neutral
 CC lipid binding or a transfer activity of CERP. The vaccine elicits
 CC an immune response against endogenous CERP activity, and is used to
 CC treat or prevent a cardiovascular disease, such as atherosclerosis.
 XX

SQ Sequence 31 AA:

Query Match 100.0%; Score 162; DB 17; Length 31;
 Best Local Similarity 100.0%; Pred. No. 4.6e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 COYIRANSKFIGITERGFEPEHLVDPIQSLS 31
 |||||
 DB 1 cgyikanskfigitfegfpehlvdfigls 31

RESULT 2

AAW02470
 ID AAW02470 standard; protein; 31 AA.

AC AAW02470;

DT 14-JUL-1999 (first entry)

DE Fusion of a tetanus toxoid fragment and C-terminal of human CERP.

XX Vaccine; antibody; endogenous; cholesteryl ester transfer protein; CERP;
 KW high-density lipoprotein-associated cholesterol; metabolism;
 KM low-density lipoprotein-associated cholesterol; atherosclerotic lesion;
 KM cholesterol; atherosclerosis; heart disease.

OS Synthetic.

PN WO9920302-A1.

PD 29-APR-1999.

PE 20-OCT-1998; 98WO-US22145.

PR 20-OCT-1997; 97US-0954643.

PA (AVANT) AVANT IMMUNOTHERAPEUTICS INC.

PI Rittershaus CW, Thomas LJ;

DR WPI; 1999-302645/25.

XX Vaccine against cholesteryl ester transfer protein

XX Disclosure; Page 55; 61pp; English.

XX The specification describes a vaccine that promotes the production of
 CC antibodies that bind endogenous cholesteryl ester transfer protein

CC (CERP). The vaccines (and equivalent plasmid-based vaccines) are
 CC used to increase the ratio of circulating high-density lipoprotein
 CC (HDL)-associated cholesterol to low-density lipoprotein (LDL)-associated
 CC cholesterol; to decrease the level of endogenous CERP activity in humans
 CC or other animals; to alter metabolism of LDL-associated cholesterol, for
 CC inhibiting development of atherosclerotic lesions; to lower circulating
 CC levels of LDL and total cholesterol; and to treat or prevent
 CC atherosclerosis (or more generally heart disease). The present sequence
 CC was used in the course of the invention.

SQ Sequence 31 AA:

Query Match 100.0%; Score 162; DB 20; Length 31;
 Best Local Similarity 100.0%; Pred. No. 4.6e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 COYIRANSKFIGITERGFEPEHLVDPIQSLS 31
 |||||
 DB 1 cgyikanskfigitfegfpehlvdfigls 31

RESULT 3

AAW06131
 ID AAW06131 standard; Peptide; 50 AA.

AC AAW06131;

DT 07-FEB-1997 (first entry)

DE Anti-cholesteryl ester transfer multivalent vaccine peptide.

XX Cholesteryl ester transfer protein; CERP; antigen; vaccine;
 KW cardiovascular disease; atherosclerosis.

OS Synthetic.

XX Key Location/Qualifiers

FT MISC-difference 1 /note- "C-terminal Cys residue is present for use
 FT in linking the peptide to itself or other
 FT molecules"

FT Region 2..15 /label- "T-cell-epitope
 FT /note- "T-cell epitope comprises amino acids
 FT 830-843 of tetanus toxoid protein"

FT Region 16..34 /label- "B-cell-epitope
 FT /note- "B-cell epitope comprises amino acids
 FT 349-367 of human CERP"

FT Region 35..50 /label- "B-cell epitope
 FT /note- "B-cell epitope comprises the C-terminal 16
 FT amino acids of human CERP, involved in
 FT neutral lipid binding or transfer activity"

WO9634888-A1.

PD 07-NOV-1996.

PE 01-MAY-1996; 96WO-US06147.

PR 01-MAY-1995; 95US-0432483.

PA (TCCL-) T CELL SCI INC.

PI Rittershaus CW, Thomas LJ;

DR WPI; 1996-506103/50.

XX Cholesteryl ester transfer protein B cell epitope linked to T cell
 PT epitope - used to generate vaccine to regulate CERP activity for
 PT decreasing the risk of developing a cardiovascular disease e.g.

```
PT atherosclerosis
XX
PS Disclosure; Page 7; 72pp; English.
XX
CC A multivalent vaccine comprises an immunogenic helper T-cell
CC epitope of tetanus toxoid protein covalently linked to the B-cell
CC also AAM06133). The vaccine elicits an immune response against
CC endogenous CERP activity, and is used to treat or prevent a
CC cardiovascular disease, such as atherosclerosis.
CC
XX
SQ Sequence 50 AA;

Query Match 88.0%; Score 142.5; DB 17; Length 50;
Best Local Similarity 62.0%; Pred. NO. 8.5e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 19; Gaps 1;

OY 1 GYIKANSKFIGITE-----FGFPEHLVDFLOSLS 31
   |||||
DB 1 cgyikanskfigitefprpdqghvayrfeedifgfphehlvdfllqsls 50

RESULT 4
AAM06132
ID AAM06132 standard; Peptide: 50 AA.
XX
AC AAM06132;
XX
DT 07-FEB-1997 (first entry)
XX
DE Anti-cholesterol ester transfer multivalent vaccine peptide.
XX
KW Cholesteryl ester transfer protein; CERP; antigen; vaccine;
KW cardiovascular disease; atherosclerosis.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT 2..15
FT /label= "T-cell epitope
FT /note= "T-cell epitope comprises amino acids
FT 830-843 of tetanus toxoid protein"
FT 16..34
FT /label= "B-cell epitope
FT /note= "B-cell epitope comprises amino acids
FT 350-368 of rabbit CERP"
FT 35..50
FT /label= "B-cell epitope
FT /note= "B-cell epitope comprises the C-terminal 16
FT amino acids of rabbit CERP, involved in
FT neutral lipid binding or transfer activity"
FT
XX
PN WO9634888-A1.
XX
PD 07-NOV-1996.
XX
PF 01-MAY-1996; 96WO-US06147.
XX
PR 01-MAY-1995; 95US-0432483.
XX
PA (TCEL-) T CELL SCI INC.
XX
PI Rittershaus CW, Thomas LJ;
XX
DR WPI: 1996-506103/50.
XX
XX Cholesteryl ester transfer protein B cell epitope linked to T cell
PT epitope - used to generate vaccine to regulate CERP activity for
PT decreasing the risk of developing a cardiovascular disease e.g.
PT atherosclerosis
XX
PS Disclosure; Page 7; 72pp; English.
```

```
XX
CC A multivalent vaccine comprises an immunogenic helper T-cell
CC epitope of tetanus toxoid protein covalently linked to the B-cell
CC epitopes of rabbit cholesteryl ester transfer protein (CERP) (see
CC also AAM06133). The vaccine elicits an immune response against
CC endogenous CERP activity, and is used to treat or prevent a
CC cardiovascular disease, such as atherosclerosis.
CC
XX
SQ Sequence 50 AA;

Query Match 79.9%; Score 129.5; DB 17; Length 50;
Best Local Similarity 59.2%; Pred. NO. 8.9e-13;
Matches 29; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

OY 2 GYIKANSKFIGITE-----FGFPEHLVDFLOSLS 31
   |||||
DB 2 gylkanskfigiterfprpdgreavayrfeedifgfphehlvdfllqsls 50

RESULT 5
AAM46447
ID AAM46447 standard; Peptide: 50 AA.
XX
AC AAM46447;
XX
DT 18-MAY-1998 (first entry)
XX
DE CERP B cell epitope/tetanus toxoid construct for a plasmid vaccine.
XX
KW Cholesteryl ester transfer protein; CERP; cholesteryl ester;
KW high density lipoprotein; HDL; very low density lipoprotein; VLDL;
KW low density lipoprotein; LDL; atherosclerosis; neutral lipid binding;
KW transfer activity; immunogenic; B cell epitope; antibody;
KW DNA plasmid-based vaccine; broad range helper T cell epitope;
KW treatment; cardiovascular disease; chimeric.
XX
OS Chimeric - Clostridium tetani.
OS Chimeric - Oryctolagus sp.
XX
FH Key Location/Qualifiers
FT 2..15
FT /label= "tetanus toxoid broad range helper T cell
FT /note= "tetanus toxoid broad range helper T cell
FT 16..34
FT /label= "CERP epitope
FT /note= "CERP epitope of amino acids 350-368 of
FT 35..50
FT /label= "CERP epitope of amino acids 481-496 of
FT /note= "CERP epitope of amino acids 481-496 of
FT AAM46445"
FT
XX
PN WO9741227-A1.
XX
PD 06-NOV-1997.
XX
PF 01-MAY-1997; 97WO-US07294.
XX
PR 21-FEB-1997; 97US-0802967.
XX
PR 01-MAY-1996; 96US-0640713.
XX
PA (TCEL-) T CELL SCI INC.
XX
PI Thomas LJ;
XX
DR WPI: 1997-549731/50.
DR N-PSDB; AAV05128.
XX
XX DNA plasmid-based vaccine encodes CERP B cell and helper T cell
PT epitope(s) - used for elevating high density lipoprotein levels, and
PT for treating cardiovascular disease
XX
PS Claim 8; Page 22; 67pp; English.
```

Query Match	79.9%;	Score 129.5;	DB 18;	Length 50;
Best Local Similarity	59.2%;	Pred. No. 8.9e-13;		
Matches	29;	Conservative	0;	Indels 19; Gaps 1
		Mismatches		

RESULT	6
AAV91236	
ID	AAV91236 standard; peptide; 35 AA.

AC	AA91236;
XX	
DT	22-MAY-2000 (first entry)

Modified HBVsurface Ag/CTP peptide, SEQ ID NO:114.

[illegible]

OS Chimeric - Hepatitis B virus.
OS Chimeric - Homo sapiens.

PN W09966957-A2.

PD 29-DEC-1999.

PF 21-JUN-1999; 99WO-US13975.

PR 20-JUN-1998; 98US-0100412.

PA (UNBI-) UNITED BIOMEDICAL INC.

PI Wang CY;

DR WPI; 2000-160564/14.

PT	New artificial T helper cell epitope and derived immunogens with target
PT	antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT	or human immune deficiency virus -

The invention relates to novel promiscuous T helper cell epitopes (Th), and immunogenic peptides comprising the Th epitopes of the invention along with B cell epitopes. The Th epitopes and peptide immunogens containing them, are used to induce a T helper cell response, specifically against Plasmodium falciparum, cholesterol ester transport protein (CEP) or HIV epitopes, but more generally against any pathogen, immunoreactive self-antigen or tumour antigen. The Th epitopes and peptide immunogens may be used for prevention and/or treatment of infections (HIV, foot-and-mouth disease or malaria); for cancer immunotherapy; for inhibition of the action of lutealising hormone releasing hormone (LHRH) for contraception, treatment of hormone-dependent cancer, prevention of boar taint in meat, and immunocastration); for promoting the growth of animals; or for treating allergies or arteriosclerosis. Incorporation of a promiscuous Th (functional in genetically diverse subjects) into an immunogen improves capacity to induce a strong T helper cell-mediated immune response, resulting in production of antibodies against a target antigen. Th can replace carrier proteins and pathogen-derived T helper epitopes. Sequence AA91121 represents a promiscuous T helper epitope from the measles virus F (MVF) protein and sequences AA91122-931142, AA91226 and AA91245-931246 represent synthetic Th epitopes based on MVE Th epitope. Sequence AA91143 represents a promiscuous Th epitope from hepatitis B virus (HBV) surface antigen, and sequences

CC AAAY1144-191155 are synthetic epitopes derived from this HBV epitope.
CC AAAY1156-191196, AAAY1227 and AAAY1242-191244 are antigenic peptides
CC competing to form conjugates with anti-HBc antibody.

is the LHRH target antigenic peptide used in these LHRH antipeptides. AA9119/100 is gonadotropin releasing hormone (GnRH) and AA9119/100 is gonadotropin releasing hormone (GnRH) and AA9119/100 is gonadotropin releasing hormone (GnRH).

peptides comprising somatostatin and a Th epitope. Somatostatin immunogens may be used to promote growth in livestock. AAV91208 is a

CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVH Th
CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV

infection of T cells. AAY90212 is a modified version of a human IgE (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/TGF CH3

CC antigenic peptides which may be used in the treatment of allergies.
CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)

CC VPI capsid protein and AAY91221-Y91222 comprise this peptide and a 7th
CC epitope. AAY91223 is a *Plasmodium falciparum* circumsporozoite (CS) target

CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th
CC epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent
CC epitopes that may be used in a malaria vaccine.

CC CEMP peptide and a Th epitope which may be used to prevent or treat
CC arteriole and cardiovascular diseases.
CC
CC
CC CEMP-derived peptides and AA9Y1232-Y91241 are immunogens comprising a
CC
CC

are HIV-1 neutralising B-cell epitopes, and AA191248-Y191251 and AA191258-Y191273 are antigenic peptides comprising *env* gp120 and gp120-125 regions of HIV-1 and cardiovascular disease. AA191247 and AA191252-Y191257

epitope which may be used as a component in an anti-HIV-1 vaccine.
AAV91198 and AAV91199 are respectively an immunostimulatory toxin
CC CC

protein epitope from *Yersinia* species, and hinge spacer peptide, both of which may optionally be used in the antigenic peptides of the CC

CC invention.
XX

Sequence 35 AA.

Query Match	53.7%;	Score 87;	DB 21;	Length 35;
Best Local Similarity	80.5%;	Score 90;	DB 22;	Length 35;

base local similarity 85.38; file. NO. 2.3E-V0;
Matches 17; Conservative 1; Mismatches 1; Indels 0;
Gaps 0

QY 13 I T E F G F P E H L L V D F L Q S L S 31

```
Db 17 idkfgfpehlvdfflqs1s 35
```

RESULT 7

AY13815 standard, root id: 22 x
AY13815

100-443815-1

08-JUL-1999 /first entry

XX 5
6
7
8
9

DE Rabbit CERP immunogenic fragment.
 XX
 KW CERP; cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;
 KW antibody production; cholesteryl ester transfer; therapy;
 KW high density lipoprotein; HDL cholesterol concentration;
 KW pro-atherogenic dyslipoproteinaemia.
 XX
 OS Oryctolagus sp.
 XX
 PN WO9915655-A1.
 XX
 PD 01-APR-1999.
 XX
 PF 17-SEP-1998; 98WO-US19366.
 XX
 PR 19-SEP-1997; 97US-0934367.
 XX
 PA (MONS) MONSANTO CO.
 XX
 PI Glenn K, Needleman P;
 XX
 DR WPI: 1999-276984/23.
 XX
 PT New recombinant DNA vaccines
 XX
 PS Disclosure; Page 75; 99pp; English.
 XX
 CC This sequence represents an immunogenic fragment of the rabbit
 CC cholesteryl ester transferase protein (CERP).
 CC The invention relates to recombinant DNA vaccines that contain DNA
 CC encoding CERP, which can be used for producing antibodies to lessen the
 CC transfer of cholesteryl esters from high density lipoprotein (HDL). The
 CC method can provide an autogenic immunological process for lessening the
 CC transfer of cholesteryl esters from HDL particles and for increasing the
 CC HDL cholesterol concentration of a mammal whose blood also contains
 CC CERP. The method may be useful in treating human pro-atherogenic
 CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
 CC method can have an effect that lasts for months as compared to the
 CC short-term effects of the small molecule drugs now available.
 CC
 SQ Sequence 22 AA;
 XX

Query Match 52.5%; Score 85; DB 20; Length 22;
 Best Local Similarity 94.1%; Pred. No. 2.8e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 15 EFGFPEHLVDPLQSL 31
 :|||||
 Db 6 dfgfpehlvdplqsls 22

RESULT 8
 AAY13821
 ID AAY13821 standard; peptide; 22 AA.
 XX
 AC AAY13821;
 XX
 DT 08-JUL-1999 (first entry)
 XX
 DE Human CERP immunogenic fragment.
 XX
 KW CERP; cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;
 KW antibody production; cholesteryl ester transfer; therapy;
 KW high density lipoprotein; HDL cholesterol concentration;
 KW pro-atherogenic dyslipoproteinaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO9915655-A1.
 XX
 PD 01-APR-1999.
 XX

PF 17-SEP-1998; 98WO-US19366.
 XX
 PR 19-SEP-1997; 97US-0934367.
 XX
 PA (MONS) MONSANTO CO.
 XX
 PI Glenn K, Needleman P;
 XX
 DR WPI: 1999-276984/23.
 XX
 PT New recombinant DNA vaccines
 XX
 PS Disclosure; Page 88; 99pp; English.
 XX
 CC This sequence represents an immunogenic fragment of the human
 CC cholesteryl ester transferase protein (CERP).
 CC The invention relates to recombinant DNA vaccines that contain DNA
 CC encoding CERP, which can be used for producing antibodies to lessen the
 CC transfer of cholesteryl esters from high density lipoprotein (HDL). The
 CC method can provide an autogenic immunological process for lessening the
 CC transfer of cholesteryl esters from HDL particles and for increasing the
 CC HDL cholesterol concentration of a mammal whose blood also contains
 CC CERP. The method may be useful in treating human pro-atherogenic
 CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
 CC method can have an effect that lasts for months as compared to the
 CC short-term effects of the small molecule drugs now available.
 CC
 SQ Sequence 22 AA;
 XX

Query Match 52.5%; Score 85; DB 20; Length 22;
 Best Local Similarity 94.1%; Pred. No. 2.8e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 15 EFGFPEHLVDPLQSL 31
 :|||||
 Db 6 dfgfpehlvdplqsls 22

RESULT 9
 AAW06128
 ID AAW06128 standard; peptide; 26 AA.
 XX
 AC AAW06128;
 XX
 DT 07-FEB-1997 (first entry)
 XX
 DE Human cholesteryl ester transfer protein C-terminal B-cell epitope.
 XX
 KW Cholesteryl ester transfer protein; CERP; antigen; vaccine;
 KW cardiovascular disease; atherosclerosis; B-cell epitope.
 XX
 OS Homo sapiens.
 XX
 PN WO9634888-A1.
 XX
 PD 07-NOV-1996.
 XX
 PF 01-MAY-1996; 96WO-US06147.
 XX
 PR 01-MAY-1995; 95US-0432483.
 XX
 PA (TCEL-) T CELL SCI INC.
 XX
 PI Rittershaus CW, Thomas LJ;
 XX
 DR WPI: 1996-506103/50.
 XX
 PT Cholesteryl ester transfer protein B cell epitope linked to T cell
 PT epitope - used to generate vaccine to regulate CERP activity for
 PT decreasing the risk of developing a cardiovascular disease e.g.
 atherosclerosis
 XX

PS Claim 5; Page 41; 72pp; English.

XX
CC A B-cell epitope (AAW06128) comprising the C-terminal 26 amino acids
CC of human liver mature cholesteryl ester transfer protein (CETP)
CC (see also AAW06127) is involved in a neutral lipid binding or a
CC transfer activity of CETP. It can be linked to a universal or a
CC broad range immunogenic T-cell epitope, such as that found at amino
CC acids 830-843 of tetanus toxoid protein, to produce a synthetic
CC vaccine (see also AAW06129) that elicits an immune response against
CC endogenous CETP activity, thereby treating or preventing
CC cardiovascular disease, such as atherosclerosis. It may also be
CC incorporated into a multivalent vaccine (see also AAW06131)
CC including another CETP B-cell epitope.

SQ Sequence 26 AA;

Query Match 52.5%; Score 85; DB 17; Length 26;
Best Local Similarity 94.1%; Pred. No. 3.4e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 15 EFGFPEHLVDPLQSLSS 31
:|||||
Db 10 dfqfpehlvdfqlqsls 26

RESULT 10
AA113801
ID AAY13801 standard; peptide: 26 AA.
XX
AC AAY13801;
XX
DT 08-JUL-1999 (first entry)
XX
DE Rabbit CETP immunogenic fragment.
XX
KM CETP, cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;
KM antibody production; cholesteryl ester transfer; therapy;
KM high density lipoprotein; HDL cholesterol concentration;
KM pro-atherogenic dyslipoproteinaemia.
XX
OS Oryctolagus sp.
XX
PN WO9915655-A1.
XX
PD 01-APR-1999.
XX
PF 17-SEP-1998; 98WO-US19366.
XX
PR 19-SEP-1997; 97US-0934367.
XX
PA (MONS) MONSANTO CO.
XX
PI Glenn K. Needleman P;
XX
DR WPI; 1999-276984/23.
XX
PT New recombinant DNA vaccines
XX
PS Claim 15; Page 85; 99pp; English.

This sequence represents an immunogenic fragment of the rabbit
CC cholesteryl ester transferase protein (CETP).
CC The invention relates to recombinant DNA vaccines that contain DNA
CC encoding CETP, which can be used for producing antibodies to lessen the
CC transfer of cholesteryl esters from high density lipoprotein (HDL). The
CC method can provide an autogenic immunological process for lessening the
CC transfer of cholesteryl esters from HDL particles and for increasing the
CC HDL cholesterol concentration of a mammal whose blood also contains
CC CETP. The method may be useful in treating human pro-atherogenic
CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
CC method can have an effect that lasts for months as compared to the
CC short-term effects of the small molecule drugs now available.

XX
SQ Sequence 26 AA;

Query Match 52.5%; Score 85; DB 20; Length 26;
Best Local Similarity 94.1%; Pred. No. 3.4e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 15 EFGFPEHLVDPLQSLSS 31
:|||||
Db 10 dfqfpehlvdfqlqsls 26

RESULT 11
AAY91228
ID AAY91228 standard; peptide: 26 AA.
XX
AC AAY91228;
XX
DT 22-MAY-2000 (first entry)
XX
DE Human cholesteryl transport protein (CETP) peptide, SEQ ID NO:106.
XX
KM Promiscuous T-cell epitope; measles virus F protein; MVF;
KM hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KM interleukin-6 releasing hormone; IL6RH; contraceptive; anticancer;
KM somatostatin; growth promotion; CD4 receptor; HIV-1; anti-allergic;
KM foot and mouth disease virus; immunoglobulin E; IGE; anti-allergic;
KM Plasmodium falciparum; circumporozoite; antimalarial; CETP;
KM cholesteryl ester transport protein; anti-arteriosclerotic.
XX
OS Homo sapiens.
XX
PN WO9966957-A2.
XX
PD 29-DEC-1999.
XX
PF 21-JUN-1999; 99WO-US13975.
XX
PR 20-JUN-1998; 98US-0100412.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI; 2000-160564/14.
XX
PT New artificial T helper cell epitope and derived immunogens with target
PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT or human immune deficiency virus
XX
PS Claim 10; Page 49; 129pp; English.

The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response,
CC specifically against Plasmodium falciparum, cholesteryl ester transport
CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC peptide immunogens may be used for prevention and/or treatment of
CC infections (HIV, foot-and-mouth disease or malaria); for cancer
CC immunotherapy; for inhibition of the action of interleukin hormone
CC releasing hormone (LHRH) for contraception, treatment of hormone-
CC dependent cancer, prevention of boar taint in meat, and
CC immunocastration); for promoting the growth of animals; or for
CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
CC Th (functional in genetically diverse subjects) into an immunogen
CC improves capacity to induce a strong T helper cell-mediated immune
CC response, resulting in production of antibodies against a target
CC antigen. Th can replace carrier proteins and pathogen-derived T helper
CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
CC from the measles virus F (MVF) protein and sequences AAY91122-Y91142,

AAV91220 and AAV91245-Y91246 represent synthetic Th epitopes based on the Mφ Th epitope. Sequence AA91914 represents a promiscuous Th epitope from hepatitis B virus (HBV) surface antigens, and sequences AAV91144-Y91155 are synthetic epitopes derived from th.s HBV epitope. AAV91156-Y91196, AAV91227 and AAV91242-Y91244 are antigenic peptides comprising an LHRH sequence joined to a promiscuous Th epitope. AAV91197 is the LHRH target antigenic peptide used in these LHRH antigenic peptides. AAV91200 is somatostatin, and AAV91201-Y91207 are antigenic peptides comprising somatostatin and a Th epitope. Somatostatin immunogens may be used to promote growth in livestock. AAV91208 is a human CD4 CDR2-like domain antigenic site, and AAV91207-Y90211 are Mφ Th epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV infection of T cells. AAV90212 is a modified version of a human IGE (immunoglobulin E) Cε3 domain, and AAV90213-Y90219 are Th epitope/IgE Cε3 antigenic peptides which may be used in the treatment of allergies. AAV91220 is a peptide derived from foot and mouth disease virus (FMDV) VP1 capsid protein and AAV91221-Y91222 comprise this peptide and a Th epitope. AAV91223 is a plasmidium falciparum circumsporozoite (CS) target antigen, and AAV91224-Y91225 comprise the CS antigen and an Mφ Th epitope and may be used in a malaria vaccine. AAV91228-Y91231 represent CEMP-derived peptides and AAV91232-Y91241 are immunogens comprising a CEMP peptide and a Th epitope which may be used to prevent or treat arteriosclerosis and cardiovascular disease. AAV91247 and AAV91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAV91248-Y91251 and AAV91258-Y91273 are antigenic peptides comprising Mφ Th and HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1 vaccine. AAV91198 and AAV91199 are respectively an immunostimulatory invasion protein epitope from *Yersinia* species, and hinge spacer peptide, both of which may optionally be used in the antigenic peptides of the invention. Note: Sequence AAV91227 is also designated SEQ ID NO:106 in the specification.

Query Match	52.5%	Score 85	DB 21	Length 26
Best Local Similarity	94.1%	Pred. No. 3,4e-06		
Matches 16	Conservative 1	Mismatches 0	Indels 0	Gaps 0
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	:		31	
Db	10	dfgfpehlvdfllqsls	26	
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ID	AA91232			
AC	AA91232 standard; peptide; 46 AA.			
DT	22-MAY-2000 (first entry)			
DE	Modified MVF Th epitope/CERP peptide, SEQ ID NO:110.			
XX	Promiscuous T-cell epitope; measles virus F protein; MVF;			
XX	hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;			
XX	luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;			
XX	somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;			
XX	foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;			
XX	Plasmodium falciparum; circumsporozoite; antimalarial; CERP;			
XX	cholesterol ester transport protein; anti-arteriosclerotic.			
XX	Chimeric - Measles virus.			
XX	OS	Chimeric - Homo sapiens.		
XX	PN	MO9966957-A2.		
XX	PD	29-DEC-1999.		
XX	PF	21-JUN-1999; 99MO-US13975.		
XX	PR	20-JUN-1998; 98US-0100412.		

PA (UNBI-) UNITED BIOMEDICAL, INC.
XX
XX
PI Wang CY;
XX
XX
DR WPI; 2000-160564/14.
XX
XX New artificial T helper cell epitope and derived immunogens with target
PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT or human immune deficiency virus -
XX
XX
PS Claim 11: Page 104; 129pp; English.

The invention relates to novel promiscuous T helper cell epitopes (Th), and immunogenic peptides comprising the Th epitopes and peptide immunogens along with B cell epitopes. The Th epitopes and peptide immunogens containing them, are used to induce a T helper cell response, specifically against Plasmodium falciparum, cholesterol ester transport protein (CEMP) or HIV epitopes, but more generally against any pathogen, immunoreactive self-antigen or tumour antigen. The Th epitopes and peptide immunogens may be used for prevention and/or treatment of infections (HIV, foot-and-mouth disease or malaria); for cancer immunotherapy; for inhibition of the action of interleukin hormone releasing hormone (LHRH) for contraception, treatment of hormone-dependent cancer, prevention of boar taint in meat, and immunocastration); for promoting the growth of animals; or for treating allergies or arteriosclerosis. Incorporation of a promiscuous Th (functional in genetically diverse subjects) into an immunogen improves capacity to induce a strong T helper cell-mediated immune response, resulting in production of antibodies against a target antigen. Th can replace carrier proteins and pathogen-derived T helper epitopes. Sequence AA911121 represents a promiscuous T helper epitope from the measles virus F (W/F) protein and sequences AA911122-Y91142, AA912126 and AA912145-Y91246 represent synthetic Th epitopes based on the W/F Th epitope. Sequence AA911143 represents a promiscuous Th epitope from hepatitis B virus (HBV) surface antigen, and sequences AA911144-Y91155 are synthetic epitopes derived from this HBV epitope. AA911156-Y91196, AA912127 and AA912142-Y91244 are antigenic peptides comprising an LHRH sequence joined to a promiscuous Th epitope. AA911197 is the LHRH target antigenic peptide used in these LHRH antigenic peptides. AA912100 is somatostatin, and AA912101-Y91207 are antigenic peptides comprising somatostatin and a Th epitope. Somatostatin immunogens may be used to promote growth in livestock. AA912108 is a human CD4 CDR2-like domain antigenic site, and AA912109-Y90211 are W/H Th infection/CD4 CDR2 antigenic peptides which may be used to prevent HIV infection of T cells. AA90212 is a modified version of a human IGE (immunoglobulin E) CH3 domain, and AA90213-Y90219 are Th epitope/IGE CH3 antigenic peptides which may be used in the treatment of allergies. AA912120 is a peptide derived from foot and mouth disease virus (FMDV) VP1 capsid protein and AA912121-Y91222 comprises this peptide and a Th epitope. AA912123 is a Plasmodium falciparum circumsporozoite (CS) target antigen, and AA912124-Y91225 comprise the CS antigen and an W/F Th epitope and may be used in a malaria vaccine. AA912128-Y91231 represent CEMP-derived peptides and AA912123-Y91241 are immunogens comprising a CEMP peptide and a Th epitope which may be used to prevent or treat arteriosclerosis and cardiovascular disease. AA912147 and AA912152-Y91257 are HIV-1 neutralising B-cell epitopes, and AA912148-Y91251 and AA912158-Y91273 are antigenic peptides comprising W/H Th and HIV-1 B-cell epitopes which may be used as a component in an anti-HIV-1 vaccine. AA912198 and AA912199 are respectively an immunostimulatory invasive protein epitope from *Yersinia* species, and hinge spacer peptide, both of which may optionally be used in the antigenic peptides of the invention.

```
Query Match      52.5%; Score 85; DB 21; Length 46;
Best Local Similarity 94.1%; Pred. No. 6.6e-06;
Matches 16; Conservative 0; Indels 0; Gaps 0.
```

RESULT 13
 AAY91233
 ID AAY91233 standard; peptide; 46 AA.
 XX
 AC AAY91233;
 XX
 DT 22-MAY-2000 (first entry)
 XX
 DE Modified MVF Th epitope/CEP peptide, SEQ ID NO:111.
 XX
 KM Promiscuous T-cell epitope; measles virus F protein; MVF;
 KM hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KM interleukin-6; interleukin-6 releasing hormone; LHRH; contraceptive; anticancer;
 KM somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
 KM foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 KM Plasmodium falciparum; circumsporozoite; antimalarial; CEP;
 KM cholesterol ester transport protein; anti-arteriosclerotic.
 XX
 OS Chimeric - Measles virus.
 OS Chimeric - Homo sapiens.
 XX
 PN WO966957-A2.
 XX
 PD 29-DEC-1999.
 XX
 PF 21-JUN-1999; 99WO-US13975.
 XX
 PR 20-JUN-1998; 98US-0100412.
 XX
 PA (UNBI-) UNITED BIOMEDICAL INC.
 XX
 PI Wang CY;
 XX
 DR WPI: 2000-160564/14.
 XX
 PT New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus -
 PT
 PS Claim 11; Page 104-105; 129pp; English.
 XX
 CC The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response.
 CC Specifically against Plasmodium falciparum, cholesterol ester transport
 CC protein (CEP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of interleukin-6 releasing
 CC hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunocastration; for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAY9121 represents a promiscuous T helper epitope
 CC from the measles virus F (MVF) protein and sequences AAY91122-Y91142,
 CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
 CC MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
 CC peptides comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AAY91208 is a

CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVF Th
 CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
 CC infection of T cells. AAY90212 is a modified version of a human IgE
 CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IgE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
 CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th
 CC epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent
 CC CEP-derived peptides and AAY91232-Y91241 are immunogens comprising a
 CC CEP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
 CC AAY91258-Y91273 are antigenic peptides comprising MVF Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91198 and AAY91199 are respectively an immunostimulatory invasin
 CC protein epitope from Yersinia species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.
 XX
 SQ Sequence 46 AA;
 XX
 Query Match 52.5%; Score 85; DB 21; Length 46;
 Best Local Similarity 94.1%; Pred. No. 6,6e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 15 ERGFPEHLVDLOSLS 31
 Db 30 diGFpHLVDfLgSLs 46
 :|||||
 RESULT 14
 AAY06127
 ID AAY06127 standard; Protein; 476 AA.
 XX
 AC AAY06127;
 XX
 DT 07-FEB-1997 (first entry)
 XX
 DE Human cholesterol ester transfer protein.
 XX
 KM Cholesterol ester transfer protein; CEP; antigen; vaccine;
 KM cardiovascular disease; atherosclerosis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 349..367
 FT /label= B-cell_epitope
 FT Region 461..476
 FT /label= B-cell_epitope
 FT /note= "C-terminal epitope involved in neutral
 FT lipid binding or a transfer activity of
 FT CEP (Claim 5)"
 XX
 PN MO9634888-A1.
 XX
 PD 07-NOV-1996.
 XX
 PF 01-MAY-1996; 96WO-US06147.
 XX
 PR 01-MAY-1995; 95US-0432483.
 XX
 PA (TCEL-) T CELL SCI INC.
 XX
 PI Rittershaus CW, Thomas LJ;
 XX
 DR WPI: 1996-506103/50.
 XX
 PT Cholesterol ester transfer protein B cell epitope linked to T cell
 PT epitope - used to generate vaccine to regulate CEP activity for

PT decreasing the risk of developing a cardiovascular disease e.g.
 PT atherosclerosis
 XX
 XX
 PS Claim 2: Page 44-47; 72pp: English.
 CC Human liver mature cholesterol ester transfer protein (CETP) (AAW06127)
 CC plays a role in altering the relative profile of circulating
 CC lipoproteins to one associated with an increased risk of
 CC cardiovascular disease. B-cell epitopes (see also AAW06128) of CETP
 CC can be used in novel peptide vaccines (see also AAW06129, AAW06131)
 CC that elicit an immune response against endogenous CETP activity,
 CC thereby treating or preventing cardiovascular disease, such as
 CC atherosclerosis.
 XX
 SQ Sequence 476 AA;
 Query Match 52.5%; Score 85; DB 17; Length 476;
 Best Local Similarity 94.1%; Pred. No. 9.7e-05;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 15 EFGPEHLVDFLOSLS 31
 :|||||
 Db 460 dfgfpehllydfllqsls 476
 RESULT 15
 AAW46446
 ID AAW46446 standard; Peptide: 476 AA.
 XX
 AC AAW46446;
 XX
 DT 18-MAY-1998 (first entry)
 XX
 DE Human mature cholesterol ester transfer protein (CETP).
 XX
 XX Cholesterol ester transfer protein: CETP; cholesterol ester;
 KM high density lipoprotein; HDL; very low density lipoprotein; VLDL;
 KM low density lipoprotein; LDL; atherosclerosis; neutral lipid binding;
 KW transfer activity; immunogenic; B cell epitope; antibody; TP2;
 KM DNA plasmid-based vaccine; broad range helper T cell epitope;
 KM treatment; cardiovascular disease.
 XX
 OS Homo sapiens.
 XX
 PN WO97/41227-A1.
 XX
 PD 06-NOV-1997.
 XX
 PF 01-MAY-1997; 97WO-US07294.
 XX
 PR 21-FEB-1997; 97US-0802967.
 PR 01-MAY-1996; 96US-0640713.
 XX
 PA (TCCL-) T CELL SCI INC.
 XX
 PI Thomas LJ;
 XX
 DR WPI: 1997-549731/50.
 DR N-PSDB: AAV05127.
 XX
 PT DNA plasmid-based vaccine encodes CETP B cell and helper T cell
 PT epitope(s) - used for elevating high density lipoprotein levels, and
 PT for treating cardiovascular disease
 XX
 PS Claim 6: Pages 36-38; 67pp: English.
 CC The present sequence represents a human mature cholesterol ester transfer
 CC protein (CETP). CETP mediates the transfer of cholesterol esters from
 CC high density lipoprotein (HDL) to very low density lipoprotein (VLDL) and
 CC low density lipoprotein (LDL). An increased CETP activity
 CC produces an atherogenic lipoprotein profile and induces atherosclerosis.
 CC A 13 amino acid stretch in the human CETP (Phe463 to Leu475), and also

CC possibly Asp460, are particularly important for neutral lipid binding and
 CC transfer activity. This region has been shown to be immunogenic as a B
 CC cell epitope of CETP, and a monoclonal antibody (TP2) directed at this
 CC region has been shown to inhibit neutral lipid transfer. A second B cell
 CC epitope is defined by Arg349 to Ile367. Antibodies to this second epitope
 CC would allow the formation of immune complexes involving CETP, and promote
 CC the removal of the complexed CETP. This peptide region was selected for
 CC its potential antigenicity and high possibility for surface expression
 CC on native CETP. Sequences encoding these 2 epitopes can be used in a DNA
 CC plasmid-based vaccine which comprises sequences encoding at least 1 B
 CC cell epitope of CETP linked in frame with at least one segment encoding
 CC a broad range helper T cell epitope. The vaccines can be used to elevate
 CC the ratio of circulating HDL to circulating LDL, VLDL or total
 CC cholesterol in a human. It can also be used for decreasing the level of
 CC endogenous CETP activity in a human. The vaccine can be used to produce
 CC anti-CETP antibodies in vivo and for treating cardiovascular disease.
 XX
 SQ Sequence 476 AA;
 Query Match 52.5%; Score 85; DB 18; Length 476;
 Best Local Similarity 94.1%; Pred. No. 9.7e-05;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 15 EFGPEHLVDFLOSLS 31
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 Db 460 dfgfpehllydfllqsls 476

Search completed: June 18, 2002, 08:08:27
 Job time: 156 sec

GenCore version 4.5
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OM protein - protein search, using sw model

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(without alignments)
53.068 Million cell updates/sec

Title: US-09-943-334-2

Perfect score: 162
Sequence: 1 COYKANSKFTGITEFGPEHLVDPLQSL 31

Scoring table:

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Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 350:263

Minimum DB seq length: 0
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Maximum Match 100%

Listing first 45 summaries

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Pending Patents, AA, Main:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	162	100.0	31	13 US-08-954-643-7	Sequence 7, Appl1
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16	87	53.7	35	1 PCT-US99-139758-114	Sequence 114, App
17	87	53.7	35	21 US-09-701-568-114	Sequence 114, App
18	85	52.5	22	11 US-08-785-997-10	Sequence 10, Appl
19	85	52.5	22	11 US-08-785-997-34	Sequence 34, Appl
20	85	52.5	22	11 US-08-788-882-10	Sequence 10, Appl
21	85	52.5	22	11 US-08-788-882-34	Sequence 34, Appl
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26	85	52.5	22	17 US-09-387-340-10	Sequence 10, Appl
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44	85	52.5	470	19 US-09-518-598-14	Sequence 14, Appl
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ALIGNMENTS

RESULT 1
US-08-432-483-2
; Sequence 2, Application US/08432483
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles, W.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
; TITLE OF INVENTION: TRANSFER PROTEIN (CEP) ACTIVITY
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: Ten South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-7407
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/432,483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Leon R. Yankwich
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: 95,179(TCS-95179)

```

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL:
; ANTI-SENSE:
; FEATURE:
; NAME/KEY:
; LOCATION:
; US-08-432-483A-2

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Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-08-432-483A-2
; Sequence 2, Application US/08432483A
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
; TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: Ten South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-7407
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/432,483A
; FILING DATE: 1-May-1995
; CLASSIFICATION: 424
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Leon R. Yankwich
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: 95,179(TCS-95179)
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL:
; ANTI-SENSE:
; FEATURE:
; NAME/KEY:
; LOCATION:
; US-08-432-483A-2

Query Match          100.0%; Score 162; DB 8; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 COYIKANSKFIGITTEFGPEHLVDPLQSL 31
```

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Db      1 COYIKANSKFIGITTEFGPEHLVDPLQSL 31
        |||||||||||||||||||||||||||||

RESULT 3
US-08-945-289-2
; Sequence 2, Application US/08945289
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles, W.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
; TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/945,289
; FILING DATE: October 17, 1997
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/432,483
; FILING DATE: May 1, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Leon R. Yankwich
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: TCS-411.1P US
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL:
; ANTI-SENSE:
; FEATURE:
; NAME/KEY:
; LOCATION:
; US-08-945-289-2

Query Match          100.0%; Score 162; DB 13; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 COYIKANSKFIGITTEFGPEHLVDPLQSL 31
        |||||||||||||||||||||||||||||
        1 COYIKANSKFIGITTEFGPEHLVDPLQSL 31

RESULT 4
US-08-954-643-7
; Sequence 7, Application US/08954643
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles, W.
; TITLE OF INVENTION: XENOGENIC CHOLESTERYL ESTER
; TITLE OF INVENTION: TRANSFER PROTEIN (CETP) FOR MODULATION OF CETP ACTIVITY
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: MA
```

COUNTRY: U.S.A.
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,643
FILING DATE: concurrently herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: TCS-420.0 US
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-954-643-7

Query Match 100.0%; Score 162; DB 13; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 COYIKANSKFIGITTEGPEPHLLVDFLOSLS 31
DB 1 COYIKANSKFIGITTEGPEPHLLVDFLOSLS 31

RESULT 5
US-09-529-762-7
; Sequence 7, Application US/09529762
; GENERAL INFORMATION:
; APPLICANT: AVANT Immunotherapeutics, Inc.
; APPLICANT: Rittershaus, Charles
; TITLE OF INVENTION: Xenogeneic Cholesteryl Ester Transfer Protein (CETP) for
; FILE REFERENCE: sequence listing for TCS-420.1 PCT
; CURRENT APPLICATION NUMBER: US/09/529,762
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: USSN 08/954,643
; PRIOR FILING DATE: 1997-10-20
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 7
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: fusion protein containing tetanus toxoid segment
; OTHER INFORMATION: Linked to human CETP C-terminus
US-09-529-762-7

Query Match 100.0%; Score 162; DB 19; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 COYIKANSKFIGITTEGPEPHLLVDFLOSLS 31
DB 1 COYIKANSKFIGITTEGPEPHLLVDFLOSLS 31

RESULT 6

US-09-943-334-2
; Sequence 2, Application US/09943334
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; APPLICANT: Thomas, Lawrence J.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVI
; FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
; CURRENT APPLICATION NUMBER: US/09/943,334
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 08/432,483
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: PCT/US96/06147
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/945,289
; PRIOR FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: vaccine peptide of the invention
US-09-943-334-2

Query Match 100.0%; Score 162; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 COYIKANSKFIGITTEGPEPHLLVDFLOSLS 31
DB 1 COYIKANSKFIGITTEGPEPHLLVDFLOSLS 31

RESULT 7
US-09-943-548-2
; Sequence 2, Application US/09943548
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; APPLICANT: Thomas, Lawrence J.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVI
; FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
; CURRENT APPLICATION NUMBER: US/09/943,548
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 08/432,483
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: PCT/US96/06147
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/945,289
; PRIOR FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: vaccine peptide of the invention
US-09-943-548-2

Query Match 100.0%; Score 162; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 COYIKANSKFIGITTEGPEPHLLVDFLOSLS 31
DB 1 COYIKANSKFIGITTEGPEPHLLVDFLOSLS 31

RESULT 8
US-08-945-289-8

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; Sequence 8, Application US/08945289
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
; TITLE OF INVENTION: TRANSFER PROTEIN (CEP) ACTIVITY
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; City: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/945,289
; FILING DATE: October 17, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/432,483
; FILING DATE: May 1, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Leon R. Yankwich
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: TCS-411.1P US
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL:
; ANTI-SENSE:
; FEATURE:
; NAME/KEY:
; LOCATION:
; US-08-945-289-8

Query Match      88.0%; Score 142.5; DB 13; Length 50;
Best Local Similarity 62.0%; Pred. No. 6.9e-14;
Matches 31; Conservative 0; Mismatches 0; Indels 19; Gaps 1;

QY 1 COYKANSKFIGITE-----FGPPEHLVDFLOSLS 31
DB 1 COYKANSKFIGITELFPPRDOQHSVAYTFEEDIFGPEHLVDFLOSLS 50

RESULT 9
US-09-943-334-8
; Sequence 8, Application US/09943334
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CEP) ACTIVITY
; FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
; CURRENT APPLICATION NUMBER: US/09/943,334
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 08/432,483
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: PCT/US96/06147
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/945,289
; PRIOR FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 50

```

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: vaccine peptide of the invention
US-09-943-334-8

Query Match      88.0%; Score 142.5; DB 23; Length 50;
Best Local Similarity 62.0%; Pred. No. 6.9e-14;
Matches 31; Conservative 0; Mismatches 0; Indels 19; Gaps 1;

QY 1 COYKANSKFIGITE-----FGPPEHLVDFLOSLS 31
DB 1 COYKANSKFIGITELFPPRDOQHSVAYTFEEDIFGPEHLVDFLOSLS 50

RESULT 10
US-09-943-548-8
; Sequence 8, Application US/09943548
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CEP) ACTIVITY
; FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
; CURRENT APPLICATION NUMBER: US/09/943,548
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 08/432,483
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: PCT/US96/06147
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/945,289
; PRIOR FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: vaccine peptide of the invention
US-09-943-548-8

Query Match      88.0%; Score 142.5; DB 23; Length 50;
Best Local Similarity 62.0%; Pred. No. 6.9e-14;
Matches 31; Conservative 0; Mismatches 0; Indels 19; Gaps 1;

QY 1 COYKANSKFIGITE-----FGPPEHLVDFLOSLS 31
DB 1 COYKANSKFIGITELFPPRDOQHSVAYTFEEDIFGPEHLVDFLOSLS 50

RESULT 11
US-08-640-713-7
; Sequence 7, Application US/08640713
; GENERAL INFORMATION:
; APPLICANT: Thomas, Lawrence J.
; TITLE OF INVENTION: PLASMIN-BASED VACCINE FOR TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 75 State Street
; City: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/08/640,713
FILING DATE: May 1, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,1102(TCS-205-999)
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL:
ANTI-SENSE:
FEATURE: amino acid sequence of peptide encoded by
bases 10 to 159 of SEQ ID NO:5
NAME/KEY:
LOCATION:
US-08-640-713-7

Query Match 79.9%; Score 129.5; DB 10; Length 50;
Best Local Similarity 59.2%; Pred. No. 6.9e-12;
Matches 29; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

QY 2 QYKANSKFIGITE-----FGPPEHLVDFLOSL 31
Db 2 QYKANSKFIGITERPPRGREAVAYRFEEDIFGPPKHLVDFLOSL 50

RESULT 12
US-08-802-967A-7
Sequence 7, Application US/08802967A
GENERAL INFORMATION:
APPLICANT: Thomas, Lawrence J.
TITLE OF INVENTION: PLASMID-BASED VACCINE FOR
TITLE OF INVENTION: TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word 7
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,967A
FILING DATE: 21-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/640,713
FILING DATE: 01-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: TCS 414.1 US
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL:
ANTI-SENSE:
FEATURE:

NAME/KEY: amino acid sequence of peptide encoded
NAME/KEY: by bases 10 to 159 of SEQ ID NO:5
LOCATION:
US-08-802-967A-7

Query Match 79.9%; Score 129.5; DB 12; Length 50;
Best Local Similarity 59.2%; Pred. No. 6.9e-12;
Matches 29; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

QY 2 QYKANSKFIGITE-----FGPPEHLVDFLOSL 31
Db 2 QYKANSKFIGITERPPRGREAVAYRFEEDIFGPPKHLVDFLOSL 50

RESULT 13
US-08-945-289-9
Sequence 9, Application US/08945289
GENERAL INFORMATION:
APPLICANT: Rittershaus, Charles, W.
TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,289
FILING DATE: October 17, 1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/432,483
FILING DATE: May 1, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: TCS-411.1P US
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL:
ANTI-SENSE:
FEATURE:
NAME/KEY:
LOCATION:
US-08-945-289-9

Query Match 79.9%; Score 129.5; DB 13; Length 50;
Best Local Similarity 59.2%; Pred. No. 6.9e-12;
Matches 29; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

QY 2 QYKANSKFIGITE-----FGPPEHLVDFLOSL 31
Db 2 QYKANSKFIGITERPPRGREAVAYRFEEDIFGPPKHLVDFLOSL 50

RESULT 14
US-09-943-334-9
Sequence 9, Application US/09943334

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; GENERAL INFORMATION:
; APPLICANT: Riltershaus, Charles W.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVITY
; FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
; CURRENT APPLICATION NUMBER: US/09/943,334
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 08/432,483
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: PCT/US96/06147
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/945,289
; PRIOR FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: vaccine peptide of the invention
US-09-943-334-9
```

```
Query Match          79.9%; Score 129.5; DB 23; Length 50;
Best local Similarity 59.2%; Pred. No. 6,9e-12;
Matches 29; Conservative 1; Mismatches 0; Indels 19; Gaps 1;
```

```
OY 2 QYIKANSKFIGITE-----FGFPEHLVDFLOSLS 31
DB 2 QYIKANSKFIGITERPPDGRAVAYRPEEDIFGPKHLVDFLOSLS 50
```

```
RESULT 15
US-09-943-548-9
; Sequence 9, Application US/09943548
; GENERAL INFORMATION:
; APPLICANT: Riltershaus, Charles W.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVITY
; FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
; CURRENT APPLICATION NUMBER: US/09/943,348
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 08/432,483
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: PCT/US96/06147
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/945,289
; PRIOR FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: vaccine peptide of the invention
US-09-943-548-9
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```
Query Match          79.9%; Score 129.5; DB 23; Length 50;
Best local Similarity 59.2%; Pred. No. 6,9e-12;
Matches 29; Conservative 1; Mismatches 0; Indels 19; Gaps 1;
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```
OY 2 QYIKANSKFIGITE-----FGFPEHLVDFLOSLS 31
DB 2 QYIKANSKFIGITERPPDGRAVAYRPEEDIFGPKHLVDFLOSLS 50
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Search completed: June 18, 2002, 08:11:59
Job time: 368 sec

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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:07:29 ; Search time 26.23 Seconds

(without alignments)
99,954 Million cell updates/sec

Title: US-09-943-334-2

Sequence: 162
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Gapop 10.0, Gapext 0.5

Searched: 257105 seqs, 84670655 residues

Total number of hits satisfying chosen parameters: 257105

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	85	52.5	470	5	US-09-446-415B-6
2	78.5	48.5	24	6	US-10-128-711-110
3	71.5	44.1	27	6	US-10-076-674-7
4	71.5	44.1	27	6	US-10-076-674A-7
5	70	43.2	14	5	US-09-707-738-5
6	70	43.2	14	5	US-09-543-608A-38
7	70	43.2	14	5	US-09-709-774-5
8	70	43.2	14	5	US-09-942-052-710
9	70	43.2	14	5	US-09-260-714B-1
10	70	43.2	14	6	US-10-128-711-95
11	70	43.2	14	6	US-10-001-469-1403
12	70	43.2	15	5	US-09-413-186A-11
13	70	43.2	17	1	PCT-US02-10293-3
14	70	43.2	25	5	US-09-413-186A-14
15	70	43.2	25	5	US-09-413-186A-15
16	70	43.2	25	5	US-09-413-186A-16
17	70	43.2	27	6	US-10-128-711-111
18	70	43.2	27	6	US-10-128-711-112
19	70	43.2	1315	6	US-10-018-997-1
20	53	32.7	11	5	US-09-523-033A-3
21	51	31.5	348	7	US-60-360-039-850
22	49	30.2	80	5	US-09-620-393B-4183
23	49	30.2	80	5	US-09-620-393B-8965
24	49	30.2	99	5	US-09-620-393B-4182
25	49	30.2	99	5	US-09-620-393B-8964
26	49	30.2	120	5	US-09-620-393B-4181

27	49	30.2	120	5	US-09-620-393B-8963	Sequence 8963, Ap
28	48.5	29.9	735	6	US-10-032-361-2	Sequence 2, Appl
29	48.5	29.9	826	1	PCT-US02-08886-10	Sequence 10, Appl
30	48.5	29.9	826	1	PCT-US02-08864-6	Sequence 6, Appl
31	48.5	29.9	826	1	PCT-US02-08946-2	Sequence 2, Appl
32	48.5	29.9	826	1	PCT-US02-08946-5	Sequence 5, Appl
33	48.5	29.9	826	1	PCT-US02-08946-6	Sequence 6, Appl
34	48.5	29.9	826	1	PCT-US02-08946-7	Sequence 7, Appl
35	48.5	29.9	826	5	US-09-555-362-10	Sequence 10, Appl
36	48.5	29.9	826	6	US-10-032-361-1	Sequence 1, Appl
37	48.5	29.9	826	6	US-10-113-872-330	Sequence 330, App
38	48.5	29.9	826	6	US-10-028-158-23	Sequence 23, Appl
39	48.5	29.9	826	6	US-10-007-255-4	Sequence 4, Appl
40	47	29.0	391	6	US-09-540-209B-8239	Sequence 8239, Ap
41	47	29.0	535	6	US-10-102-806-729	Sequence 729, Appl
42	47	29.0	538	1	PCT-US02-11152-5	Sequence 5, Appl
43	46	28.4	555	6	US-10-104-047-2011	Sequence 2011, Ap
44	46	28.4	1038	5	US-09-935-625-16166	Sequence 16166, A
45	46	28.4	1124	5	US-09-935-625-22443	Sequence 22443, A

ALIGNMENTS

```
RESULT 1
US-09-446-415B-6
; Sequence 6, Application 94/09446415B
; GENERAL INFORMATION:
; APPLICANT: Beamer, Lesa J.
; APPLICANT: Eisenberg, David J.
; TITLE OF INVENTION: BACTERICIDAL/PERMEABILITY-INCREASING PROTEIN:
; TITLE OF INVENTION: CRYSTALLIZATION, X-RAY DIFFRACTION, THREE-DIMENSIONAL
; TITLE OF INVENTION: STRUCTURE DETERMINATION, RATIONAL DRUG DESIGN AND
; TITLE OF INVENTION: MOLECULAR MODELING OF RELATED PROTEINS
; FILE REFERENCE: 11034US02
; CURRENT APPLICATION NUMBER: US/09/446,415B
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 08/879,565
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; OTHER INFORMATION: 5)
; OTHER INFORMATION: 5)
US-09-446-415B-6
Query Match 52.5%; Score 85; DB 5; Length 470;
Best Local Similarity 94.1%; Pred. No. 5e+05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Cy 15 EFGPEHLVDFLOSLS 31
Db 454 DFGPEHLVDFLOSLS 470
RESULT 2
US-10-128-711-110
; Sequence 110, Application US/10128711
; GENERAL INFORMATION:
; APPLICANT: VITTELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Steffen
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
```

```

CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Hourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/128,711
FILING DATE: 22-Apr-2002
CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/197,484
FILING DATE: 16-FEB-1994
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (206) 623-6793

INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 110:
US-10-128-711-110

Query Match      48.5%; Score 78.5; DB 6; Length 24;
Best Local Similarity 65.5%; Pred. No. 1.8e-05;
Matches 19; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

OY      2 OYKANSKFIGITTEGPEHLVDFLOSL 30
DB      1 OYKANSKFIGITTEF-----LPSPDFPSV 24

RESULT      3
US-10-076-674-7
; Sequence 7, Application US/10076674
; GENERAL INFORMATION:
; APPLICANT: SOKOLL, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/076,674
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Human
US-10-076-674-7

Query Match      44.1%; Score 71.5; DB 6; Length 27;

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Best Local Similarity 80.0%; Pred. No. 0.00024;
Matches 16; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

OY      2 OYKANSKFIGITTEGPEFH 21
DB      3 OYKANSKFIGITEL---EH 19

RESULT      4
US-10-076-674A-7
; Sequence 7, Application US/10076674A
; GENERAL INFORMATION:
; APPLICANT: SOKOLL, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/076,674A
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Human
US-10-076-674A-7

Query Match      44.1%; Score 71.5; DB 6; Length 27;
Best Local Similarity 80.0%; Pred. No. 0.00024;
Matches 16; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

OY      2 OYKANSKFIGITTEGPEFH 21
DB      3 OYKANSKFIGITEL---EH 19

RESULT      5
US-09-707-738-5
; Sequence 5, Application US/09707738
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Gaeta, Federico
; APPLICANT: Grey, Howard M.
; APPLICANT: Sidney, John
; APPLICANT: Alexander, Jeffery L.
; TITLE OF INVENTION: Induction of Immune Response Against
; FILE REFERENCE: Desired Determinants
; CURRENT APPLICATION NUMBER: US/09/707,738
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 08/121,101
; PRIOR FILING DATE: 1993-09-14
; PRIOR APPLICATION NUMBER: US 08/305,871
; PRIOR FILING DATE: 1994-09-14
; PRIOR APPLICATION NUMBER: US 08/485,218
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 60/010,510
; PRIOR FILING DATE: 1996-01-24
; PRIOR APPLICATION NUMBER: US 08/788,822
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 09/310,462
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Tet Tox 830-843, T-helper epitope from tetanus
; OTHER INFORMATION: toxin p2, peptide 553.01
US-09-707-738-5

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Query Match : 43.2%; Score 70; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OYIKANSKFIGITE 15
|||||
DB 1 OYIKANSKFIGITE 14

RESULT 6
US-09-543-608A-38

; Sequence 38, Application US/09543608A
; GENERAL INFORMATION:
; APPLICANT: Flakes, John D.
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Cells, Esteban
; APPLICANT: Keogh, Elissa A.
; APPLICANT: Chesnut, Robert
; APPLICANT: Eplimmune Inc.
; TITLE OF INVENTION: HLA Class I A2 Tumor Associated Antigen
; FILE REFERENCE: 018623-015710US
; CURRENT APPLICATION NUMBER: US/09/543,608A
; CURRENT FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: tetanus toxoid positions 830-843, Standard Peptide
; OTHER INFORMATION: 553.01
US-09-543-608A-38

Query Match : 43.2%; Score 70; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OYIKANSKFIGITE 15
|||||
DB 1 OYIKANSKFIGITE 14

RESULT 7
US-09-709-774-5

; Sequence 5, Application US/09709774
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Gaeta, Federico
; APPLICANT: Grey, Howard M.
; APPLICANT: Sidney, John
; APPLICANT: Alexander, Jeffery L.
; APPLICANT: Eplimmune Inc.
; TITLE OF INVENTION: Alteration of Immune Response Using Pan DR-Binding
; FILE REFERENCE: 018623-006240US
; CURRENT APPLICATION NUMBER: US/09/709,774
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 08/121,101
; PRIOR FILING DATE: 1993-09-14
; PRIOR APPLICATION NUMBER: US 08/305,871
; PRIOR FILING DATE: 1994-09-14
; PRIOR APPLICATION NUMBER: US 60/010,510
; PRIOR FILING DATE: 1996-01-24
; PRIOR APPLICATION NUMBER: US 08/788,822
; PRIOR FILING DATE: 1997-01-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Tet Tox 830-843
US-09-709-774-5

Query Match : 43.2%; Score 70; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OYIKANSKFIGITE 15
|||||
DB 1 OYIKANSKFIGITE 14

RESULT 8
US-09-942-052-710

; Sequence 710, Application US/09942052
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Rid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 710
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Tetanus toxoid
US-09-942-052-710

Query Match : 43.2%; Score 70; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OYIKANSKFIGITE 15
|||||
DB 1 OYIKANSKFIGITE 14

RESULT 9
US-09-260-714B-1

; Sequence 1, Application US/09260714B
; GENERAL INFORMATION:
; APPLICANT: Eplimmune Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chesnut, Robert
; APPLICANT: Sidney, John
; TITLE OF INVENTION: PEPTIDES WITH INCREASED BINDING AFFINITY
; FILE REFERENCE: 39963-20028.00
; CURRENT APPLICATION NUMBER: US/09/260,714B
; CURRENT FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 14

TYPE: PRT
ORGANISM: Tetanus toxoid
US-09-260-714B-1

Query Match 43.2%; Score 70; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OYKANSKFIGITE 15
Db 1 OYKANSKFIGITE 14

RESULT 10
US-10-128-711-95

Sequence 95, Application US/10128711
GENERAL INFORMATION:

APPLICANT: VITIELLO, Maria A.
CHESTNOT, Robert W.
SETTE, Alessandro D.
CELIS, Esteban
GRAY, Howard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
CTL IMMUNITY

NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/128,711
FILING DATE: 22-Apr-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/197,484
FILING DATE: 16-Feb-1994
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-Aug-1992
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-Apr-1992
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-Jan-1992
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-Aug-1991

ATTORNEY/AGENT INFORMATION:

NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (206) 623-6793

INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:

NAME/KEY: Peptide

LOCATION: 1..14

OTHER INFORMATION: /note= "Tetanus toxoid 830-843"
US-10-128-711-95

Query Match 43.2%; Score 70; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OYKANSKFIGITE 15
Db 1 OYKANSKFIGITE 14

RESULT 11
US-10-001-469-1403

Sequence 1403, Application US/10001469
GENERAL INFORMATION:

APPLICANT: JAKOBOVITS, AYA
APPLICANT: RAITANO, ARTHUR
APPLICANT: AFAR, DANIEL
APPLICANT: SAFERAN, DOUGLAS
APPLICANT: HUBERT, RENE
APPLICANT: FARIS, MARY
APPLICANT: CHALITA-BID, PTA

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
TITLE OF INVENTION: 101P3A11 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20024.20

CURRENT APPLICATION NUMBER: US/10/001,469

CURRENT FILING DATE: 2002-05-20

PRIOR APPLICATION NUMBER: 60/157,902

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: 60/291,118

PRIOR FILING DATE: 2001-05-15

PRIOR APPLICATION NUMBER: 09/680,728

PRIOR FILING DATE: 2000-10-05

NUMBER OF SEQ ID NOS: 2888

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1403

LENGTH: 14

TYPE: PRT

ORGANISM: Clostridium sp.

US-10-001-469-1403

Query Match 43.2%; Score 70; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OYKANSKFIGITE 15
Db 1 OYKANSKFIGITE 14

RESULT 12
US-09-413-186A-11

Sequence 11, Application US/09413186A
GENERAL INFORMATION:

APPLICANT: Steinaa, Lucilla
APPLICANT: Mouritsen, Soren
APPLICANT: Gautam, Anand
APPLICANT: Haaning, Jesper
APPLICANT: Dalum, Iben
APPLICANT: Birk, Peter
APPLICANT: Leach, Dana
APPLICANT: Nielsen, Klaus

TITLE OF INVENTION: NOVEL METHODS FOR THERAPEUTIC VACCINATION
FILE REFERENCE: 3631-0115P

CURRENT APPLICATION NUMBER: US/09/413,186A

CURRENT FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: 60/105,011

PRIOR FILING DATE: 1998-10-20

PRIOR APPLICATION NUMBER: PA 1998 01261

PRIOR FILING DATE: 1998-10-05

NUMBER OF SEQ ID NOS: 36
US-10-128-711-95

SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 15
TYPE: PRT
ORGANISM: Clostridium tetani
US-09-413-186A-11

Query Match 43.2%; Score 70; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 QYKANSKFIGITE 15
DB 1 QYKANSKFIGITE 14

RESULT 13
PCT-US02-10293-3
Sequence 3, Application PC/TUS0210293
GENERAL INFORMATION:
APPLICANT: Wang, Chang YI
TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
FILE REFERENCE: 1151-4167
CURRENT APPLICATION NUMBER: PCT/US02/10293
CURRENT FILING DATE: 2002-04-02
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 17
TYPE: PRT
ORGANISM: Clostridium tetani
PCT-US02-10293-3

Query Match 43.2%; Score 70; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 QYKANSKFIGITE 15
DB 3 QYKANSKFIGITE 16

RESULT 14
US-09-413-186A-14
Sequence 14, Application US/09413186A
GENERAL INFORMATION:
APPLICANT: Steinna, Lucilla
APPLICANT: Mouritsen, Soren
APPLICANT: Gautam, Anand
APPLICANT: Haaning, Jesper
APPLICANT: Dalum, Iben
APPLICANT: Birk, Peter
APPLICANT: Leach, Dana
APPLICANT: Nielsen, Klaus
TITLE OF INVENTION: NOVEL METHODS FOR THERAPEUTIC VACCINATION
FILE REFERENCE: 3631-0115P
CURRENT APPLICATION NUMBER: US/09/413,186A
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/105,011
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: PA 1998 01261
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 25
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Fusion of tetanus toxoid epitope and PSM
US-09-413-186A-14

Query Match 43.2%; Score 70; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 QYKANSKFIGITE 15
DB 6 QYKANSKFIGITE 19

RESULT 15
US-09-413-186A-15
Sequence 15, Application US/09413186A
GENERAL INFORMATION:
APPLICANT: Steinna, Lucilla
APPLICANT: Mouritsen, Soren
APPLICANT: Gautam, Anand
APPLICANT: Haaning, Jesper
APPLICANT: Dalum, Iben
APPLICANT: Birk, Peter
APPLICANT: Leach, Dana
APPLICANT: Nielsen, Klaus
TITLE OF INVENTION: NOVEL METHODS FOR THERAPEUTIC VACCINATION
FILE REFERENCE: 3631-0115P
CURRENT APPLICATION NUMBER: US/09/413,186A
CURRENT FILING DATE: 1999-10-05
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: PA 1998 01261
PRIOR FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 25
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fusion of tetanus toxoid epitope and PSM
US-09-413-186A-15

Query Match 43.2%; Score 70; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 QYKANSKFIGITE 15
DB 6 QYKANSKFIGITE 19

Search completed: June 18, 2002, 08:07:29
Job time: 98 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:06:56 ; Search time 21.81 Seconds
(without alignments)
34.686 Million cell updates/sec

Title: US-09-943-334-2
Perfect score: 162
Sequence: 1 COYIKANSKFGITGTFEPPEHLVDPLQSLIS 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/1aa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	129.5	79.9	50	4	US-09-171-969-7
2	85	52.5	470	3	US-08-879-565-14
3	85	52.5	476	4	US-09-171-969-4
4	81	50.0	496	4	US-09-171-969-2
5	78.5	48.5	24	5	PCT-US92-07218-25
6	78.5	48.5	24	5	PCT-US95-02121-110
7	78.5	48.5	27	5	PCT-US92-07218-32
8	77.5	47.8	37	1	US-08-446-692-63
9	77.5	47.8	37	2	US-08-488-351A-63
10	76.5	47.2	47	1	US-08-446-692-35
11	76.5	47.2	47	1	US-08-488-351A-35
12	76	46.9	37	2	US-08-446-692-57
13	76	46.9	37	2	US-08-488-351A-57
14	71.5	44.1	27	1	US-08-446-692-13
15	71.5	44.1	27	2	US-08-488-351A-13
16	70	43.2	14	1	US-08-186-266-5
17	70	43.2	14	1	US-08-305-871A-5
18	70	43.2	14	1	US-08-465-167A-18
19	70	43.2	14	2	US-08-817-933A-9
20	70	43.2	14	5	PCT-US92-07218-15
21	70	43.2	14	5	PCT-US92-07218-90
22	70	43.2	14	5	PCT-US95-02121-95
23	70	43.2	15	2	US-08-319-704-10
24	70	43.2	15	2	US-08-661-052-6
25	70	43.2	15	2	US-08-460-502-7
26	70	43.2	15	4	US-09-046-373-2
27	70	43.2	15	4	US-09-188-082-6

28	70	43.2	15	5	PCT-US93-11703-69	Sequence 69, Appl
29	70	43.2	16	4	US-09-248-588-55	Sequence 55, Appl
30	70	43.2	17	1	US-08-446-692-4	Sequence 4, Appl
31	70	43.2	17	2	US-08-488-351A-4	Sequence 4, Appl
32	70	43.2	17	3	US-09-100-409A-40	Sequence 40, Appl
33	70	43.2	17	5	PCT-US95-08596-23	Sequence 23, Appl
34	70	43.2	17	5	PCT-US95-13841-7	Sequence 31, Appl
35	70	43.2	24	5	PCT-US92-07218-31	Sequence 31, Appl
36	70	43.2	27	5	PCT-US92-07218-26	Sequence 26, Appl
37	70	43.2	27	5	PCT-US92-07218-27	Sequence 27, Appl
38	70	43.2	27	5	PCT-US92-07218-28	Sequence 28, Appl
39	70	43.2	27	5	PCT-US95-02121-111	Sequence 111, App
40	70	43.2	27	5	PCT-US95-02121-112	Sequence 11, App
41	70	43.2	29	3	US-09-075-257A-13	Sequence 13, Appl
42	70	43.2	29	3	US-09-075-257A-14	Sequence 14, Appl
43	70	43.2	29	4	US-09-534-639-13	Sequence 13, Appl
44	70	43.2	29	4	US-09-534-639-14	Sequence 14, Appl
45	70	43.2	30	5	PCT-US92-07218-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-09-171-969-7
; Sequence 7, Application US/09171969
; Patent No. 6284533
GENERAL INFORMATION:
; APPLICANT: Thomas, Lawrence J.
; TITLE OF INVENTION: PLASMID-BASED VACCINE FOR TREATING ATHEROSCLEROSIS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 75 State Street, Suite 2300
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1807
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/171,969
; FILING DATE: 01 May 1997 (01.05.97)
; CLASSIFICATION: 514
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/640,713
; FILING DATE: 01 May 1996 (01.05.96)
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/802,967
; FILING DATE: 21 February 1997 (21.02.97)
ATTORNEY/AGENT INFORMATION:
; NAME: Leon R. Yankwich
; REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: TCS 414.1 PCT (05672)
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL:
; ANTI-SENSE:
; FEATURE: amino acid sequence of peptide encoded
; NAME/KEY: by bases 10 to 159 of SEQ ID NO:5
; LOCATION:
; US-09-171-969-7

Query Match 79.9%; Score 129.5; DB 4; Length 50;

Best Local Similarity 59.2%; Pred. No. 2.2e-14;
Matches 29; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

OY 2 OYKANSKFIGITE-----FGFPEHLVDFLOSL 31
|||||
DB 2 OYKANSKFIGITERPPDGRNAVYREEDIFGPKHLVDFLOSL 50

RESULT 2
US-08-879-565-14

; Sequence 14, Application US/08879565A

; Patent No. 6093573

; GENERAL INFORMATION:

; APPLICANT: Beamer, Lesa J.

; APPLICANT: Carroll, Stephen F.

; APPLICANT: Eisenberg, David

; TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF

; FILE REFERENCE: 1103/110340S01

; CURRENT APPLICATION NUMBER: US/08/879,565A

; CURRENT FILING DATE: 1997-06-20

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14

; LENGTH: 470

; TYPE: PRT

; ORGANISM: Human

; FEATURE:

; OTHER INFORMATION: cholesterol ester transfer protein (CETP) (Figure

; OTHER INFORMATION: 5)

US-08-879-565-14

Query Match 52.5%; Score 85; DB 3; Length 470;
Best Local Similarity 94.1%; Pred. No. 6.7e-06;

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 15 EFGFPEHLVDFLOSL 31
:|||||

DB 454 DFGFPEHLVDFLOSL 470

RESULT 3

US-09-171-969-4

; Sequence 4, Application US/09171969

; Patent No. 6284533

; GENERAL INFORMATION:

; APPLICANT: Thomas, Lawrence J.

; TITLE OF INVENTION: PLASMID-BASED VACCINE FOR TREATING ATHEROSCLEROSIS

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Banner & Witcoff, Ltd.

; STREET: 75 State Street, Suite 2300

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1807

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WordPerfect 6.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/171,969

; FILING DATE: 01 May 1997 (01.05.97)

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/640,713

; FILING DATE: 01 May 1996 (01.05.96)

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/802,967

; FILING DATE: 21 February 1997 (21.02.97)

; ATTORNEY/AGENT INFORMATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Leon R. Yankwich
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: TCS 414.1 PCT (05872)

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 476 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL:

; ANTI-SENSE:

; FEATURE:

; NAME/KEY: Amino acid sequence of mature human

; NAME/KEY: CETP

; LOCATION:

; PUBLICATION INFORMATION:

; AUTHORS: Dayana, Dennis, et al.

; TITLE: Cloning and sequencing of human

; TITLE: cholesterol ester transfer cDNA

; JOURNAL: Nature

; VOLUME: 327

; ISSUE:

; PAGES: 632 - 634

; DATE: 18-JUN-1987

; RELEVANT RESIDUES IN SEQ ID NO: 4: FROM 1 TO 476

US-09-171-969-4

Query Match 52.5%; Score 85; DB 4; Length 476;
Best Local Similarity 94.1%; Pred. No. 6.8e-06;

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 15 EFGFPEHLVDFLOSL 31
:|||||

DB 460 DFGFPEHLVDFLOSL 476

RESULT 4

US-09-171-969-2

; Sequence 2, Application US/09171969

; Patent No. 6284533

; GENERAL INFORMATION:

; APPLICANT: Thomas, Lawrence J.

; TITLE OF INVENTION: PLASMID-BASED VACCINE FOR TREATING ATHEROSCLEROSIS

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Banner & Witcoff, Ltd.

; STREET: 75 State Street, Suite 2300

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1807

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WordPerfect 6.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/171,969

; FILING DATE: 01 May 1997 (01.05.97)

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/640,713

; FILING DATE: 01 May 1996 (01.05.96)

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/802,967

; FILING DATE: 21 February 1997 (21.02.97)

; ATTORNEY/AGENT INFORMATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Leon R. Yankwich

; REGISTRATION NUMBER: 30,237

; REFERENCE/DOCKET NUMBER: TCS 414.1 PCT (05872)

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

LENGTH: 496 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL:
ANTI-SENSE:
FEATURE:
NAME/KEY: amino acid sequence for mature
NAME/KEY: rabbit CERP protein.
LOCATION:
PUBLICATION INFORMATION:
AUTHORS: Nagashima, Mariko, et al.
TITLE: Cloning and mRNA tissue
TITLE: distribution of rabbit
TITLE: cholesterol ester transfer
TITLE: protein
JOURNAL: J. Lipid Res.
VOLUME: 29
ISSUE:
PAGES: 1643 - 1649
DATE: 1988
RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 496
US-09-171-969-2

Query Match 50.0%; Score 81; DB 4; Length 496;
Best Local Similarity 88.2%; Pred. No. 3.3e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 15 ERGPEHLVDFLOSL 31
DB 480 DFGFPHLLVDFLOSL 496

RESULT 5
PCT-US92-07218-25
Sequence 25, Application PC/TUS9207218
GENERAL INFORMATION:
APPLICANT: Vitello, Maria A.
TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS CTL
TITLE OF INVENTION: EPTOPES
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07218
FILING DATE: 19920826
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14137-26-3
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US92-07218-25

Query Match 48.5%; Score 78.5; DB 5; Length 24;
Best Local Similarity 65.5%; Pred. No. 2.2e-06;
Matches 19; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

QY 2 QYKANSKFTGTERGPEHLVDFLOSL 30
DB 1 QYKANSKFTGTERGPEHLVDFLOSL 24

RESULT 6
PCT-US95-02121-110
Sequence 110, Application PC/TUS9502121
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: CTL IMMUNITY
NUMBER OF SEQUENCES: 153
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02121
FILING DATE: 16-FEB-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,484
FILING DATE: 16-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US95-02121-110

Query Match 48.5%; Score 78.5; DB 5; Length 24;
Best Local Similarity 65.5%; Pred. No. 2.2e-06;
Matches 19; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

```
QY      2 QYKANSKFIGITEFGPEHLLVDLQSL    30
          ||||| | | | | | | | | | | :
Db      1 QYKANSKFIGITEF-----LPSDFFPSV    24
```

RESULT 7
PCT-US92-07218-32

Sequence 32, Application PC/VUSS9207218
GENERAL INFORMATION:
APPLICANT: Vitello, Maria A.
APPLICANT: Chesnut, Robert W.
TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS C
TITLE OF INVENTION: EPTIOPES
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

RESULT 8
US-08-446-692-63
; Sequence 63, Application US/08446692
; Patent No. 5759551
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi

1
 2 APPLICANT: Zamb, Timothy
 3 TITLE OF INVENTION: Immunogenic LHRH peptide constructs
 4 TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
 5 NUMBER OF SEQUENCES: 114
 6
 7 CORRESPONDENCE ADDRESS:

Query Match	47.88;	Score 77.5;	DB 1;	Length 37;
Best Local Similarity	63.08;	Pred. No. 5.5e-06;		
Matches 17; Conservative	1;	Mismatches 2;	Indels 7;	Gaps 1;

RESULT 9
 US-08-488-351A-63
 : Sequence 63, Application US/08488351A
 : Patent No. 5843446
 : GENERAL INFORMATION:
 : APPLICANT: Ladd, Anna
 : APPLICANT: Wang, Chang Yi
 : APPLICANT: Zamb, Timothy
 : TITLE OF INVENTION: Immunogenic LHRH peptide constructs
 : TITLE OF INVENTION: and sythetic universal immune stimulatois for vaccines
 : NUMBER OF SPOUGNCES: 114
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Maria C.H. Lin
 : STREET: 345 Park Avenue
 : CITY: New York
 : STATE: NY
 : COUNTRY: US
 : ZIP: 10154-0053
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/488.351A
 : FILING DATE: 7-JUN-1995
 : CLASSIFICATION: 424
 : PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,275
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,166
; FILING DATE: 27-APR-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-488-351A-63

Query Match 47.88; Score 77.5; DB 2; Length 37;
Best Local Similarity 65.08; Pred. No. 5.5e-06;
Matches 17; Conservative 1; Mismatches 2; Indels 7; Gaps 1;

QY 2 QYKANSKFGITGTEG-----PPEH 21
Db 5 QYKANSKFGITGTEGSKAKSKFPSPY 31

RESULT 10
US-08-446-692-35
; Sequence 35, Application US/08446692
; Patent No. 5759551
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang YI
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulatores for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 amino acids
```

```

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-446-692-35

Query Match 47.28; Score 76.5; DB 1; Length 47;
Best Local Similarity 85.08; Pred. No. 1.1e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 2 QYKANSKFGITGTEGPEH 21
Db 21 QYKANSKFGITGTEG-GEH 39

RESULT 11
US-08-488-351A-35
; Sequence 35, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang YI
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulatores for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,351A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,275
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,166
; FILING DATE: 27-APR-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-488-351A-35

Query Match 47.28; Score 76.5; DB 2; Length 47;
Best Local Similarity 85.08; Pred. No. 1.1e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
```

QY 2 QYKANSKFIGHTFEGP 21
| | | | | | | | | | | | | | | | | |
DB 21 QYKANSKFIGHTELG-GEH 39

RESULT 12

US-08-446-692-57
Sequence 57, Application US/08446692

Patent No. 5759551

GENERAL INFORMATION:

APPLICANT: Ladd, Anna

APPLICANT: Wang, Chang Yi

TITLE OF INVENTION: Immunogenic LHRH peptide constructs

TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines

NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:

ADDRESSEE: Maria C.H. Lin

STREET: 345 Park Avenue

CITY: New York

STATE: NY

COUNTRY: US

ZIP: 10154-0053

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/446,692

FILING DATE: 7-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Maria C.H. Lin

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1151-4146 US2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)415-8745

TELEFAX: (516)751-6849

INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:

LENGTH: 37 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-446-692-57

Query Match 46.9%; Score 76; DB 1; Length 37;

Best Local Similarity 93.8%; Pred. No. 9.7e-06;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYKANSKFIGHTFEG 17

| | | | | | | | | | | | | | | | | |

DB 21 QYKANSKFIGHTELG 36

RESULT 13

US-08-488-351A-57

Sequence 57, Application US/08488351A

Patent No. 5843446

GENERAL INFORMATION:

APPLICANT: Ladd, Anna

APPLICANT: Wang, Chang Yi

TITLE OF INVENTION: Immunogenic LHRH peptide constructs

TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines

NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:

ADDRESSEE: Maria C.H. Lin

STREET: 345 Park Avenue

CITY: New York

STATE: NY

COUNTRY: US

ZIP: 10154-0053

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,351A

FILING DATE: 7-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/446,692

FILING DATE: 7-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/229,275

FILING DATE: 14-APR-1994

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/057,166

FILING DATE: 27-APR-1992

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Maria C.H. Lin

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1151-4146 US2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)415-8745

TELEFAX: (516)751-6849

INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:

LENGTH: 37 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-488-351A-57

Query Match 46.9%; Score 76; DB 2; Length 37;

Best Local Similarity 93.8%; Pred. No. 9.7e-06;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QYKANSKFIGHTFEG 17

| | | | | | | | | | | | | | | | | |

DB 21 QYKANSKFIGHTELG 36

RESULT 14

US-08-446-692-13

Sequence 13, Application US/08446692

Patent No. 5759551

GENERAL INFORMATION:

APPLICANT: Ladd, Anna

APPLICANT: Wang, Chang Yi

TITLE OF INVENTION: Immunogenic LHRH peptide constructs

TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines

NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:

ADDRESSEE: Maria C.H. Lin

STREET: 345 Park Avenue

CITY: New York

STATE: NY

COUNTRY: US

ZIP: 10154-0053

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/446,692
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-446-692-13

Query Match 44.1%; Score 71.5; DB 1; Length 27;
Best Local Similarity 80.0%; Pred. No. 3.7e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

OY 2 QYIKANSKFIGITEFGFEPH 21
|||
Db 3 QYIKANSKFIGITEL---EH 19

RESULT 15
US-08-488-351A-13
Sequence 13, Application US/08488351A
Patent No. 5843446
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Mang, Chang Yi
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,351A
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,692
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/229,275
FILING DATE: 14-APR-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,166
FILING DATE: 27-APR-1992
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745

TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-488-351A-13

Query Match 44.1%; Score 71.5; DB 2; Length 27;
Best Local Similarity 80.0%; Pred. No. 3.7e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

OY 2 QYIKANSKFIGITEFGFEPH 21
|||
Db 3 QYIKANSKFIGITEL---EH 19

Search completed: June 18, 2002, 08:06:57
Job time: 66 sec

6

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:08:31 ; Search time 14.11 Seconds
(without alignments)
177.060 Million cell updates/sec

Title: US-09-943-334-1
Perfect score: 134
Sequence: 1 RDGFLLLQMDGFPENHLVDFLOSL 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 5201

Minimum DB seq length: 0
Maximum DB seq length: 26

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	20.9	19	2 A39504	octamer-binding pr
2	28	20.9	24	2 A24417	interphotoreceptor
3	28	20.9	26	2 B59018	MUC1 enhancer bind
4	27	20.1	21	2 A32521	hexokinase (EC 2.7
5	27	20.1	23	2 S43532	cytochrome-c oxida
6	27	20.1	26	2 S78374	hypothetical prote
7	26.5	19.8	20	2 A54077	cytochrome b558 -
8	26	19.4	15	2 S59492	formate dehydrogen
9	26	19.4	25	2 B24417	interphotoreceptor
10	26	19.4	26	2 C85947	hypothetical prote
11	25	18.7	15	2 S71306	heat shock protein
12	25	18.7	16	2 T44936	calmodulin kinase
13	25	18.7	16	2 C49048	T-cell receptor be
14	25	18.7	17	2 PH1607	Ig H chain V-D-J r
15	25	18.7	20	2 S77989	cytochrome-c oxida
16	25	18.7	23	2 PC4030	rRNA endonuclease
17	25	18.7	25	2 A60502	myonexin - norther
18	24.5	18.3	14	2 B61597	cytochrome P450 AL
19	24	17.9	13	2 S03879	6-phosphofructokin
20	24	17.9	14	2 A01250	angiotensin I precu
21	24	17.9	15	2 A60834	angiotensin I precu
22	24	17.9	17	2 B31769	T-cell receptor de
23	24	17.9	18	2 PN0175	glutathione transf
24	24	17.9	18	2 H75063	hypothetical prote
25	24	17.9	20	2 A60822	cytochrome P450 PB
26	24	17.9	20	2 A37984	ADP-ATP carrier pr
27	23	17.2	7	2 S36662	dermorphin (Lys-7)
28	23	17.2	14	2 PA0015	seed storage prote
29	23	17.2	17	2 S71864	glutathione transf

30	23	17.2	19	2 I46554	T-cell receptor de
31	23	17.2	21	2 T07683	proteinase inhibit
32	23	17.2	23	2 I39681	exog protein - Aer
33	23	17.2	24	2 PC2199	alicyclic amine N-
34	23	17.2	24	2 T42257	phosphoprotein pho
35	23	17.2	24	2 A53557	neurotoxin Bt-II -
36	23	17.2	25	2 S35926	T-cell receptor ga
37	23	17.2	26	2 JT0965	cytochrome-c oxida
38	23	17.2	26	2 A42218	early protein Sx1
39	22	16.4	7	1 A61324	dermorphin - Robde
40	22	16.4	11	2 P70250	Ig heavy chain CRD
41	22	16.4	12	2 C36201	I-aminocyclopropan
42	22	16.4	14	2 A61002	photosystem II oxy
43	22	16.4	19	2 B60822	cytochrome P450 UT
44	22	16.4	20	2 S72501	protein kinase C 1
45	22	16.4	20	2 A31049	calsequestrin, fas

ALIGNMENTS

RESULT 1

in, Ku-like, 72K chain - human (fragment)
us (man)
sequence_revision 30-Dec-1991 #text_change 30-Sep-1993

; Gould, H.

352-3059, 1991

and characterization of Ku-2, an octamer-binding protein relate
19504; MUID:91131605

in

Query Match 20.9%; Score 28; DB 2; Length 19;
Best Local Similarity 71.4%; Pred. No. 5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 7 LQMDGFP 13
DB 11 LEMDVGF 17

RESULT 2

A24417 Interphotoreceptor retinoid-binding protein - sheep (fragment)

N:Alternate names: Interstitial retinol-binding protein

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C>Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 21-Nov-1997

C:Accession: A24417

R:Pong, S.L.; Cook, R.G.; Alvarez, R.A.; Llou, G.I.; Landers, R.A.; Bridges, C.D.B.

FEBS Lett. 205, 309-312, 1986

A:Title: N-terminal sequence homologues in interstitial retinol-binding proteins from

A:Reference number: A91365; MUID:86301171

A:Accession: A24417

A:Molecule type: protein

A:Residues: 1-24 <FON>

C:superfamily: Interphotoreceptor retinoid-binding protein

C:Keywords: duplication

Query Match 20.9%; Score 28; DB 2; Length 24;
Best Local Similarity 35.0%; Pred. No. 6.5e+02;
Matches 7; Conservative 5; Mismatches 2; Indels 6; Gaps 1;

OY 5 LLLQMDGFP 18
DB 5 LVLDMAQVLLDNYTFPENLM 24

RESULT 3
 B59018
 MUC1 enhancer binding protein 85K chain MUC1EBP-85 - human (fragments)
 C:Species: Homo sapiens (man)
 C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 08-May-1998
 C:Accession: B59018
 R:Abbe, M.; Smith, C.J.; Larson, C.J.
 Submitted to the Protein Sequence Database, May 1998
 A:Description: Involvement of "Ku-like" proteins in the transcription of MUC1/DF3, a brc
 A:Reference number: A59018
 A:Accession: B59018
 A:Molecule type: protein
 A:Residues: 1-17,18-26 <ABE>
 A:Experimental source: breast cancer cell line MCF-7
 C:Keywords: DNA binding; heterodimer

Query Match 20.9%; Score 28; DB 2; Length 26;
 Best Local Similarity 37.5%; Pred. No. 7,1e+02;
 Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 5 LLIQMDGFPEHLVD 20
 :| | | | |
 Db 9 VVLMXMDVGFTLPFLIE 24

RESULT 4
 A32521
 hexokinase (EC 2.7.1.1) I peptide III - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 12-Apr-1995
 C:Accession: A32521
 R:Schirch, D.M.; Wilson, J.E.
 Arch. Biochem. Biophys. 257, 1-12, 1987
 A:Title: Rat brain hexokinase: amino acid sequence at the substrate hexose binding site
 A:Reference number: A90080; MUID:87324917
 A:Accession: A32521
 A:Molecule type: protein
 A:Residues: 1-21 <SCH>
 A:Superfamily: human hexokinase I; hexokinase homology
 C:Keywords: ATP; glycolysis; phosphotransferase

Query Match 20.1%; Score 27; DB 2; Length 21;
 Best Local Similarity 50.0%; Pred. No. 8e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 7 LQMDGFPEPH 16
 | | | | |
 Db 3 LGTFSPFXH 12

RESULT 5
 S43632
 cytochrome-c oxidase (EC 1.9.3.1) chain VIIa, hepatic - rainbow trout (fragment)
 C:Species: Oncorhynchus mykiss (rainbow trout)
 C>Date: 20-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
 C:Accession: S43632
 R:Freund, R.; Kadenbach, B.
 Eur. J. Biochem. 221, 1111-1116, 1994
 A:Title: Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochc
 A:Reference number: S43624; MUID:94237150
 A:Accession: S43632
 A:Molecule type: protein
 A:Residues: 1-23 <FRF>
 A>Note: the source is designated as Salmo gairdneri
 C:Genetics:
 A:Genome: nuclear
 C:Superfamily: mammalian cytochrome-c oxidase chain VIIa
 C:Keywords: liver; membrane-associated complex; mitochondrion; oxidoreductase

Query Match 20.1%; Score 27; DB 2; Length 23;

Best Local Similarity 50.0%; Pred. No. 8.9e+02;
 Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 LIQMDGFPEHL 17
 | | | | |
 Db 11 LFQAXNGIPVHL 22

RESULT 6
 S78374
 hypothetical protein 26b - Odontella sinensis chloroplast
 C:Species: chloroplast Odontella sinensis
 C>Date: 17-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 24-Apr-1998
 C:Accession: S78374
 R:Kowallik, K.V.; Stoebe, B.; Schaffran, I.; Kroth-Pancic, P.; Freier, U.
 Plant Mol. Biol. Rep. 13, 336-342, 1995
 A:Title: The chloroplast genome of a chlorophyll a+c-containing Alga, Odontella sine
 A:Reference number: S78238
 A:Accession: S78374
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-26 <KOW>
 A:Cross-references: EMBL:Z67753; NID:q1185127; PID:e211900; PID:q1185264
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
 C:Genetics:
 A:Genome: chloroplast
 C:Keywords: chloroplast

Query Match 20.1%; Score 27; DB 2; Length 26;
 Best Local Similarity 42.9%; Pred. No. 1e+03;
 Matches 6; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

QY 2 DGFL-LIQMDGFG 13
 | | | | |
 Db 11 DGFICLIMLYK 24

RESULT 7
 A54077
 cytochrome b558 - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
 C:Accession: A54077
 R:Escorriu, V.; Laporte, F.; Garin, J.; Brandolin, G.; Vignais, P.V.
 J. Biol. Chem. 269, 14007-14014, 1994
 A:Title: Purification and physical properties of a novel type of cytochrome b from ra
 A:Reference number: A54077; MUID:94245717
 A:Accession: A54077
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-20 <ESC>
 A:Experimental source: peritoneal neutrophils
 A>Note: sequence extracted from NCBI backbone (NCHIP.148739)

Query Match 19.8%; Score 26.5; DB 2; Length 20;
 Best Local Similarity 45.0%; Pred. No. 9e+02;
 Matches 9; Conservative 2; Mismatches 4; Indels 5; Gaps 1;

QY 3 GFLIQMDGFPEHLVDL 22
 | | | | |
 Db 6 GFLVLIV-----SALLVGL 20

RESULT 8
 S59492
 formate dehydrogenase alpha chain - Alcaligenes eutrophus (fragment)
 C:Species: Alcaligenes eutrophus
 C>Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
 C:Accession: S59492
 R:Friddlebold, J.; Meyer, F.; Bill, E.; Trautwein, A.X.; Bowlen, B.
 Biol. Chem. Hoppe-Seyler 376, 561-568, 1995

A:Title: Structural and immunological studies on the soluble formate dehydrogenase from
A:Reference number: S59492; MUID:56145736

A:Accession: S59492
A:Status: Preliminary
A:Molecule type: Protein
A:Residues: 1-15 <FRI>

Query Match 19.4%: Score 26; DB 2; Length 15;
Best Local Similarity 57.1%: Pred. No. 7.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 QMDPGP 14
DB 6 EIDPGP 12

RESULT 9
B24417
Interphoreceptor retinoid-binding protein - pig (fragment)
N:Alternate names: Interstitial retinol-binding protein
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 21-Nov-1997
C:Accession: B24417
R:Pong, S.L., Cook, R.G., Alvarez, R.A., Liou, G.I., Landers, R.A., Bridges, C.D.B.
FEBS Lett. 205, 309-312, 1986
A:Title: N-terminal sequence homologues in interstitial retinol-binding proteins from 10
A:Reference number: A91365; MUID:86301171
A:Accession: B24417
A:Molecule type: Protein
A:Residues: 1-25 <FRI>
C:Superfamily: Interphoreceptor retinoid-binding protein
C:Keywords: duplication

Query Match 19.4%: Score 26; DB 2; Length 25;
Best Local Similarity 38.3%: Pred. No. 1.4e+03;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 6 LQMDPGPEHL 18
DB 12 ILDMYTFPESLM 24

RESULT 10
C85947
hypothetical protein 24250 (Imported) - Escherichia coli (strain O157:H7, substrain EDL5)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: C85947
R:Perna, N.T., Plunkett III, G., Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew
Miller, L., Grobbeck, E.J., Davis, N.W., Llim, A., Dimmlanta, E., Potamousis, K., Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: AB5480; MUID:21074935; PMID:11206551
A:Accession: C85947
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-26 <STO>
A:Cross-references: GB:AE005174; NID:q12517442; PIDN:AG658039 1; GSPDB:GN00145; UMGF:242
A:Experimental source: strain O157:H7, substrain EDL53
C:Genetics:
A:Gene: 24250

Query Match 19.4%: Score 26; DB 2; Length 26;
Best Local Similarity 38.5%: Pred. No. 1.5e+03;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 14 PEHLVDPLQSL 26
DB 14 PRALIDIVSLT 26

RESULT 11

S71306
Heat shock protein 90 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998
C:Accession: S71306
R:Conconi, M., Szewda, L.I., Levine, R.L., Stadman, E.R., Frisquet, B.
Arch. Biochem. Biophys. 331, 232-240, 1996
A:Title: Age-related decline of rat liver multicatalytic proteinase activity and prot
A:Reference number: S71306; MUID:96299287
A:Accession: S71306

A:Molecule type: Protein
A:Residues: 1-15 <CON>
A:Experimental source: liver
C:Keywords: heat shock; phosphoprotein; stress-induced protein

Query Match 18.7%: Score 25; DB 2; Length 15;
Best Local Similarity 40.0%: Pred. No. 1.1e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 14 PEHLVDPLQ 23
DB 6 PDHPIVETLR 15

RESULT 12
T44936
calmodulin kinase 2 - fission yeast (Schizosaccharomyces pombe) (fragment)
C:Species: Schizosaccharomyces pombe
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C:Accession: T44936
R:Allemay, V., Alique, R.
submitted to the EMBL data library, May 1996
A:Reference number: 222873
A:Accession: T44936
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-16 <ALE>
A:Cross-references: EMBL:U57982; PIDN:AAD09466.1

Query Match 18.7%: Score 25; DB 2; Length 16;
Best Local Similarity 100.0%: Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GCFP 14
DB 5 GCFP 8

RESULT 13
C49048
T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragmen
C:Species: Homo sapiens (man)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C:Accession: C49048
R:Stoud, M., Kjeldsen-Kragh, J., Suleyman, S., Vinje, O., Natvig, J.B., Forre, O.
Eur. J. Immunol. 22, 2413-2418, 1992
A:Title: Limited heterogeneity of T cell receptor variable region gene usage in juven
A:Reference number: A49048; MUID:92387250
A:Accession: C49048
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-16 <STO>
A:Experimental source: patient EV, IL-2R+ synovial T-cells
A:Note: sequence extracted from NCBI backbone (NCBI:113265)
C:Keywords: T-cell receptor

Query Match 18.7%: Score 25; DB 2; Length 16;
Best Local Similarity 54.5%: Pred. No. 1.2e+03;

Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 3 GFLLLQMDFGF 13
 |||||
 |
 Db 3 GFYLLQGPFGY 13

RESULT 14

PH1607
 Ig H chain V-D-J region (wild-type clone 333) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C:Accession: PH1607
 R:Lewinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178: 317-329, 1993
 A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A:Reference number: PH1580; M01D:93501609
 A:Accession: PH1607
 A:Molecule type: DNA
 A:Residues: 1-17 <LEV>
 A:Experimental source: bone marrow pre-B lymphocyte
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin

Query Match 18.7%; Score 25; DB 2; Length 17;
 Best Local Similarity 40.0%; Pred. No. 1.3e+03;
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 DGFLLQMDF 11
 |||||
 |
 Db 8 DGYYYVANDY 17

RESULT 15

S77989
 Cytochrome-c oxidase (EC 1.9.3.1) chain VIIb - bigeye tuna (fragment)
 C:Species: Thunnus obesus (bigeye tuna)
 C:Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 30-Jan-1998
 C:Accession: S77989
 R:Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.
 submitted to the Protein Sequence Database, June 1997
 A:Reference number: S77980
 A:Accession: S77989
 A:Molecule type: protein
 A:Residues: 1-20 <ARY>
 A:Experimental source: heart
 C:Genetics:
 A:Genome: nuclear
 C:Function:
 A:Pathway: oxidative phosphorylation; respiratory chain
 C:Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 18.7%; Score 25; DB 2; Length 20;
 Best Local Similarity 46.2%; Pred. No. 1.6e+03;
 Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 4 FLLQMDGPPFH 16
 |||||
 |
 Db 8 FHLEFGDNGMPVH 20

Search completed: June 18, 2002, 08:13:49
 Job time: 318 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:13:32 ; Search time 10.19 Seconds
(without alignments)
98.794 Million cell updates/sec

Title: US-09-943-334-1

Perfect score: 134
Sequence: 1 RDGFLLQMDRFPPEHLVDFLOSLIS 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 1551

Minimum DB seq length: 0
Maximum DB seq length: 26

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	24.6	24	1	COXJ_SHEEP
2	28	20.9	24	1	IRBP_SHEEP
3	27	20.1	23	1	COXJ_ONCMY
4	27	20.1	24	1	CCAA_STRTI
5	27	20.1	26	1	YCXA_ODOST
6	26	19.4	25	1	AUS1_LITRA
7	26	19.4	25	1	IRBP_PIG
8	25	18.7	16	1	ARCD_PSEBU
9	25	18.7	20	1	COXN_THUDR
10	25	18.7	23	1	COXK_CANFA
11	24	17.9	14	1	ANGT_HORSE
12	24	17.9	20	1	TL22_SPIOL
13	23	17.2	18	1	MU21_LITGE
14	23	17.2	24	1	SCX2_MESTR
15	23	17.2	25	1	BORR_BOTJA
16	22	16.4	18	1	UCO3_MAIZE
17	22	16.4	20	1	CAQS_RAT
18	22	16.4	20	1	MIF_PIG
19	22	16.4	24	1	FIBG_CANFA
20	22	16.4	24	1	KPYR_CLOPA
21	22	16.4	26	1	CATG_RAT
22	22	16.4	26	1	CT21_LITCI
23	22	16.0	25	1	ALR_PSEFL
24	21	15.7	9	1	FARD_CAVIO
25	21	15.7	9	1	SAMP_MUSCA
26	21	15.7	25	1	AMP3_MELGA
27	21	15.7	25	1	PEPM_SSECO
28	20	14.9	10	1	TEPM_RANTE
29	20	14.9	11	1	CA31_LITCI
30	20	14.9	11	1	CA32_LITCI
31	20	14.9	14	1	DCMK_PSECP
32	20	14.9	16	1	MDH_SYNY4
33	20	14.9	21	1	ATPB_PHYPA

34	20	14.9	23	1	SODM_RANCA	P36215 rana catesb
35	20	14.6	25	1	AUS2_LITRA	P82402 litoria ran
36	19.5	14.6	19	1	NUO6_SOLIU	P80729 solanum tub
37	19.5	14.6	25	1	MERE_CANAL	P82610 candida alb
38	19	14.2	12	1	V23K_MSSV	P82005 white spot
39	19	14.2	19	1	OXLA_OPHNA	P81383 ophiophagus
40	19	14.2	19	1	UP21_UPEIN	P82027 uperoletia 1
41	19	14.2	19	1	UP25_UPEIN	P82031 uperoletia 1
42	19	14.2	20	1	ITRA_ALBTU	P24925 albizzia ju
43	19	14.2	20	1	SUCB_CANFA	P93507 canis fam11
44	19	14.2	21	1	DCMS_PSECA	P1921 pseudomones
45	19	14.2	21	1	SP13_SOLIU	P58516 solanum tub

ALIGNMENTS

RESULT 1	COXJ_SHEEP	STANDARD:	PRT:	24 AA.
ID	COXJ_SHEEP			
AC	Q9YR30;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Cytochrome c oxidase polypeptide VIIa-liver/heart, mitochondrial			
DE	(Ec 1.9.3.1) (Cytochrome c oxidase subunit VIIa-l) (Fragment).			
CN	COX7A2 OR COX7A1.			
OS	Ovis aries (Sheep).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Caprinae; Ovis.			
OX	NCBI_TaxID=9940;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=liver, and Heart;			
RX	MEDLINE=6092035; PubMed=8529022;			
RA	Linder D., Freund R., Kadembach B.;			
RT	"Species-specific expression of cytochrome c oxidase isozymes.";			
RL	Comp. Biochem. Physiol. 112B:461-469(1995).			
CC	-1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE			
CC	CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN			
CC	MITOCHONDRIAL ELECTRON TRANSPORT.			
CC	-1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferrocyclochrome			
CC	c + 2 H(2)O.			
CC	-1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.			
CC	-1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIA FAMILY.			
CC	Oxidoreductase; Inner membrane; Mitochondrion.			
KW	NON_TER			
FT	SEQUENCE 24 AA: 2795 MM; D49D27C03B61F803 CRC64;			
QY	6 LQMDRFPPEHL 17			
DB	11 LFOEDNGIPVHL 22			
Query Match	24.6%; Score 33; DB 1; Length 24;			
Best local Similarity	58.3%; Pred. No. 56;			
Matches	7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;			
RESULT 2	IRBP_SHEEP	STANDARD:	PRT:	24 AA.
ID	IRBP_SHEEP			
AC	P12653;			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-OCT-1989 (Rel. 12, Last sequence update)			
DT	01-Feb-1996 (Rel. 33, Last annotation update)			
DE	Interphotoreceptor retinoid-binding protein (IRBP) (interstitial			
DE	retinol-binding protein) (Fragment).			
CN	RBP3.			
OS	Ovis aries (Sheep).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			

OX Bovidae; Caprinae; Ovis.
 NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE:
 RA MEDLINE=86301171; PubMed=3743780;
 RA Fong S.L., Cook R.G., Alvarez R.A., Liou G.I., Landers R.A.,
 RA Bridges C.D.B.:
 RT "N-terminal sequence homologues in interstitial retinol-binding
 RT proteins from 10 vertebrate species.";
 RL FEBS Lett. 205:309-312(1986).
 CC -1- FUNCTION: IRBP SHOTLES 11-CIS AND ALL TRANS RETINOIDS BETWEEN
 CC THE RETINOL ISOMERASE IN THE PIGMENT EPITHELIUM AND THE VISUAL
 CC PIGMENTS IN THE PHOTORECEPTOR CELLS OF THE RETINA.
 CC -1- SUBCELLULAR LOCATION: INTERPHOTORECEPTOR MATRIX THAT PERMEATES
 CC THE SPACE BETWEEN THE RETINA AND THE CONTIGUOUS LAYER OF PIGMENT
 CC EPITHELIUM CELLS.
 DR PIR: A24417; A24417.
 KW Vitamin A; Transport.
 FT NON_TER 24
 SQ SEQUENCE 24 AA; 2799 MW; 02DEBE61ABE4523 CRC64;

Query Match 20.1%; Score 28; DB 1; Length 24;
 Best Local Similarity 35.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 5; Mismatches 2; Indels 6; Gaps 1;
 OY 5 LLLDM-----DFGFPEHL 18
 DB 5 LVLDMAGVLLDNTYFENILM 24

RESULT 3
 COX1_ONCMY
 ID COX1_ONCMY STANDARD; PRT; 23 AA.
 AC P80333;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cytochrome c oxidase polypeptide VIa-liver (EC 1.9.3.1) (VIIC)
 DE (Fragment).
 OS Oncomyobus mykiss (Rainbow trout) (Salmo gairdneri).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 CC Proactinopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE:
 RC TISSUE=Liver;
 RX MEDLINE=94237150; PubMed=8181469;
 RA Freund R., Kadenbach B.:
 RT "Identification of tissue-specific isoforms for subunits Vb and VIa
 RT of cytochrome c oxidase isolated from rainbow trout.";
 RL Eur. J. Biochem. 221:1111-1116(1994).
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 CC MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIa FAMILY.
 DR PIR: S43632; S43632.
 KW Oxidoreductase; Inner membrane; Mitochondrion.
 FT NON_TER 23
 SQ SEQUENCE 23 AA; 2635 MW; BCBED43FBAD9C509 CRC64;

Query Match 20.1%; Score 27; DB 1; Length 23;
 Best Local Similarity 50.0%; Pred. No. 4.6e+02;
 Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 OY 6 LLQMDGFPPEHL 17
 DB 11 LFOAXNGIPVHL 22

RESULT 4
 CCAA_STRT
 ID CCAA_STRT STANDARD; PRT; 24 AA.
 AC P80436;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Chinoxalin-2-carboxylic acid activating enzyme (Fragment).
 OS Streptomyces triostinicus.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=45399;
 RN [1]
 RP SEQUENCE:
 RA Pahl A., Schlumbohm W., Keller U.;
 RL Submitted (MAR-1995) to the SWISS-PROT data bank.
 CC -1- FUNCTION: INVOLVED IN TRIOSTIN BIOSYNTHESIS.
 KW Antibiotic biosynthesis.
 FT NON_TER 24
 SQ SEQUENCE 24 AA; 2900 MW; 91C222B57CEB6D1 CRC64;

Query Match 20.1%; Score 27; DB 1; Length 24;
 Best Local Similarity 30.0%; Pred. No. 4.8e+02;
 Matches 6; Conservative 5; Mismatches 3; Indels 6; Gaps 1;
 OY 2 DGFLLQMDGFPPEHLVDF 21
 DB 3 DGFV-----PMPDHLADEY 16

RESULT 5
 YCXD_ODOST
 ID YCXD_ODOST STANDARD; PRT; 26 AA.
 AC P49839;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical 3.2 kDa protein in RPOC2-Rps2 intergenic region (ORF26B).
 OS Odontella sinensis.
 CC Chloroplast.
 CC Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;
 CC Bidulophycidae; Eupodiscaceae; Eupodiscaceae; Odontella.
 OX NCBI_TaxID=2839;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kowalik K.V., Stoebe B., Schaffran I., Kroth-Pancic P., Freier U.:
 RT "The chloroplast genome of a chlorophyll a+c-containing alga,
 RT Odontella sinensis.";
 RL Plant Mol. Biol. Rep. 13:336-342(1995).
 CC -----
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 CC -----
 DR EMBL: Z67753; CAA91747.1;
 KW Chloroplast; Hypothetical protein.
 KW SEQUENCE 26 AA; 3137 MW; 8305B587C0A30B36 CRC64;

Query Match 20.1%; Score 27; DB 1; Length 26;
 Best Local Similarity 42.9%; Pred. No. 5.3e+02;
 Matches 6; Conservative 4; Mismatches 2; Indels 2; Gaps 1;
 OY 2 DGFLL--LLQMDGCF 13
 DB 11 DGFTECLMLNRYF 24

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RESULT 6
AC A051_LITRA STANDARD: PRT: 25 AA.
AC P82401;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Aurein 5.1
OS Litoria raniformis (Southern bell frog), and
OS Litoria aurea (Green and golden bell frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria;
OX NCBI_TaxID=116057, 8371;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Granular dorsal gland;
RX MEDLINE=20408845; PubMed=10951191;
RA Rozek T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A.,
  Wallace J.C., Tyler M.J.;
RT "The antibiotic and anticancer active aurein peptides from the
  Australian bell frogs Litoria aurea and Litoria raniformis the
  solution structure of aurein 1.2."
RL Eur. J. Biochem. 267:5330-5341(2000).
CC -1- FUNCTION: HAS NO ANTIMICROBIAL OR ANTICANCER ACTIVITY.
CC -1- SUBCELLULAR LOCATION: SECRETED.
SQ SEQUENCE 25 AA; 2547 MW; 15C6169CD98AFC27 CRC64;

Query Match 19.4%; Score 26; DB 1; Length 25;
Best Local Similarity 38.9%; Pred. No. 7.2e+02;
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 6 LIOMDFGPEHLLVDFLQ 23
DB 2 LIDIVTGLIGLILYDVLK 19

RESULT 7
AC IRBP_PIG STANDARD: PRT: 25 AA.
AC P12662;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Interphotoreceptor retinoid-binding protein (IRBP) (Interstitial
  retinol-binding protein) (Fragment).
GN RBP3.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Suis.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=86301171; PubMed=3743780;
RA Pong S.L., Cook R.G., Alvarez R.A., Liou G.I., Landers R.A.,
  Bridges C.D.B.;
RT "N-terminal sequence homologues in interstitial retinol-binding
  proteins from 10 vertebrate species."
RL PNAS Lett. 205:309-312(1986).
CC -1- FUNCTION: IRBP SHUTTLES 11-CIS AND ALL TRANS RETINOIDS BETWEEN
  THE RETINOL ISOMERASE IN THE PIGMENT EPITHELIUM AND THE VISUAL
  PIGMENTS IN THE PHOTORECEPTOR CELLS OF THE RETINA.
CC -1- SUBCELLULAR LOCATION: INTERPHOTORECEPTOR MATRIX THAT PERMEATES
  THE SPACE BETWEEN THE RETINA AND THE CONTIGUOUS LAYER OF PIGMENT
  EPITHELIUM CELLS.
CC PIR: B24417; B24417.
DR Vitamin A; Transport.
KM NON_TER 25
FT SEQUENCE 25 AA; 2813 MW; 4E751DE160231B7 CRC64;

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Query Match 19.4%; Score 26; DB 1; Length 25;
Best Local Similarity 38.5%; Pred. No. 7.2e+02;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 6 LIOMDFGPEHLL 18
DB 12 ILIDNYTPESIM 24

RESULT 8
AC ACD_PSEPU STANDARD: PRT: 16 AA.
AC P41147;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Arginine/ornithine antiporter (Fragment).
GN ACD.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 4359;
RA Wilson S.D., Wang M., Filpula D.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CATALYZES AN ELECTRONEUTRAL EXCHANGE BETWEEN ARGININE
  AND ORNITHINE TO ALLOW HIGH EFFICIENCY ENERGY CONVERSION IN THE
  ARGININE DEIMINASE PATHWAY.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
  (potential).
CC -1- SIMILARITY: BELONGS TO THE ACD/CAD/GERAB/LYSI FAMILY OF
  PERMEASES.
CC -----
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  CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: 007185; AAA16963.1;
KM Transport; Amino-acid transport; Transmembrane; Inner membrane.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1644 MW; 90B48A7C8FAA9705 CRC64;

Query Match 18.7%; Score 25; DB 1; Length 16;
Best Local Similarity 83.3%; Pred. No. 6.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 DGFLL 7
DB 11 DGFLL 16

RESULT 9
AC COXN_THUOB STANDARD: PRT: 20 AA.
AC P80380;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIb-heart (EC 1.9.3.1) (Fragment).
OS Thynnus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;

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RN [1]
 RP SEQUENCE.
 RC TISSUE-Heart;
 RX MEDLINE=97454291; PubMed=9310366;
 RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
 RA Kadenbach B.;
 RT "The subunit structure of cytochrome-c oxidase from tuna heart and
 liver.";
 RL Eur. J. Biochem. 248:99-103(1997).
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 CC MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) -> 4 ferricytochrome
 CC c + 2 H(2)O.
 KM Oxidoreductase; Mitochondrion.
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 2303 MW; 0A33BD34006E5AA6 CRC64;

Query Match 18.7%; Score 25; DB 1; Length 20;
 Best Local Similarity 46.2%; Pred. No. 8.2e+02;
 Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 FLQMDGFPEH 16
 DB 8 FHLEYGNGMPVH 20

RESULT 10
 COCK_CANFA STANDARD; PRT; 23 AA.
 AC 09RZ8;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Cytochrome c oxidase polypeptide V1a-heart, mitochondrial
 DE (EC 1.9.3.1) (Cytochrome c oxidase subunit V1a-H) (COX V1A-M)
 DE (Fragment).
 GN COX7A1 OR COX7AH.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_Taxid=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain, and Heart;
 RX MEDLINE=96092035; PubMed=8529022;
 RA Linder D., Freund R., Kadenbach B.;
 RT "Species-specific expression of cytochrome c oxidase isozymes.";
 RL Comp. Biochem. Physiol. 112B:461-469(1995).
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 CC MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) -> 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE V1A FAMILY.
 KM Oxidoreductase; Inner membrane; Mitochondrion.
 FT NON_TER 23
 SQ SEQUENCE 23 AA; 2627 MW; AD3EA34B61FF73CE CRC64;

Query Match 18.7%; Score 25; DB 1; Length 23;
 Best Local Similarity 50.0%; Pred. No. 9.5e+02;
 Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 LQMDGFPEH 17
 DB 11 LFQADNGLPVXL 22

RESULT 11
 ANGT_HORSE

ID ANGT_HORSE STANDARD; PRT; 14 AA.
 AC P01016;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Angiotensinogen [Contains: Angiotensin I; Angiotensin II] (Fragment).
 GN SERPINB8 OR AGT.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_Taxid=9796;
 RN [1]
 RP SEQUENCE.
 RA Skeggs L.T., Jr., Kahn J.R., Lentz K., Shumway N.P.;
 RT "The preparation, purification, and amino acid sequence of a
 RT polypeptide renin substrate.";
 RL J. Exp. Med. 106:439-453(1957).

CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
 CC BALANCE OF BODY FLUIDS.
 CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR PIR: A01250; A01250.
 DR InterPro: IPR000215; Serpin.
 DR PROSITE: PS00284; SERPIN; PARTIAL.
 KM Vasoconstrictor; Plasma; Serpin.
 FT PEPTIDE 1 10 ANGIOTENSIN I.
 FT NON_TER 14 8 ANGIOTENSIN II.
 FT SEQUENCE 14 AA; 1759 MW; 2E9921F8EEFBD7 CRC64;

Query Match 17.9%; Score 24; DB 1; Length 14;
 Best Local Similarity 83.3%; Pred. No. 8e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 PEHLV 19
 DB 7 PPHLLV 12

RESULT 12
 TL22_SPIOL STANDARD; PRT; 20 AA.
 AC P82796;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Thylakoid luminal 22 kDa protein (P22) (Fragment).
 OS Spinacia oleracea (Spinach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_Taxid=3562;
 RN [1]
 RP SEQUENCE.

RA Kieselbach T., Petersson U., Bystedt M., Schroeder W.P.;
 RL Submitted (SEP-2000) to the SWISS-PROT data bank.
 CC -1- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
 KM Chloroplast; Thylakoid.
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 2409 MW; 78F5B50699BB620 CRC64;

Query Match 17.9%; Score 24; DB 1; Length 20;
 Best Local Similarity 40.0%; Pred. No. 1.2e+03;
 Matches 6; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 12 GFPEHLVDPIQSLS 26
 |||:::|

Db 5 GREY--IDFDCYS 17

RESULT 13
MU21_LITGE
ID MU21_LITGE STANDARD: PRT: 18 AA.
AC P82068;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Maculatin 2.1.
OS Litoria genimaculata (Green-eyed tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
OX NCBI_TaxID=95132;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RX MEDLINE=98281937; PubMed=9620615;
RA Kozek T., Waugh R.J., Steindorner S.T., Bowle J.H., Tyler M.J.,
RA Wallace J.C.;
RT "The maculatin peptide from the skin glands of the tree frog
RT Litoria genimaculata. A comparison of the structures and
RT antibacterial activities of maculatin 1.1 and caerin 1.1.";
RL J. Pept. Sci. 4:111-115(1998).
CC -1- FUNCTION: SHOWS ANTIBACTERIAL ACTIVITY AGAINST B.CEREUS,
CC L.INNOCUA, M.LUTEUS, S.AUREUS, S.EPIDERMISAND S.UBRRIS.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MW=1878; METHOD=FAV.
KW Amphibian skin; Amlidation; Antibiotic.
FT MOD_RES 18 18 AMIDATION.
SQ SEQUENCE 18 AA; 1879 MW; 98A1F86BB4FACBBE CRC64;

Query Match 17.2%; Score 23; DB 1; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 19 VDFLGSLIS 26
Db 3 VDFLKKVA 10

RESULT 14
SCX2_MESTA
ID SCX2_MESTA STANDARD: PRT: 24 AA.
AC P45668;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neurotoxin II (BT-II) (Fragment).
OS Mesobuthus tamulus (Eastern Indian scorpion) (Buthus tamulus).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butioidae; Butiidae; Mesobuthus.
OX NCBI_TaxID=34647;
RN [1]
RP SEQUENCE.
RC TISSUE-Venom;
RX MEDLINE=94287436; PubMed=8016854;
RA Lala K., Narayanan P.;
RT "Purification, N-terminal sequence and structural characterization of
RT a toxic protein from the Indian scorpion venom Butus tamulus.";
RL Toxicon 32:325-338(1994).
CC -1- FUNCTION: BINDS TO SODIUM CHANNELS AND INHIBITS THE INACTIVATION
CC OF THE ACTIVATED CHANNELS, THEREBY BLOCKING NEURONAL TRANSMISSION.
CC THIS TOXIN IS ACTIVE AGAINST MAMMALS. LD(50) IS 2.25 MG/KG IN MICE
CC BY SUBCUTANEOUS INJECTION.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.
CC ALPHA-TOXIN SUBFAMILY.
KW Neurotoxin; Sodium channel inhibitor.
FT NON_TER 24 24
SQ SEQUENCE 24 AA; 2686 MW; DA1990C8FF8E2769 CRC64;

Query Match 17.2%; Score 23; DB 1; Length 24;
Best Local Similarity 80.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGFLL 6
Db 2 DGYLL 6

RESULT 15
BOTR_BOTJA
ID BOTR_BOTJA STANDARD: PRT: 25 AA.
AC P22028;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Botrocetin (Platelet coagglutinin) (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE-Venom;
RX MEDLINE=91129280; PubMed=1993206;
RA Fujimura Y., Titani K., Usami Y., Suzuki M., Oyama R., Matsui T.,
RA Fukui H., Sugimoto M., Ruggeri Z.M.;
RT "Isolation and chemical characterization of two structurally and
RT functionally distinct forms of botrocetin, the platelet coagglutinin
RT isolated from the venom of Bothrops jararaca.";
RL Biochemistry 30:1957-1964(1991).
CC -1- FUNCTION: THERE ARE TWO DISTINCT FORMS OF THE VON WILLEBRAND
CC FACTOR-DEPENDENT PLATELET COAGGLUTININ. THE DIMERIC FORM IS
CC 34-TIMES MORE ACTIVE THAN THE ONE-CHAIN BOTROCTETIN IN PROMOTING
CC VWF BINDING TO PLATELETS.
CC -1- SUBUNIT: MONOMER. VWF AND BOTROCTETIN FORM A SOLUBLE COMPLEX.
CC -1- PTM: CONTAINS NUMEROUS INTRACHAIN DISULFIDE BONDS.
CC -1- SIMILARITY: TO OTHER MEMBERS OF THE C-TYPE LECTIN FAMILY.
DR Interpro: IPR001304; Lectin_C
DR PROSITE: PS00615; C_TYPE_LECTIN_1; PARTIAL.
DR PROSITE: PS50041; C_TYPE_LECTIN_2; PARTIAL.
KW Glycoprotein; Venom.
FT VARIANT 2 2 I -> V.
FT NON_TER 25 25
SQ SEQUENCE 25 AA; 2655 MW; D25D9031A705CAF8 CRC64;

Query Match 17.2%; Score 23; DB 1; Length 25;
Best Local Similarity 44.4%; Pred. No. 2.1e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 8 QMDFGPEH 16
Db 17 ECDXGTPEN 25

Search completed: June 18, 2002, 08:16:45
Job time: 193 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:13:12 ; Search time 23.95 Seconds
(without alignments)
187,724 Million cell updates/sec

Title: US-09-943-334-1

Perfect score: 134

Sequence: 1 RDGFLLQLQMFQFPFELLVDFLQSL 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 9143

Minimum DB seq length: 0

Maximum DB seq length: 26

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_RVIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	23.1	19	6	Q9TRR6
2	30.5	22.8	17	4	Q9UJH1
3	30	22.4	21	2	P70861
4	29	21.6	20	5	Q9TWH5
5	28	20.9	23	11	Q9UJNO
6	27	20.1	12	4	Q9UGS1
7	27	20.1	14	6	Q9TRQ7
8	27	20.1	22	10	Q9S8E1
9	27	20.1	26	11	Q9JTW8
10	26.5	19.8	20	6	Q9TRC2
11	26.5	19.8	21	2	Q9ZG55
12	26	19.4	9	4	Q96KPF
13	26	19.4	12	2	Q9K3B4
14	26	19.4	12	2	Q9L8H6
15	26	19.4	12	2	Q9L8H8
16	26	19.4	22	6	O02830

17	26	19.4	23	4	Q96CD6	Q96cd6 homo sapien
18	26	19.4	24	2	Q46081	Q46081 clostridium
19	26	19.4	25	13	P82401	P82401 iltoria ran
20	25	18.7	16	3	O94554	O94554 schizosacch
21	25	18.7	19	13	Q9PS70	Q9ps70 gallus gall
22	25	18.7	20	10	Q9S878	Q9s878 petunia hyb
23	25	18.7	21	12	Q93044	Q93044 maize strea
24	25	18.7	21	12	Q93046	Q93046 maize strea
25	25	18.7	21	12	Q93047	Q93047 maize strea
26	25	18.7	21	12	Q933P6	Q933P6 heliobacte
27	25	18.7	24	2	Q93361	Q93361 homo sapien
28	25	18.7	24	12	Q69137	Q69137 human herpe
29	24.5	18.3	22	13	Q9PS42	Q9ps42 gallus gall
30	24.5	18.3	23	12	Q10423	Q10423 influenza a
31	24.5	18.3	25	13	Q9PS41	Q9ps41 gallus gall
32	24.5	18.3	26	11	Q99LX4	Q99LX4 mus musculu
33	24	17.9	13	2	Q34622	Q34622 borrelia bu
34	24	17.9	13	2	Q31364	Q31364 borrelia ga
35	24	17.9	13	2	Q31365	Q31365 borrelia ga
36	24	17.9	18	17	Q9UYK7	Q9uyk7 pyrococcus
37	24	17.9	20	6	Q9XTG3	Q9xtg3 ateles belz
38	24	17.9	21	2	Q9X3D0	Q9x3d0 prochloroco
39	24	17.9	21	12	Q93050	Q93050 maize strea
40	24	17.9	22	4	Q9UQ31	Q9uq31 homo sapien
41	24	17.9	22	5	Q95NM7	Q95nm7 heliconius
42	24	17.9	22	6	Q9XTA7	Q9xta7 cercopithec
43	24	17.9	22	6	Q9XTA6	Q9xta6 canis famli
44	24	17.9	22	11	Q9WV72	Q9wv72 cricetus
45	24	17.9	22	11	Q9WV71	Q9wv71 rattus norv

ALIGNMENTS

RESULT 1
Q9TRR6 PRELIMINARY; PRT; 19 AA.
AC Q9TRR6; ID Q9TRR6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CALCYCLIN-ASSOCIATED PROTEIN, CAP50-CA2+/PHOSPHOLIPID-BINDING PROTEIN
DE L-14 FRAGMENT.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Cranista; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP MEDLINE=92250478; PubMed=1533622;
RX Tokumitsu H., Mizutani A., Minami H., Kobayashi R., Hataka H.;
RA "A calyculin-associated protein is a newly identified member of the
RT Ca2+/phospholipid-binding proteins, annexin family.";
RL J. Biol. Chem. 267:8919-8924(1992).
SQ SEQUENCE 19 AA; 2018 MW; 9A54062504B8322E CRC64;

Query Match 23.1%; Score 31; DB 6; Length 19;
Best Local Similarity 43.8%; Pred. NO. 4.1e+02;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
OY 11 FGPFELLVDFLQSL 26
DB 2 FCTDEQAATIDYGSRS 17
RESULT 2
Q9UJH1 PRELIMINARY; PRT; 17 AA.
AC Q9UJH1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

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DE DJ436M11.2 (RETINOSCHISIS (X-LINKED, JUVENILE) 1 (XLRSL))
DE (FRAGMENT).
GN RSL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gratham D.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z94056; CAB40073.1; -.
FT NON_TER 17
SQ SEQUENCE 17 AA; 2029 MW; 810DE1B78C52C7FB CRC64;

Query Match 22.8%; Score 30.5; DB 4; Length 17;
Best Local Similarity 58.3%; Pred. No. 4.3e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 2 DGFLLQMDPGF 13
Db 6 EGFLLLL-FGY 16

RESULT 3
P70861 PRELIMINARY; PRT; 21 AA.
AC P70861;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE THDF (FRAGMENT).
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-212;
RX MEDLINE=97312006; PubMed=9168617;
RT Ge Y., Old I.G., Girones I.S., Charon N.W.;
RT "The flag motility operon of Borrelia burgdorferi is initiated by a
RT sigma 70-like promoter."
RL Microbiology 143:1681-1690(1997).
DR EMBL; U62901; AAB62742.1; -.
FT NON_TER 21
SQ SEQUENCE 21 AA; 2432 MW; F33B1BC548BD5B33 CRC64;

Query Match 22.4%; Score 30; DB 2; Length 21;
Best Local Similarity 50.0%; Pred. No. 6.6e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 9 MDGFFPHLL 18
Db 7 IEDFPEGL 16

RESULT 4
O9TWH5 PRELIMINARY; PRT; 20 AA.
AC O9TWH5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE 40 KDA GAP JUNCTION PROTEIN (FRAGMENT).
OS Heliothis virescens (Noctuid moth) (Oilet moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Noctuoidea; Noctuidae; Heliothinae; Heliothis.
OX NCBI_TaxID=7102;
RN [1]
RP SEQUENCE.

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RX MEDLINE=95347000; PubMed=7621522;
RA Ryerse J.S.;
RT "Immunocytochemical, electrophoresis, and immunoblot analysis of
RT Heliothis virescens gap junctions isolated in the presence and absence
RT of protease inhibitors."
RL Cell Tissue Res. 281:179-186(1995).
SQ SEQUENCE 20 AA; 2304 MW; A298D3EB3E89586B CRC64;

Query Match 21.6%; Score 29; DB 5; Length 20;
Best Local Similarity 35.3%; Pred. No. 8.9e+02;
Matches 6; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 5 LLLQMDGFFPHLLVDF 21
Db 3 VIFNIDGYLEFLTRDF 19

RESULT 5
O9JINO PRELIMINARY; PRT; 23 AA.
AC O9JINO;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE GAP JUNCTION SUBUNIT PROTEIN CONNEXIN37 (FRAGMENT).
GN GJ44.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-129/SVJ;
RX MEDLINE=20461860; PubMed=11004519;
RA Seul K.H., Beyer E.C.;
RT "Mouse connexin37: gene structure and promoter analysis."
RL Blochim. Biophys. Acta 1492:499-504(2000).
DR EMBL; AF216831; AAF91222.1; -.
FT MGD; MGI:95715; GJ44.
FT NON_TER 23
SQ SEQUENCE 23 AA; 2617 MW; 2E879CA19105F7F8 CRC64;

Query Match 20.9%; Score 28; DB 1; Length 23;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 DGFPEPHLL 18
Db 3 DWGFLEKLL 11

RESULT 6
O9UGS1 PRELIMINARY; PRT; 12 AA.
AC O9UGS1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE DJ796117.4 (NOVEL PROTEIN SIMILAR TO GS2) (FRAGMENT).
GN DJ796117.4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL035398; CAB63074.1; -.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1430 MW; AF7740ABECB69AA6 CRC64;

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Query Match
Best Local Similarity 44.4%; Score 27; DB 4; Length 12;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 5 LLLQMDGFG 13
: : : : :
Db 1 MILEWDMSF 9

RESULT 7
O9TR07 PRELIMINARY; PRT; 14 AA.
AC O9TR07;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE CALCYCLIN-ASSOCIATED PROTEIN PEPTIDE L-8, CAP-50-ANNEXIN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE
RX MEDLINE=92317074; PubMed=1618851;
RA Mizutani A., Usuda N., Tokumitsu H., Minami H., Yasui K.,
RT Kobayashi R., Hidaka H.;
RT "CAP-50, a newly identified annexin, localizes in nuclei of cultured
fibroblast 3Y1 cells";
RL J. Biol. Chem. 267:13498-13504(1992).
SO SEQUENCE 14 AA; 1446 MW; C832EB96DD9C6C6 CRC64;

Query Match
Best Local Similarity 41.7%; Score 27; DB 6; Length 14;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 11 FGPEHLVDFL 22
: : : : :
Db 2 FGTEQALIDXL 13

RESULT 8
O9SBE1 PRELIMINARY; PRT; 22 AA.
AC O9SBE1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE ANNEXIN (FRAGMENT).
OS Capsicum annuum (Bell pepper).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Capsicum.
OX NCBI_TaxID=4072;
RN [1]
RP SEQUENCE
RX MEDLINE=95353219; PubMed=7627125;
RA Hoshino T., Mizutani A., Chida M., Hidaka H., Mizutani J.;
RT "Plant annexin form homodimer during Ca(2+)-dependent liposome
aggregation";
RL Biochem. Mol. Biol. Int. 35:749-755(1995).
SO SEQUENCE 22 AA; 2465 MW; A36D1A1FE311F0F CRC64;

Query Match
Best Local Similarity 41.7%; Score 27; DB 10; Length 22;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 11 FGPEHLVDFL 22
: : : : :
Db 11 FGPEHLVDFL 22

Db 3 WGTDEKLIIDIL 14

RESULT 9
O99JW8 PRELIMINARY; PRT; 26 AA.
ID O99JW8
AC O99JW8;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 3.1 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005613; AAH05613.1; -
KW Hypothetical protein.
SO SEQUENCE 26 AA; 3090 MW; 4759778C1D32AC98 CRC64;

Query Match
Best Local Similarity 41.7%; Score 27; DB 11; Length 26;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 2 DGFLLQMDGFG 13
: : : : :
Db 4 DSFLMLMRAP 15

RESULT 10
O9TRC2 PRELIMINARY; PRT; 20 AA.
ID O9TRC2
AC O9TRC2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE HEMOPROTEIN P-30 (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE
RX MEDLINE=94245717; PubMed=8188680;
RA Escrivou V., Laporte F., Garin J., Brandolin G., Vignais P.V.;
RT "Purification and physical properties of a novel type of cytochrome b
from rabbit peritoneal neutrophils";
RL J. Biol. Chem. 269:14007-14014(1994).
SO SEQUENCE 20 AA; 2198 MW; 2301B618163DA419 CRC64;

Query Match
Best Local Similarity 45.0%; Score 26.5; DB 6; Length 20;
Matches 9; Conservative 2; Mismatches 4; Indels 5; Gaps 1;

OY 3 GFLLLQMDGFGPEHLVDFL 22
: : : : :
Db 6 GFLVLLV-----SALLVGL 20

RESULT 11
O9ZG55 PRELIMINARY; PRT; 21 AA.
ID O9ZG55
AC O9ZG55;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE ATP-BINDING PROTEIN (FRAGMENT).
GN RECF.

```
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=12 434b;
RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;
RT "Gene identification of Chlamydia trachomatis by random DNA
sequencing.";
RL Submitted (Aug-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF087306; AAD04082.1; -.
KW ATP-binding.
FT NON_TER 1 1
FT NON_TER 21 21
SQ SEQUENCE 21 AA; 2336 MW; 0185D9AC428276D9 CRC64;

Query Match 19.8%; Score 26.5; DB 2; Length 21;
Best Local Similarity 41.7%; Pred. No. 2.3e+03;
Matches 5; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

OY 6 HLQMDGFEHL 17
Db 8 ILQL-TSPFKH 18

RESULT 12
O96KF6 PRELIMINARY; PRT; 9 AA.
AC O96KF6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE STEAROYL-COA DESATURASE (FRAGMENT).
GN SCD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=HEPATOCYTES, LIVER, HAIR FOLLICLE, AND BRAIN;
RA Zhang L., Ge L., Tran T., Steen K., Protty S.M.;
RT "Isolation and Characterization of the Human Stearyl-CoA Desaturase
Gene Promoter: Requirement of a Conserved CCAAT cis-Element.";
RL Biochem. J. 0:0-(2001).
DR EMBL; AF320307; AAK54510.1; -.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1039 MW; 3593B6D72721EDC7 CRC64;

Query Match 19.4%; Score 26; DB 4; Length 9;
Best Local Similarity 71.4%; Pred. No. 5.6e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 14 PEHLVD 20
Db 2 PAHLDP 8

RESULT 13
O9K3B4 PRELIMINARY; PRT; 12 AA.
AC O9K3B4;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE HYPOTHETICAL 1.5 KDa PROTEIN (FRAGMENT).
OS Enterococcus faecium (Streptococcus faecium).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
OC Enterococcus.
OX NCBI_TaxID=1352;
RN (1)
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```
RP SEQUENCE FROM N.A.
RC STRAIN-VARIOUS STRAINS; TRANSPOSON-TN5382;
RX MEDLINE=20307504; PubMed=10846225;
RA Dahl K.H., Lundblad E.W., Roekenes T.P., Olsvik O., Sundsfjord A.;
RT "Genetic linkage of the vanB2 gene cluster to TN5382 in vancomycin
resistant enterococci and characterization of two novel insertion
sequences.";
RL Microbiology 146:1469-1479(2000).
DR EMBL; AF203417; AAF70584.1; -.
DR EMBL; AF203405; AAF70560.1; -.
DR EMBL; AF203406; AAF70562.1; -.
DR EMBL; AF203407; AAF70584.1; -.
DR EMBL; AF203409; AAF70568.1; -.
DR EMBL; AF203412; AAF70574.1; -.
DR EMBL; AF203413; AAF70576.1; -.
DR EMBL; AF203414; AAF70578.1; -.
DR EMBL; AF203415; AAF70580.1; -.
DR EMBL; AF203416; AAF70582.1; -.
KW Hypothetical protein.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1476 MW; 1613207414D1EBAB CRC64;
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Query Match 19.4%; Score 26; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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OY 16 HLLVDF 21
Db 7 HALIDF 12
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RESULT 14
O9L8H6 PRELIMINARY; PRT; 12 AA.
AC O9L8H6; O9L810; O9L812;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HYPOTHETICAL 1.5 KDa PROTEIN (FRAGMENT).
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
OC Enterococcus.
OX NCBI_TaxID=1351;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=TUH7-54, TUH4-67, AND TUH1-75; TRANSPOSON-TN5382;
RX MEDLINE=20307504; PubMed=10846225;
RA Dahl K.H., Lundblad E.W., Roekenes T.P., Olsvik O., Sundsfjord A.;
RT "Genetic linkage of the vanB2 gene cluster to TN5382 in vancomycin
resistant enterococci and characterization of two novel insertion
sequences.";
RL Microbiology 146:1469-1479(2000).
DR EMBL; AF203411; AAF70572.1; -.
DR EMBL; AF203408; AAF70566.1; -.
DR EMBL; AF203404; AAF70558.1; -.
KW Hypothetical protein.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1476 MW; 1613207414D1EBAB CRC64;
```

```
Query Match 19.4%; Score 26; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 16 HLLVDF 21
Db 7 HALIDF 12
```

```
RESULT 15
O9L8H8 PRELIMINARY; PRT; 12 AA.
ID O9L8H8
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AC Q9LBH8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HYPOHETICAL 1.5 KDA PROTEIN (FRAGMENT).
OS Enterococcus gallinarum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
OC Enterococcus.
OX NCBI_TaxID=1353;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TUH7-16; TRANSPOSON-TN5382;
RX MEDLINE=20307504; PubMed=10846225;
RA Dahl K.H., Lundblad E.W., Koekenes T.P., Olsvik O., Sundsfjord A.;
RT "Genetic linkage of the vanB2 gene cluster to Tn5382 in vancomycin
RT resistant enterococci and characterization of two novel insertion
RT sequences.";
RL Microbiology 146:1469-1479(2000).
DR EMBL: AF203410; AAF70570.1; -.
KW Hypothetical protein.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1476 MW; 1613207414DIEAB CRC64;

Query Match 19.4%; Score 26; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 16 HLLVDF 21
| | | |
Db 7 HALIDF 12

Search completed: June 18, 2002, 08:16:29
Job time: 197 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:13:52 ; Search time 29.43 Seconds
(without alignments)
98,128 Million cell updates/sec

Title: US-09-943-334-1

Sequence: 1 RRGFLILQMDPFGPEHLVDFLOSLIS 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 258094

Minimum DB seq length: 0
Maximum DB seq length: 26

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_032802.*
1: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
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20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	134	100.0	26	17	AAW06128	Human cholesteryl
2	134	100.0	26	20	AAV13801	Rabbit CERP immuno
3	134	100.0	26	21	AAV91228	Human cholesteryl
4	117	87.3	26	20	AAV13802	Rabbit CERP immuno
5	117	87.3	26	21	AAV91231	Human cholesteryl
6	111	82.8	22	20	AAV13815	Rabbit CERP immuno
7	111	82.8	22	20	AAV13821	Human CERP immuno
8	107	79.9	22	20	AAV13809	Rabbit CERP immuno
9	83	61.9	16	21	AAV91229	Human cholesteryl
10	79	59.0	16	21	AAV91230	Human cholesteryl
11	53	39.6	11	18	AAW24294	Human/Rabbit CERP

12	34	25.4	22	22	AAW64866	Human secreted pro
13	34	25.4	25	20	AAV12067	Human 5' EST seque
14	33	24.6	12	4	AAV30225	Sequence of inter
15	33	24.6	12	9	AAV80053	Sequence of human
16	33	24.6	14	20	AAV27814	Human secreted pro
17	33	24.6	21	18	AAW38080	PPPY motif contai
18	33	24.6	22	22	AAW11445	Interferon-alpha2
19	33	24.6	22	22	AAW22196	Endogenous TCR alp
20	32.5	24.3	22	22	AAW89172	HIV gp120 protein
21	32	23.9	21	19	AAW65690	Fibronectin bindin
22	32	23.9	22	20	AAV19066	Lectihin:cholester
23	32	23.9	22	20	AAV18812	Lectihin:cholester
24	32	23.9	22	20	AAV18549	Lectihin:cholester
25	32	23.9	22	20	AAV19320	Lectihin:cholester
26	31.5	23.5	26	21	AAV69931	Human IL-1 recepto
27	31	23.1	12	20	AAV32796	Mammalian prolacti
28	31	23.1	21	19	AAW65666	Fibronectin bindin
29	31	23.1	22	19	AAW65669	Peptide #13. Synt
30	30	22.4	17	21	AAV68335	Amyotrophic latera
31	30	22.4	19	22	ABW41585	Peptide #0091 enco
32	30	22.4	19	22	AAW62456	Human brain expres
33	30	22.4	19	22	AAW75265	Human bone marrow
34	30	22.4	19	22	AAW35377	Peptide #9414 enco
35	30	22.4	20	15	AAW61276	Transactivating pr
36	30	22.4	20	19	AAW41190	Tax protein fragme
37	30	22.4	22	17	AAW95899	Fragment #4 of 7-a
38	30	22.4	25	22	ABW32318	Peptide #4969 enco
39	30	22.4	25	22	ABW22871	Protein #4870 enco
40	30	22.4	26	22	ABW19835	Murine muscle-spec
41	29	21.6	10	19	AAW78506	SH2 domain binding
42	29	21.6	11	20	AAW99442	Interleukin-2 rece
43	29	21.6	11	21	AAW82915	Peptide exhibiting
44	29	21.6	11	22	AAE12095	Target-receptor-D1
45	29	21.6	13	18	AAW10883	MAB anti-HBsAg bin

ALIGNMENTS

RESULT 1	AAW06128	standard; Peptide: 26 AA.
XX	XX	
AC	AAW06128;	
XX	XX	
DT	07-FEB-1997 (first entry)	
XX	XX	
DE	Human cholesteryl ester transfer protein C-terminal B-cell epitope.	
XX	XX	
KW	Cholesteryl ester transfer protein; CERP; antigen; vaccine;	
KW	cardiovascular disease; atherosclerosis; B-cell epitope.	
XX	XX	
OS	Homo sapiens.	
XX	XX	
PN	W09634888-A1.	
XX	XX	
PD	07-NOV-1996.	
XX	XX	
PE	01-MAY-1996; 96WO-0506147.	
XX	XX	
PR	01-MAY-1995; 95US-0432483.	
XX	XX	
PA	(TCEL-) T CELL SCI INC.	
XX	XX	
PI	Rittershaus CW, Thomas LJ;	
XX	XX	
DR	WPI; 1996-506103/50.	
XX	XX	
PT	Cholesteryl ester transfer protein B cell epitope linked to T cell	
PT	epitope - used to generate vaccine to regulate CERP activity for	
PT	decreasing the risk of developing a cardiovascular disease e.g.	
PT	atherosclerosis	
XX	XX	

PS Claim 5; Page 41; 72pp; English.

XX A B-cell epitope (AAW06128) comprising the C-terminal 26 amino acids

CC of human liver mature cholesteryl ester transfer protein (CETP)

CC (see also AAW06127) is involved in a neutral lipid binding or a

CC transfer activity of CETP. It can be linked to a universal or a

CC broad range immunogenic T-cell epitope, such as that found at amino

CC acids 830/843 of tetanus toxoid protein, to produce a synthetic

CC vaccine (see also AAW06129) that elicits an immune response against

CC endogenous CETP activity, thereby treating or preventing

CC cardiovascular disease, such as atherosclerosis. It may also be

CC incorporated into a multivalent vaccine (see also AAW06131)

CC including another CETP B-cell epitope.

XX Sequence 26 AA:

SO

Query Match 100.0%; Score 134; DB 17; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.2e-13;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFTLLQMDFGFPEHLVDFLQSL 26

1 rdgftllqmdfgfpelhlvdfqls 26

DB

RESULT 2

AA13801

ID AA13801 standard; peptide: 26 AA.

XX AAY13801;

AC

XX 08-JUL-1999 (first entry)

DT

XX Rabbit CETP immunogenic fragment.

DE

XX CETP: cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;

KW antibody production; cholesteryl ester transfer; therapy;

KW high density lipoprotein; HDL cholesterol concentration;

KW pro-atherogenic dyslipoproteinaemia.

XX

XX Oryctolagus sp.

OS

XX WO9115655-A1.

PN

XX 01-APR-1999.

PD

XX 17-SEP-1998; 98WO-US19366.

XX

XX 19-SEP-1997; 97US-0934367.

XX

XX (MONS) MONSANTO CO.

PA

XX Glenn K, Needleman P;

PI

XX WPI; 1999-276984/23.

DR

XX

XX New recombinant DNA vaccines

PT

XX Claim 15; Page 85; 99pp; English.

PS

XX This sequence represents an immunogenic fragment of the rabbit

CC cholesteryl ester transferase protein (CETP).

CC The invention relates to recombinant DNA vaccines that contain DNA

CC encoding CETP, which can be used for producing antibodies to lessen the

CC transfer of cholesteryl esters from high density lipoprotein (HDL). The

CC method can provide an autogenic immunological process for lessening the

CC transfer of cholesteryl esters from HDL particles and for increasing the

CC HDL cholesterol concentration of a mammal whose blood also contains

CC CETP. The method may be useful in treating human pro-atherogenic

CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The

CC method can have an effect that lasts for months as compared to the

CC short-term effects of the small molecule drugs now available.

XX Sequence 26 AA:

SO

Query Match 100.0%; Score 134; DB 20; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.2e-13;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFTLLQMDFGFPEHLVDFLQSL 26

1 rdgftllqmdfgfpelhlvdfqls 26

DB

RESULT 3

AA91228

ID AA91228 standard; peptide: 26 AA.

XX AAY91228;

AC

XX 22-MAY-2000 (first entry)

DT

XX Human cholesteryl transport protein (CETP) peptide, SEQ ID NO:106.

DE

XX Promiscuous T-cell epitope; measles virus F protein; MVF;

KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;

KW interleukin 6; growth promoting hormone; LHRH; contraceptive; anticancer;

KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;

KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;

KW Plasmodium falciparum; circumsporozoite; antimalarial; CETP;

KW cholesteryl ester transport protein; anti-arteriosclerotic.

XX

XX Homo sapiens.

OS

XX WO966957-A2.

PN

XX 29-DEC-1999.

PD

XX 21-JUN-1999; 99WO-US13975.

XX

XX 20-JUN-1998; 98US-0100412.

XX

XX (UNBI-) UNITED BIOMEDICAL INC.

PA

XX Wang CY;

PI

XX WPI; 2000-160564/14.

DR

XX

XX New artificial T helper cell epitope and derived immunogens with target

PT antigenic site, for immunization against e.g. malaria, arteriosclerosis

PT or human immune deficiency virus

PT

XX Claim 10; Page 49; 129pp; English.

PS

XX The invention relates to novel promiscuous T helper cell epitopes (Th),

CC and immunogenic peptides comprising the Th epitopes of the invention

CC along with B cell epitopes. The Th epitopes and peptide immunogens

CC containing them, are used to induce a T helper cell response,

CC specifically against Plasmodium falciparum, cholesteryl ester transport

CC protein (CETP) or HIV epitopes, but more generally against any pathogen,

CC immunoreactive self-antigen or tumour antigen. The Th epitopes and

CC peptide immunogens may be used for prevention and/or treatment of

CC infections (HIV, foot-and-mouth disease or malaria); for cancer

CC immunotherapy; for inhibition of the action of interleukin 6; for hormone-

CC releasing hormone (LHRH) for contraception, treatment of hormone-

CC dependent cancer, prevention of boar taint in meat, and

CC immunosuppression; for promoting the growth of animals; or for

CC treating allergies or arteriosclerosis. Incorporation of a promiscuous

CC Th (functional in genetically diverse subjects) into an immunogen

CC improves capacity to induce a strong T helper cell-mediated immune

CC response, resulting in production of antibodies against a target

CC antigen. Th can replace carrier proteins and pathogen-derived T helper

CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope

CC from the measles virus F (MVF) protein and sequences AAY91122-191142,

PA (MONS) MONSANTO CO.
XX
PI Glenn K. Needleman P;
XX
DR WPI: 1999-276984/23.
XX
PT New recombinant DNA vaccines
XX
PS Disclosure: Page 88; 99pp; English.
XX
CC This sequence represents an immunogenic fragment of the human
CC cholesterol ester transferase protein (CETP).
CC The invention relates to recombinant DNA vaccines that contain DNA
CC encoding CETP, which can be used for producing antibodies to lessen the
CC transfer of cholesteryl esters from high density lipoprotein (HDL). The
CC method can provide an autogenic immunological process for lessening the
CC transfer of cholesteryl esters from HDL particles and for increasing the
CC HDL cholesterol concentration of a mammal whose blood also contains
CC CETP. The method may be useful in treating human pro-atherogenic
CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
CC method can have an effect that lasts for months as compared to the
CC short-term effects of the small molecule drugs now available.
SQ Sequence 22 AA:

Query Match 82.8%; Score 111; DB 20; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 LLLQMDFGPEHLVDPLQSL 26
Db 1 lllqmdfgpehlvdplqsls 22
|||||
RESULT 8
AAV13809
ID AAV13809 standard; peptide: 22 AA.
AC AAV13809;
XX
XX 08-JUL-1999 (first entry)
DT
DE Rabbit CETP immunogenic fragment.
XX
XX CETP; cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;
KM antibody production; cholesteryl ester transfer; therapy;
KM high density lipoprotein; HDL cholesterol concentration;
KM pro-atherogenic dyslipoproteinaemia.
XX
OS Oryctolagus sp.
XX
XX W09915655-A1.
PN
XX 01-APR-1999.
PD
XX 17-SEP-1998; 98WO-US19366.
PF
XX 19-SEP-1997; 97US-0934367.
PR
XX (MONS) MONSANTO CO.
PA
XX
PI Glenn K. Needleman P;
XX
DR WPI: 1999-276984/23.
XX
PT New recombinant DNA vaccines
XX
XX Example 1; Page 73; 99pp; English.
XX
CC This sequence represents an immunogenic fragment of the rabbit
CC cholesteryl ester transferase protein (CETP).
CC The invention relates to recombinant DNA vaccines that contain DNA

CC encoding CETP, which can be used for producing antibodies to lessen the
CC transfer of cholesteryl esters from high density lipoprotein (HDL). The
CC method can provide an autogenic immunological process for lessening the
CC transfer of cholesteryl esters from HDL particles and for increasing the
CC HDL cholesterol concentration of a mammal whose blood also contains
CC CETP. The method may be useful in treating human pro-atherogenic
CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
CC method can have an effect that lasts for months as compared to the
CC short-term effects of the small molecule drugs now available.
SQ Sequence 22 AA:

Query Match 79.9%; Score 107; DB 20; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.4e-09;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 LLLQMDFGPEHLVDPLQSL 26
Db 1 lllqmdfgpehlvdplqsls 22
|||||
RESULT 9
AAV91229
ID AAV91229 standard; peptide: 16 AA.
AC AAV91229;
XX
XX 22-MAY-2000 (first entry)
DT
XX
XX Human cholesteryl transport protein (CETP) peptide, SEQ ID NO:107.
DE
XX
XX Promiscuous T-cell epitope: measles virus F protein; MVE;
KM hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KM interleukin hormone releasing hormone; LHRH; contraceptive; anticancer;
KM somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
KM foot and mouth disease virus; Immunoglobulin E; IGE; anti-allergic;
KM Plasmodium falciparum; circumsporozoite; antimalarial; CETP;
KM cholesteryl ester transport protein; anti-arteriosclerotic.
XX
XX Homo sapiens.
OS
XX
XX W09966957-A2.
FN
XX 29-DEC-1999.
PD
XX 21-JUN-1999; 99WO-US13975.
PF
XX 20-JUN-1998; 98US-0100412.
PR
XX (UNBI -) UNITED BIOMEDICAL INC.
PA
XX
XX Wang CY;
PI
XX
XX WPI: 2000-160564/14.
DR
XX
XX New artificial T helper cell epitope and derived immunogens with target
PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT or human immune deficiency virus
XX
XX
XX Claim 10; Page 50; 129pp; English.
PS
XX
XX The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response,
CC specifically against Plasmodium falciparum, cholesteryl ester transport
CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC peptide immunogens may be used for prevention and/or treatment of
CC infections (HIV, foot-and-mouth disease or malaria); for cancer
CC immunotherapy; for inhibition of the action of interleukin hormone
CC releasing hormone (LHRH) for contraception, treatment of hormone-

Query Match 59.0%; Score 79; DB 21; Length 16;
 Best Local Similarity 93.8%; Pred. No. 1.9e-05;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 11 FGPEHLVDFLOSLUS 26
 Db 1 fgfphkhlvdfllgsls 16

RESULT 11
 AAW24294 standard; peptide: 11 AA.
 AAW24294 standard; peptide: 11 AA.

AC AAW24294;
 DT 17-OCT-1997 (first entry)
 DE Human/Rabbit CERP common peptide.

XX Immune response; high density lipoprotein; HDL; cholesterol; human;
 KW serum; epitope; cholesterol ester transfer protein; CERP; rabbit.
 XX Oryctolagus cuniculus.
 OS Homo sapiens.

XX WO9639168-A1.

PD 12-DEC-1996.

PF 05-JUN-1996; 96WO-US09143.

PR 06-JUN-1995; 95US-0482454.

PA (IMMUNE RESPONSE CORP.

PI Brostoff SM, Carlo DJ, Kwch DY;

DR WPI; 1997-042849/04.

PT Stimulating an immune response to increase high density lipoprotein
 PT - avoids repeated administration of toxic drugs to lower cholesterol
 PT ester transfer protein levels

PS Claim 5; Page 16; 26pp; English.

XX The sequences given in AAW24292-94 were used in the method of the
 CC invention to stimulate an immune response to increase high density
 CC lipoprotein (HDL) cholesterol in a mammal exhibiting low levels of
 CC serum HDL. These peptides represent immunogenic epitopes of
 CC cholesterol ester transfer protein (CERP). The method utilizes
 CC the body's own immune system to lower CERP levels, thereby increasing
 CC the level of beneficial HDL cholesterol, preferably in serum. The
 CC method avoids the problems associated with the repeated administration
 CC of drugs which have undesirable side effects. This peptide represents
 CC a region of CERP which is common to both human and rabbit proteins.

XX Sequence 11 AA;

Query Match 39.6%; Score 53; DB 18; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16 HLYVDFLOSLUS 26
 Db 1 hllyvdfllgsls 11

RESULT 12

AAAB64886
 ID AAB64886 standard; Protein: 22 AA.

AC AAB64886;

XX 23-MAR-2001 (first entry)
 DT Human secreted protein sequence encoded by gene 5 SEQ ID NO:64.
 DE

XX Human; secreted protein; diagnosis; immunomodulatory; antisclerotic;
 KW dermatological; immunosuppressive; anti-inflammatory; anti-HIV;
 KW immunostimulant; cytostatic; cartiant; vascular; anti-angiogenic;
 KW ophthalmological; neuroprotectant; nootropic; anticonvulsant; vulnary;
 KW antialzheimers; antiparkinsonian; antimicrobial; immune disorder;
 KW multiple sclerosis; systemic lupus erythematosus; HIV; infection;
 KW hyperproliferative disorder; cancer; Gaucher's disease; wound healing;
 KW cardiovascular disease; sclerular syndrome; Chaga's cardiomyopathy;
 KW coronary arteriosclerosis; angiogenic disorder; diabetic retinopathy;
 KW corneal graft neovascularisation; neurological disorder; regeneration;
 KW Huntington's chorea; Alzheimer's disease; Parkinson's disease;
 KW infectious disease; chemotaxis; chromosome 1.

XX Homo sapiens.

XX WO200076530-A1.

PD 21-DEC-2000.

PF 01-JUN-2000; 2000WO-US14933.

PR 11-JUN-1999; 99US-0138572.

PA (HUMA-) HUMAN GENOME SCI INC.

PI (ROSE/) ROSEN C A.

PI Rosen CA, Ruben SM, Komatsoulis GA;

DR WPI; 2001-071147/08.

DR N-PSDB; AAF33217.

PT Nucleic acids encoding 49 human secreted polypeptides, useful for
 PT preventing, diagnosing and/or treating e.g. cancers, Parkinson's
 PT disease and diabetic retinopathy -

PS Claim 11; Page 486; 554pp; English.

XX The polynucleotide sequences given in AAF33213 to AAF33261 encode the
 CC human secreted proteins given in AAB64882 to AAB64930. AAB64931 to
 CC AAB64991 represent human secreted polypeptide sequences and proteins
 CC homologous to them, which are given in the exemplification of the present
 CC invention. Human secreted proteins have activities based on the tissues
 CC and cells the genes are expressed in. Examples of activities include:
 CC immunomodulatory; antisclerotic; dermatological; immunosuppressive;
 CC anti-inflammatory; anti-HIV; immunostimulant; cytostatic; cartiant;
 CC vascular; antimicrobial; anti-angiogenic; ophthalmological;
 CC neuroprotectant; anticonvulsant; nootropic; antialzheimers;
 CC antiparkinsonian; and vulnary. The polynucleotides and polypeptides can
 CC be used in the prevention, diagnosis and treatment of diseases associated
 CC with inappropriate polypeptide expression. Disorders that may be
 CC prevented, diagnosed and/or treated by the above methods include immune
 CC disorders (e.g. multiple sclerosis, systemic lupus erythematosus and
 CC human immunodeficiency virus (HIV) infections), hyperproliferative
 CC disorders (e.g. cancers and Gaucher's disease), cardiovascular diseases
 CC (e.g. sclerular syndrome, Chaga's cardiomyopathy and coronary
 CC arteriosclerosis), angiogenic disorders (e.g. corneal graft
 CC neovascularisation and diabetic retinopathy), neurological disorders
 CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease),
 CC infectious diseases and/or for promoting wound healing, regeneration and
 CC /or chemotaxis. AAF33204 to AAF33212 and AAB64881 represent sequences
 CC used in the exemplification of the present invention.

XX Sequence 22 AA;

Query Match 25.4%; Score 34; DB 22; Length 22;
 Best Local Similarity 60.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 GFEPEHLVDF 21
 111 : 111
 Db 10 gfpdytvd 19

RESULT 13
 AAY12067
 ID AAY12067 standard; Protein; 25 AA.

AC AAY12067;
 XX
 DT 18-JUN-1999 (first entry)
 XX

DE Human 5' EST secreted protein SEQ ID NO: 380.

XX Human; secreted protein; EST; expressed sequence tag; diagnosis;
 KM forensic; gene therapy; chromosome mapping; signal peptide;
 KM upstream regulatory sequence; cytokine activity; cell proliferation;
 KM differentiation; haematopoiesis regulation; tissue growth regulation;
 KM reproductive hormone regulation; chemotactic; chemokinetic; hemostatic;
 KM thrombolytic; anti-inflammatory; tumour inhibition.

OS Homo sapiens.
 XX
 PN WO9906554-A2.
 XX
 PD 11-FEB-1999.

XX 31-JUL-1998; 98WO-IB01238.
 XX
 PR 01-AUG-1997; 97US-0905134.

XX (GEST) GENSET.
 PA
 PI Duclert A, Dumas Milne Edwards J, Lacroix B;

XX WPI: 1999-153784/13.
 DR N-PSDB: AAX40900.
 XX

PT New nucleic acids encoding human secreted proteins - obtained from
 PT cDNA libraries prepared from kidney, fetal kidney, dystrophic
 PT muscle, muscle and heart tissue

PS Claim 34; Page 500-501; 622pp; English.

XX AAX40826 to AAX41093 represent 5' expressed sequence tags (ESTs) for
 CC human secreted proteins, and encode the proteins given in AAY01602 and
 CC AAY11994 to AAY12260, respectively. The proteins given represent the
 CC signal peptide and an N-terminal fragment of a secreted protein. The
 CC nucleic acid sequences can be used for producing secreted human gene
 CC products. They can also be used to develop products for diagnosis and
 CC therapy. The proteins obtained may have cytokine activity, cell
 CC proliferation/differentiation activity, haematopoiesis regulating
 CC activity, tissue growth regulating activity, reproductive hormone
 CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
 CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
 CC activity, tumour inhibition activity or other activities. The products
 CC can be used in forensic, gene therapy and chromosome mapping procedures.
 CC The sequences can also be used for obtaining corresponding promoter
 CC sequences. The nucleic acids encoding the signal peptide can be used
 CC for directing extracellular secretion of a polypeptide or the insertion
 CC of a polypeptide into a membrane, or importing a polypeptide into
 CC a cell.
 XX

Sequence 25 AA;

Query Match 25.4%; Score 34; DB 20; Length 25;
 Best Local Similarity 50.0%; Pred. No. 2.2e+02;
 Matches 2; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 9 MDGPEHLVDFLOSLS 26
 1 1 1 1 : 1 1 1 1
 Db 1 mggiiaesfclnclvls 18

RESULT 14
 AAP30225
 ID AAP30225 standard; Protein; 12 AA.

AC AAP30225;
 XX
 DT 25-MAY-1992 (first entry)
 XX

DE Sequence of interferon (HuIFN) -alpha-61A around amino acid 40.

XX Hybrid interferon; antiviral; therapy; cancer; tumour.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Misc-difference 7
 FT /label= AA No. 40

PN WO8302461-A.
 XX
 PD 21-JUL-1983.
 XX

XX 18-JAN-1983; 83WO-0900607.
 XX
 PR 19-JAN-1982; 82US-0340782.
 PR 03-FEB-1983; 83US-0463574.
 PR 15-JUL-1985; 85US-0755265.

XX (CENTU-) CETUS CORP.
 PA
 PI Mark DF, Creasey AA;

XX WPI: 1983-723186/30.
 DR N-PSDB: AAN30158.
 XX

PT Multi-class hybrid interferon poly:peptide(s) - with restricted
 PT antiviral and cell growth regulatory activities
 PT
 PS Example: Fig 17; 61pp; English.

XX The inventors claim a multiclass hybrid interferon polypeptide and a
 CC DNA unit having a nucleotide sequence which encodes it. Pref. IF1 is
 CC AA sequence consists of alpha and beta interferons. Pref. IF1 is
 CC (1) the 1-73 AA seq. of HuIFN-alpha-1 (and IF2 is the 74-166 AA seq.
 CC of HuIFN-beta-1) (see AAN30155, AAP30222); or (1i) the 1-41 AA seq. of
 CC HuIFN-alpha-61A (and IF2 is the 43-166 AA seq. of HuIFN-beta-1) (see
 CC AAN30160, AAP30227). Alternatively, IF1 is the amino terminal end of a
 CC beta-IF and IF2 is the carboxy terminal of an alpha-IF (esp. the
 CC 1-73 seq. of HuIFN-beta-1 and the 74-167 seq. of HuIFN-alpha-1
 CC resp.) (see AAN30156, AAP30223). In the examples plasmids pGV5 and
 CC pDM101/tyr/beta-1 and p-alpha-61A were used (see AAN30151, AAN30152,
 CC AAN30157). HinfI was used to digest the DNA sequences in the region
 CC of significant handicaps (see AAN30153, AAN30154, AAN30158, AAN30159),
 CC and the restriction fragments were ligated to form hybrid DNA.
 XX

Sequence 12 AA;

Query Match 24.6%; Score 33; DB 4; Length 12;
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 DRGPE 15
 11111 :
 Db 2 dfgp 7

RESULT 15

Job time: 209 sec

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AAP80053
ID AAP80053 standard: protein: 12 AA.
XX
AC AAP80053;
XX
DT 17-NOV-1990 (first entry)
XX
DE Sequence of human Interferon (huIFN) alpha-61A gene around AA 40.
XX
KM Alpha-beta hybrid Interferon: multi-class hybrid Interferon;
XX antitumour; antiviral; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 7
FT /note="Residue 40"
XX
XX
PN US4758428-A.
XX
PD 19-JUL-1988.
XX
PF 15-JUL-1985; 85US-0755265.
XX
PR 15-JUL-1985; 85US-0755265.
XX
PR 19-JAN-1983; 83CA-0419758.
XX
PA (CETUS ) CETUS CORP.
XX
PI Mark DF, Creasey AA;
XX
XX WPI; 1988-219882/31.
XX
DR N-PSDB; AANB0050.
XX
XX
PT Multi-class hybrid Interferon polypeptide(s) -
PT having sequence from Interferon-alpha-1 and sequence from
PT Interferon-beta-1 for restricted activity
XX
XX
PS Example; Fig 17; 24pp; English.
XX
XX
CC Multi-class hybrid IFN polypeptides having an AA sequence composed
CC of 2 distinct subsequences are claimed. The plasmids used in the
CC construction of huIFN-alpha-61A-beta-1 hybrid are plasmids palpa61A and
CC pDM101/trp/beta-1. Assembly of the palpa61A plasmid involved replacing
CC the DNA fragment encoding the 23 AA signal polypeptide of preinterferon
CC with a 120BP EcoRI/Sau3A promoter fragment E.coli trp promoter,
CC operator, and trp leader ribosome binding site preoperator, encoding an
CC Arg initiation codon and using HindIII site that was inserted, 59
CC nucleotides 3'-end of the TGA translational stop codon, to insert the
CC gene into the plasmid pDM11 (a deriv of pBR322 having a deletion between
CC the HindIII and PvuII sites). The complete DNA sequence of the promoter
CC and gene fragments inserted between the EcoRI and HindIII sites of pDM11
CC is shown in AANB0049. The hybrid gene was constructed by taking advantage
CC of the homologies between huIFN alpha-61A & huIFN beta-1 at around AA 40
CC of both proteins. The DNA sequence 5'-proximal to the DdeI restriction
CC enzyme cutting site of the huIFN alpha-61A DNA is ligated to the DNA
CC sequence 3'-proximal to the site of huIFN beta-1, to create a fusion of
CC the two genes while preserving the translational reading frame of both.
XX
SQ Sequence 12 AA:

Query Match 24.6%; Score 33; DB 9; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 10 DFGFPE 15
   11111:
Db 2 dfgfpq 7

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Search completed: June 18, 2002, 08:17:21

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2002, 08:12:01 ; Search time 102.57 Seconds
(without alignments)
89,222 Million cell updates/sec

Title: US-09-943-334-1
Perfect score: 134
Sequence: 1 RDGFLLLQMDGFPPEHLVDFLOSL 26

Scoring table:

BLOSUM62
Gapop 10.0 0, Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 2173486

Minimum DB seq length: 0
Maximum DB seq length: 26

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending Patents AA.Main: *
1: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US08_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US08_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US08_COMB.pep.*
8: /cgn2_6/ptodata/2/paa/US08_COMB.pep.*
9: /cgn2_6/ptodata/2/paa/US08_COMB.pep.*
10: /cgn2_6/ptodata/2/paa/US08_COMB.pep.*
11: /cgn2_6/ptodata/2/paa/US08_COMB.pep.*
12: /cgn2_6/ptodata/2/paa/US08_COMB.pep.*
13: /cgn2_6/ptodata/2/paa/US08_COMB.pep.*
14: /cgn2_6/ptodata/2/paa/US09_COMB.pep.*
15: /cgn2_6/ptodata/2/paa/US09_COMB.pep.*
16: /cgn2_6/ptodata/2/paa/US09_COMB.pep.*
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22: /cgn2_6/ptodata/2/paa/US09_COMB.pep.*
23: /cgn2_6/ptodata/2/paa/US09_COMB.pep.*
24: /cgn2_6/ptodata/2/paa/US10_COMB.pep.*
25: /cgn2_6/ptodata/2/paa/US10_COMB.pep.*
26: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	134	100.0	26	1	PCT-US99-139758-106
2	134	100.0	26	8	US-08-432-483-1
3	134	100.0	26	8	US-08-432-483A-1
4	134	100.0	26	11	US-08-785-997-29
5	134	100.0	26	11	US-08-788-882-29
6	134	100.0	26	13	US-08-934-367-29
7	134	100.0	26	13	US-08-945-289-1

8	134	100.0	26	17	US-09-386-591-29	Sequence 29, Appl
9	134	100.0	26	17	US-09-387-340-29	Sequence 29, Appl
10	134	100.0	26	21	US-09-701-588-106	Sequence 106, Appl
11	134	100.0	26	23	US-09-943-334-1	Sequence 1, Appl1
12	134	100.0	26	23	US-09-943-334-1	Sequence 1, Appl1
13	117	87.3	26	23	PCT-US99-139758-109	Sequence 109, Appl
14	117	87.3	26	11	US-08-785-997-50	Sequence 50, Appl
15	117	87.3	26	13	US-08-788-882-50	Sequence 50, Appl
16	117	87.3	26	13	US-08-934-367-50	Sequence 50, Appl
17	117	87.3	26	17	US-09-386-591-50	Sequence 50, Appl
18	117	87.3	26	17	US-09-387-340-50	Sequence 50, Appl
19	117	87.3	26	21	US-09-701-588-109	Sequence 109, Appl
20	111	82.8	22	11	US-08-785-997-34	Sequence 34, Appl
21	111	82.8	22	11	US-08-788-882-34	Sequence 34, Appl
22	111	82.8	22	11	US-08-934-367-34	Sequence 34, Appl
23	111	82.8	22	13	US-08-788-882-34	Sequence 34, Appl
24	111	82.8	22	13	US-08-934-367-34	Sequence 34, Appl
25	111	82.8	22	13	US-08-934-367-34	Sequence 34, Appl
26	111	82.8	22	17	US-09-386-591-34	Sequence 34, Appl
27	111	82.8	22	17	US-09-387-340-34	Sequence 34, Appl
28	111	82.8	22	17	US-09-387-340-34	Sequence 34, Appl
29	111	82.8	22	11	US-08-785-997-4	Sequence 4, Appl1
30	107	79.9	22	11	US-08-788-882-4	Sequence 4, Appl1
31	107	79.9	22	13	US-08-934-367-4	Sequence 4, Appl1
32	107	79.9	22	13	US-08-934-367-4	Sequence 4, Appl1
33	107	79.9	22	17	US-09-386-591-4	Sequence 4, Appl1
34	107	79.9	22	17	US-09-387-340-4	Sequence 4, Appl1
35	83	61.9	16	1	PCT-US99-139758-107	Sequence 107, Appl
36	83	61.9	16	21	US-09-701-588-107	Sequence 107, Appl
37	79	59.0	16	1	PCT-US99-139758-108	Sequence 108, Appl
38	79	59.0	16	21	US-09-701-588-108	Sequence 108, Appl
39	53	39.6	11	8	US-08-482-454-3	Sequence 3, Appl1
40	38	28.4	13	20	US-09-675-849-22	Sequence 22, Appl
41	36.5	27.2	26	26	US-60-169-842-4506	Sequence 4506, Ap
42	36	26.9	21	1	PCT-US01-14827-13017	Sequence 13017, A
43	34	25.4	21	19	US-09-538-038-1267	Sequence 1267, Ap
44	34	25.4	21	23	US-09-950-083-4435	Sequence 4435, Ap
45	34	25.4	22	1	PCT-US00-14933-64	Sequence 64, Appl

ALIGNMENTS

RESULT 1
PCT-US99-139758-106
Sequence 106, Application PC/TUS9913975B
GENERAL INFORMATION:
APPLICANT: UNITED BIOMEDICAL INC., ET AL.
TITLE OF INVENTION: ARTIFICIAL T HELPER CELL
TITLE OF INVENTION: EPITOPES AS IMMUNE STIMULATORS FOR SYNTHETIC
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/13975B
FILING DATE: 21-JUNE-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,412
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin

```

;
;   REGISTRATION NUMBER: 29,323
;   REFERENCE/DOCKET NUMBER: 1151-4158PCL
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 212-758-4800
;   TELEFAX: 212-751-6849
;   INFORMATION FOR SEQ ID NO: 106:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 26 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   PCT-US99-13975B-106

Query Match      100.0%; Score 134; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RDGFLLLQMDGFGFPEHLLVDFLQSL 26
Db      1 RDGFLLLQMDGFGFPEHLLVDFLQSL 26

RESULT      2
US-08-432-483-1
; Sequence 1, Application US/08432483
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles, W.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
; TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: Ten South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-7407
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/432,483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Leon R. Yankwich
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: 95,179(TCS-95179)
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL:
; ANTI-SENSE:
; FEATURE:
; NAME/KEY: Carboxyl terminal 26 amino acids of
; NAME/KEY: human CETP
; LOCATION:
; PUBLICATION INFORMATION:
; AUTHORS: Drayna, Dennis, et al.
; TITLE: Cloning and sequencing of human
; TITLE: cholesterol ester transfer CDNA
; JOURNAL: Nature
; VOLUME: 327
; ISSUE:
; PAGES: 632-634
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;   DATE: 18-JUN-1987
;   RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 26
;   US-08-432-483-1

Query Match      100.0%; Score 134; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RDGFLLLQMDGFGFPEHLLVDFLQSL 26
Db      1 RDGFLLLQMDGFGFPEHLLVDFLQSL 26

RESULT      3
US-08-432-483A-1
; Sequence 1, Application US/08432483A
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
; TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: Ten South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-7407
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/432,483A
; FILING DATE: 1-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Leon R. Yankwich
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: 95,179(TCS-95179)
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL:
; ANTI-SENSE:
; FEATURE:
; NAME/KEY: Carboxyl terminal 26 amino acids of
; NAME/KEY: human CETP
; LOCATION:
; PUBLICATION INFORMATION:
; AUTHORS: Drayna, Dennis, et al.
; TITLE: Cloning and sequencing of human
; TITLE: cholesterol ester transfer CDNA
; JOURNAL: Nature
; VOLUME: 327
; ISSUE:
; PAGES: 632-634
; DATE: 18-JUN-1987
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 26
; US-08-432-483A-1

Query Match      100.0%; Score 134; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,367
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gamson Ph.D., Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1500
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PUBLICATION INFORMATION:
AUTHORS: Swenson, T. L.
AUTHORS: et al.,
JOURNAL: J. Biol. Chem.
VOLUME: 264
PAGES: 14318-14326
DATE: 1989
US-08-934-367-29

Query Match 100.0%; Score 134; DB 13; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLQMDFGPEPHLLVDPLQSL 26
DB 1 RDGFLLQMDFGPEPHLLVDPLQSL 26

RESULT 7
US-08-945-289-1
Sequence 1, Application US/08945289
GENERAL INFORMATION:
APPLICANT: Riltershau, Charles, W.
APPLICANT: Thomas, Lawrence J.
TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,289
FILING DATE: October 17, 1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/432,483
FILING DATE: May 1, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: TCS-411.1P US
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL:
ANTI-SENSE:
FEATURE:
NAME/KEY: Carboxyl terminal 26 amino
NAME/KEY: acids of human CETP
LOCATION:
PUBLICATION INFORMATION:
AUTHORS: Drayna, Dennis, et al.
TITLE: Cloning and sequencing of human cholesterol ester transfer cDNA
JOURNAL: Nature
VOLUME: 327
ISSUE:
PAGES: 632-634
DATE: 18-JUN-1987
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 26
US-08-945-289-1

Query Match 100.0%; Score 134; DB 13; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLQMDFGPEPHLLVDPLQSL 26
DB 1 RDGFLLQMDFGPEPHLLVDPLQSL 26

RESULT 8
US-09-386-591-29
Sequence 29, Application US/09386591
GENERAL INFORMATION:
APPLICANT: Needleman, Philip
APPLICANT: Glenn, Kevin
TITLE OF INVENTION: An Immunological Process and Constructs
TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration by DNA
TITLE OF INVENTION: Vaccination
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/386,591
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gamson Ph.D., Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1500
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PUBLICATION INFORMATION:
AUTHORS: Swenson, T. L.
AUTHORS: et al.,
JOURNAL: J. Biol. Chem.

VOLUME: 264
PAGES: 14318-14326
DATE: 1989
US-09-386-591-29

Query Match 100.0%; Score 134; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDGFPFPHLLVDFLOSL 26
Db 1 RDGFLLLQMDGFPFPHLLVDFLOSL 26

RESULT 9
US-09-387-340-29
; Sequence 29, Application US/09387340
; GENERAL INFORMATION:
; APPLICANT: Needleman, Philip
; APPLICANT: Glenn, Kevin
; APPLICANT: Krul, Elaine
; APPLICANT: Ganson, Edward P.
; TITLE OF INVENTION: An Immunological Process and Constructs
; TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 120 South Riverside Plaza, 22nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/387,340
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ganson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)655-1500
; TELEFAX: (312)655-1501
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PUBLICATION INFORMATION:
; AUTHORS: Swenson, T. L.
; AUTHORS: et al.,
; JOURNAL: J. Biol. Chem.
; VOLUME: 264
; PAGES: 14318-14326
; DATE: 1989
US-09-387-340-29

Query Match 100.0%; Score 134; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDGFPFPHLLVDFLOSL 26
Db 1 RDGFLLLQMDGFPFPHLLVDFLOSL 26

RESULT 10
US-09-701-588-106

; Sequence 106, Application US/09701588
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Y1
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 122
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Morgan & Flinnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY

COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/701,588
FILING DATE: 29-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998

ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-158051
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849

INFORMATION FOR SEQ ID NO: 106
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 106

US-09-701-588-106

Query Match 100.0%; Score 134; DB 21; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDGFPFPHLLVDFLOSL 26
Db 1 RDGFLLLQMDGFPFPHLLVDFLOSL 26

RESULT 11
US-09-943-334-1

; Sequence 1, Application US/09943334
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; APPLICANT: Thomas, Lawrence J.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVI
; FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
; CURRENT APPLICATION NUMBER: US/09/943,334
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 08/432,483
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: PCT/US96/06147
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/945,289
; PRIOR FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1

US-09-943-334-1

SEQ ID NO 1
LENGTH: 26
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: C - terminal 26 amino acids of Human CETP
US-09-943-334-1

Query Match 100.0%; Score 134; DB 23; Length 26;
Best Local Similarity 100.0%; Pred. No. 1,5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDGFPFPHLLVDFLOSLS 26
Db 1 RDGFLLLQMDGFPFPHLLVDFLOSLS 26

RESULT 12
US-09-943-548-1
Sequence 1, Application US/09943548
GENERAL INFORMATION:
APPLICANT: Riltershaus, Charles W.
TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVITY
FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
CURRENT APPLICATION NUMBER: US/09/943,548
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: 08/432,483
PRIOR FILING DATE: 1995-05-01
PRIOR APPLICATION NUMBER: PCT/US96/06147
PRIOR FILING DATE: 1996-05-01
PRIOR APPLICATION NUMBER: 08/945,289
PRIOR FILING DATE: 1997-10-17
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 26
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: C - terminal 26 amino acids of Human CETP
US-09-943-548-1

Query Match 100.0%; Score 134; DB 23; Length 26;
Best Local Similarity 100.0%; Pred. No. 1,5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDGFPFPHLLVDFLOSLS 26
Db 1 RDGFLLLQMDGFPFPHLLVDFLOSLS 26

RESULT 13
PCT-US99-13975B-109
Sequence 109, Application PC/TUS9913975B
GENERAL INFORMATION:
APPLICANT: UNITED BIOMEDICAL INC., ET AL.
TITLE OF INVENTION: ARTIFICIAL T HELPER CELL
TITLE OF INVENTION: EPITOPES AS IMMUNE STIMULATORS FOR SYNTHETIC
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Flanagan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/13975B
FILING DATE: 21-JUNE-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,412
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4158PC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US99-13975B-109

Query Match 87.3%; Score 117; DB 1; Length 26;
Best Local Similarity 92.0%; Pred. No. 5,4e-10;
Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DGLLLQMDGFPFPHLLVDFLOSLS 26
Db 2 DGLLLQMDGFPFPHLLVDFLOSLS 26

RESULT 14
US-08-785-997-50
Sequence 50, Application US/08785997
GENERAL INFORMATION:
APPLICANT: Needleman, Philip
TITLE OF INVENTION: An Immunological Process for Increasing
TITLE OF INVENTION: the HDL Cholesterol Concentration
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,997
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gamson Ph.D., Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-101.0 6018/68346
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1500
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:12:57 ; Search time 13.54 Seconds

(without alignments)
162.588 Million cell updates/sec

Title: US-09-943-334-1

Perfect score: 134

Sequence: 1 RCGFLLQMDRFQFPHLLVDFLOSL 26

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 44311

Minimum DB seq length: 0
Maximum DB seq length: 26

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

Pending_Patents_NA_New.*
1: /cgn2_6/prodata/1/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/prodata/1/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/prodata/1/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/prodata/1/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/prodata/1/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/prodata/1/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/prodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	53	39.6	11	5	US-09-523-033A-3
2	34	25.4	21	1	PCT-US02-09257-427
3	34	25.4	21	1	PCT-US02-09370-671
4	34	25.4	21	6	US-10-105-299-5439
5	32	24.3	12	6	US-10-145-415-68
6	32	23.9	22	5	US-09-453-834-133
7	32	23.9	22	5	US-09-453-841-133
8	32	23.9	22	6	US-10-099-574A-133
9	32	23.9	22	6	US-10-147-849-133
10	32	23.9	22	6	US-10-147-993-133
11	30	22.4	9	6	US-10-014-340-19
12	30	22.4	16	5	US-09-050-359B-136
13	30	22.4	16	5	US-09-069-827A-136
14	30	22.4	18	6	US-10-000-256A-210
15	29.5	22.0	22	5	US-09-721-506-290
16	29	21.6	21	6	US-10-105-299-4564
17	29	21.6	21	6	US-10-016-349A-215
18	28.5	21.3	15	1	PCT-US02-13200-5
19	28.5	21.3	15	6	US-10-132-100-5
20	28	20.9	11	5	US-10-105-232-72
21	28	20.9	16	5	US-09-547-938B-61
22	28	20.9	17	5	US-09-547-938B-59
23	28	20.9	17	6	US-10-105-232-324
24	28	20.9	17	6	US-10-105-232-327
25	28	20.9	18	6	US-10-105-232-333
26	28	20.9	19	6	US-10-105-232-326

27	28	20.9	22	1	PCT-US02-09188-487	Sequence 487, App
28	28	20.9	22	1	PCT-US02-09370-505	Sequence 505, App
29	28	20.9	22	5	US-09-453-834-134	Sequence 134, App
30	28	20.9	22	5	US-09-453-841-134	Sequence 134, App
31	28	20.9	22	6	US-10-105-299-3205	Sequence 3205, App
32	28	20.9	22	6	US-10-099-574A-134	Sequence 134, App
33	28	20.9	22	6	US-10-147-849-134	Sequence 134, App
34	28	20.9	22	6	US-10-147-993-134	Sequence 134, App
35	27	20.1	9	6	US-10-089-783-10	Sequence 10, App
36	27	20.1	9	6	US-10-089-783-61	Sequence 61, App
37	27	20.1	10	6	US-10-089-783-23	Sequence 23, App
38	27	20.1	10	6	US-10-089-783-24	Sequence 24, App
39	27	20.1	13	1	PCT-US02-09135-151	Sequence 151, App
40	27	20.1	13	1	PCT-US02-09105-121	Sequence 121, App
41	27	20.1	13	1	PCT-US02-09257-299	Sequence 299, App
42	27	20.1	13	1	PCT-US02-09922-285	Sequence 285, App
43	27	20.1	13	6	US-10-105-299-3814	Sequence 3814, App
44	27	20.1	20	1	PCT-US02-01109-141	Sequence 141, App
45	27	20.1	22	6	US-10-115-123-516	Sequence 516, App

ALIGNMENTS

RESULT 1
US-09-523-033A-3
; Sequence 3, Application US/09523033A
; GENERAL INFORMATION:
; APPLICANT: Kwoh, Deborah Y.
; APPLICANT: Brostloff, Steven W.
; TITLE OF INVENTION: METHOD FOR INCREASING HDL CHOLESTEROL LEVEL
; FILE REFERENCE: TCS-428.0 US-1
; CURRENT APPLICATION NUMBER: US/09/523,033A
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 08/482,454
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-523-033A-3

Query Match 39.6%; Score 53; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HLLVDFLOSL 26
DB 1 HLLVDFLOSL 11

RESULT 2
PCT-US02-09257-427
; Sequence 427, Application PC/TUS0209257
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS957PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09257
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/950,082
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 09/950,083
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 994
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 427

LENGTH: 21
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-09257-427

Query Match 25.4%; Score 34; DB 1; Length 21;
Best Local Similarity 60.0%; Pred. No. 99;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 GPEHLLVDF 21
||| : |||
DB 10 GPTTFYVDF 19

RESULT 3
PCT-US02-09370-671
Sequence 671, Application PC/TUS0209370
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: P8934PCT
CURRENT APPLICATION NUMBER: PCT/US02/09370
CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/278,650
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: US 09/950,082
PRIOR FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US 09/950,083
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 1834
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 671
LENGTH: 21
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-09370-671

Query Match 25.4%; Score 34; DB 1; Length 21;
Best Local Similarity 60.0%; Pred. No. 99;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 GPEHLLVDF 21
||| : |||
DB 10 GPTTFYVDF 19

RESULT 4
US-10-105-299-5439
Sequence 5439, Application US/10105299
GENERAL INFORMATION:
APPLICANT: Rosen, et. al
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: P8950
CURRENT APPLICATION NUMBER: US/10/105,299
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 15197
Prior Application removed - See file wrapper or palm
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5439
LENGTH: 21
TYPE: PRT
ORGANISM: Homo sapiens
US-10-105-299-5439

Query Match 25.4%; Score 34; DB 6; Length 21;
Best Local Similarity 60.0%; Pred. No. 99;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 GPEHLLVDF 21
||| : |||

DB 10 GPTTFYVDF 19

RESULT 5
US-10-145-415-68
Sequence 68, Application US/10145415
GENERAL INFORMATION:
APPLICANT: Buckel, Thomas Gunter
APPLICANT: Hammer, Philip Eugene
APPLICANT: Hill, Dwight Steven
APPLICANT: Ligon, James Madison
APPLICANT: Molnar, Istvan
APPLICANT: Pachlatko, Johannes Paul
APPLICANT: Zirkle, Ross Eric
TITLE OF INVENTION: Methods and Compositions for Making Emamectin
FILE REFERENCE: SYN-117 109846.312
CURRENT APPLICATION NUMBER: US/10/145,415
CURRENT FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: US 60/291,149
PRIOR FILING DATE: 2001-05-16
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 68
LENGTH: 12
TYPE: PRT
ORGANISM: Streptomyces tubercidicus
US-10-145-415-68

Query Match 24.3%; Score 32.5; DB 6; Length 12;
Best Local Similarity 58.3%; Pred. No. 92;
Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 6 LHMDFGPEHL 17
| : | | |||
DB 1 LHM-LGPEHL 11

RESULT 6
US-09-453-834-133
Sequence 133, Application US/09453834
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Butner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,834
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 009196-0004-999

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556

INFORMATION FOR SEQ ID NO: 133:

SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: None

US-09-453-834-133

Query Match

Best Local Similarity 58.3%; Score 32; DB 5; Length 22;

Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 15 EHLVDFLOSLS 26

Db 7 ERLEDDLQALN 18

RESULT 7

US-09-453-841-133

Sequence 133, Application US/09453841

GENERAL INFORMATION:

APPLICANT: Dasseux, Jean-Louis

APPLICANT: Sekul, Renate

APPLICANT: Butner, Klaus

APPLICANT: Cornut, Isabelle

APPLICANT: Metz, Gunther

APPLICANT: Dufourcq, Jean

TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

NUMBER OF SEQUENCES: 258

ADDRESSER: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/453,841

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/940,095

FILING DATE: 29-SEP-1997

ATTORNEY/AGENT INFORMATION:

NAME: Cornuzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 009196-0004-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556

INFORMATION FOR SEQ ID NO: 133:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: None

US-09-453-841-133

Query Match

Best Local Similarity 58.3%; Score 32; DB 5; Length 22;

Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 15 EHLVDFLOSLS 26

Db 7 ERLEDDLQALN 18

RESULT 8

US-10-099-574A-133

Sequence 133, Application US/10099574A

GENERAL INFORMATION:

APPLICANT: Dasseux, Jean-Louis

APPLICANT: Sekul, Renate

APPLICANT: Butner, Klaus

APPLICANT: Cornut, Isabelle

APPLICANT: Metz, Gunther

TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

NUMBER OF SEQUENCES: 254

ADDRESSER: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/099,574A

FILING DATE: 29-SEP-1997

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Cornuzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 009196-0005-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556

INFORMATION FOR SEQ ID NO: 133:

SEQUENCE CHARACTERISTICS:

LENGTH: 22 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: None

US-10-099-574A-133

Query Match

Best Local Similarity 58.3%; Score 32; DB 5; Length 22;

Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 15 EHLVDFLOSLS 26

Db 7 ERLEDDLQALN 18

RESULT 9

US-10-147-849-133

Sequence 133, Application US/10147849

GENERAL INFORMATION:

APPLICANT: Dasseux, Jean-Louis

```

; APPLICANT: Sekul, Renate
; APPLICANT: Butner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; NUMBER OF SEQUENCES: 254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/147,849
; FILING DATE: 29-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ. ID NO: 133:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: None
; US-10-147-849-133

Query Match      23.9%; Score 32; DB 6; Length 22;
Best Local Similarity 58.3%; Pred. No. 2.1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 15 EHLVDLFLOSLS 26
   ||| |||
DB 7 ERLLEDLLQALN 18

RESULT 10
; US-10-147-993-133
; Sequence 133, Application US/10147993
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Butner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; NUMBER OF SEQUENCES: 254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/147,993
; FILING DATE: 29-SEP-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ. ID NO: 133:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: None
; US-10-147-993-133

Query Match      23.9%; Score 32; DB 6; Length 22;
Best Local Similarity 58.3%; Pred. No. 2.1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 15 EHLVDLFLOSLS 26
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DB 7 ERLLEDLLQALN 18

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RESULT 11
; US-10-014-340-19
; Sequence 19, Application US/10014340
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Includ
; FILE REFERENCE: 9195-078
; CURRENT APPLICATION NUMBER: US/10/014,340
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ. ID NOS: 823
; SOFTWARE: PatentIn version 3.0
; SEQ. ID NO: 19
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-014-340-19

Query Match      22.4%; Score 30; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PPEHL 17
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DB 2 PPEHL 6

RESULT 12
; US-09-050-359B-136
; Sequence 136, Application US/09050359B
; GENERAL INFORMATION:
; APPLICANT: FOWLES, Dana M
; KAY, Brian K
; FREILINGER, Jeffrey A

```

HYDE-DEBUSCHER, Robin P
TITLE OF INVENTION: IDENTIFICATION OF DRUGS USING
COMPLEMENTARY COMBINATORIAL LIBRARIES
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEWMARK, P.L.L.C.
STREET: 624 Ninth Street N.W., Suite 300
City: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.3C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,359B
FILING DATE: 31-Mar-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/19638
FILING DATE: 31-OCT-1997
APPLICATION NUMBER: US 08/740,671
FILING DATE: 31-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, Iver P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: FOWLKES-4B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: peptide
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 136:
US-09-050-359B-136
Query Match 22.4%; Score 30; DB 5; Length 16;
Best Local Similarity 70.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 14 PEHLVDFLQ 23
Db 5 PESLVRLLQ 14
RESULT 13
US-09-069-827A-136
Sequence 136, Application US/09069827A
GENERAL INFORMATION:
APPLICANT: FOWLKES, Dana M
KAY, Brian K
FRELINGER, Jeffrey A
HYDE-DEBUSCHER, Robin P
TITLE OF INVENTION: IDENTIFICATION OF DRUGS USING
COMPLEMENTARY COMBINATORIAL LIBRARIES
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEWMARK, P.L.L.C.
STREET: 624 Ninth Street N.W., Suite 300
City: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,827A
FILING DATE: 30-Apr-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/050,359
FILING DATE: 31-Mar-1998
APPLICATION NUMBER: PCT/US97/19638
FILING DATE: 31-OCT-1997
APPLICATION NUMBER: US 08/740,671
FILING DATE: 31-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, Iver P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: FOWLKES-4C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 136:
US-09-069-827A-136
Query Match 22.4%; Score 30; DB 5; Length 16;
Best Local Similarity 70.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 14 PEHLVDFLQ 23
Db 5 PESLVRLLQ 14
RESULT 14
US-10-000-256A-210
Sequence 210, Application US/10000256A
GENERAL INFORMATION:
APPLICANT: Sun, Tongming
APPLICANT: Recipon, Hevve
APPLICANT: Chen, Sei-Yu
TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes a
FILE REFERENCE: DEX-0259
CURRENT APPLICATION NUMBER: US/10/000,256A
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 60/244,782
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin version 3.1
SEQ ID NO 210
LENGTH: 18
TYPE: PRT
ORGANISM: Homo sapien
US-10-000-256A-210
Query Match 22.4%; Score 30; DB 6; Length 18;
Best Local Similarity 43.8%; Pred. No. 3.3e+02;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
Oy 3 GFLLQDGFPPHL 18
Db 2 GYLGLMAAGFKERV 17
RESULT 15

US-09-721-506-290
Sequence 290, Application US/09721506
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,506
FILING DATE: 22-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 290:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..22
OTHER INFORMATION: /note="motif C peptide from human
telomerase core protein 1 (hCPI)"
SEQUENCE DESCRIPTION: SEQ ID NO: 290:
US-09-721-506-290

Best Local Similarity 40.9%; Pred. No. 4.8e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 9; Gaps 1;
QY 1 RDGELLQMDFGPEPHLLVDPL 22
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Db 2 RDGELLRLVD-----DFL 14

Search completed: June 18, 2002, 08:15:57
Job time: 180 sec

Query Match 22.0%; Score 29.5; DB 5; Length 22;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:07:31 ; Search time 12.84 Seconds

(without alignments)
49.460 Million cell updates/sec

Title: US-09-943-334-1

Perfect score: 134
Sequence: 1 RDGFLLLQMDFGFPHLLVDFLQSLUS 26Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 136340

Minimum DB seq length: 0
Maximum DB seq length: 26

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/1aa/5b.COMB.pep:*
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4: /cgn2_6/ptodata/2/1aa/6b.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	32	23.9	22	3 US-08-940-095-133	Sequence 133, App
2	32	23.9	22	3 US-08-940-093-133	Sequence 133, App
3	32	23.9	22	3 US-08-940-096-133	Sequence 133, App
4	32	23.9	22	4 US-09-453-605-133	Sequence 133, App
5	32	23.9	22	4 US-09-453-605-133	Sequence 133, App
6	32	23.9	22	5 PCT-US91-02942-98	Sequence 8, Appl
7	31	23.1	20	1 US-08-183-217-8	Sequence 2, Appl
8	30	22.4	20	1 US-08-199-508-2	Sequence 170, App
9	29.5	22.0	22	4 US-08-851-843A-170	Sequence 290, App
10	29.5	22.0	22	4 US-08-974-349A-290	Sequence 170, App
11	29.5	22.0	22	4 US-08-854-050-170	Sequence 15, Appl
12	29.5	22.0	22	4 US-09-430-323-170	Sequence 15, Appl
13	29	21.6	11	1 US-09-128-572-15	Sequence 85, Appl
14	29	21.6	11	1 US-08-399-696-85	Sequence 22, Appl
15	29	21.6	20	2 US-08-484-530-32	Sequence 3, Appl
16	29	21.6	20	2 US-08-468-540B-3	Sequence 22, Appl
17	29	21.6	20	2 US-08-827-618A-22	Sequence 337, Appl
18	29	21.6	20	4 US-08-483-952A-22	Sequence 337, Appl
19	29	21.6	24	4 US-08-905-223-337	Sequence 3, Appl
20	29	21.6	25	2 US-08-424-881-3	Sequence 3, Appl
21	29	21.6	25	4 US-08-874-763-3	Sequence 3, Appl
22	29	21.6	25	4 US-09-370-867-3	Sequence 401, App
23	28	20.9	10	3 US-08-159-339A-401	Sequence 88, Appl
24	28	20.9	10	5 PCT-US91-02942-88	Sequence 134, App
25	28	20.9	22	3 US-08-940-095-134	Sequence 134, App
26	28	20.9	22	3 US-08-940-093-134	Sequence 134, App
27	28	20.9	22	3 US-08-940-096-134	Sequence 134, App

28	28	20.9	22	4 US-09-465-719-134	Sequence 134, App
29	28	20.9	22	4 US-09-453-605-134	Sequence 134, App
30	28	20.9	26	2 US-08-482-142-22	Sequence 37, Appl
31	28	20.9	26	2 US-08-482-142-37	Sequence 160, App
32	28	20.9	26	2 US-08-482-142-134	Sequence 22, Appl
33	28	20.9	26	2 US-08-482-142-168	Sequence 37, Appl
34	28	20.9	26	2 US-08-478-572-22	Sequence 168, App
35	28	20.9	26	2 US-08-478-572-37	Sequence 134, App
36	28	20.9	26	2 US-08-478-572-134	Sequence 168, App
37	28	20.9	26	2 US-08-478-572-168	Sequence 37, Appl
38	28	20.9	26	4 US-08-484-296-22	Sequence 134, App
39	28	20.9	26	4 US-08-484-296-37	Sequence 168, App
40	28	20.9	26	4 US-08-484-296-134	Sequence 134, App
41	28	20.9	26	4 US-08-484-296-168	Sequence 30, Appl
42	28	20.9	26	5 PCT-US95-04481-13	Sequence 83, Appl
43	28	20.9	26	5 PCT-US95-04481-30	Sequence 83, Appl
44	27	20.1	9	2 US-08-765-783A-83	Sequence 83, Appl
45	27	20.1	9	4 US-09-416-557-83	Sequence 83, Appl

ALIGNMENTS

RESULT 1
US-08-940-095-133
; Sequence 133, Application US/08940095
; Patent No. 6004925
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSRO Version 2.0
; CURRENT APPLICATION NUMBER: US/08/940, 095
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzel, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 133:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6004925e
; US-08-940-095-133

COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/465,719
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,093
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6265377e
US-09-465-719-133

Query Match 23.9%; Score 32; DB 4; Length 22;
Best Local Similarity 58.3%; Pred. No. 66;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 15 EHLVDLQSL 26
| | | | | | | |
Db 7 ERLLEDLQALN 18

RESULT 5
US-09-453-605-133
; Sequence 133, Application US/09453605
; Patent No. 6329341
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Butner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,605
; FILING DATE: 26-NO. 6329341-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6329341e
SEQUENCE DESCRIPTION: SEQ ID NO: 133:
US-09-453-605-133

Query Match 23.9%; Score 32; DB 4; Length 22;
Best Local Similarity 58.3%; Pred. No. 66;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 15 EHLVDLQSL 26
| | | | | | | |
Db 7 ERLLEDLQALN 18

RESULT 6
PCT-US91-02942-98
; Sequence 98, Application PC/TUS9102942
; GENERAL INFORMATION:
; APPLICANT: ROTHLEIN, ROBERT
; APPLICANT: ADAIR, JOHN R
; APPLICANT: ATHAL, DILBERT S
; TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Ave. NW Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02942
; FILING DATE: 19910429
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9009549.8
; FILING DATE: 27-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: FOX, SAM L
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 1011.0586600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 466-0800
; TELEFAX: (202) 833-8716
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US91-02942-98

Query Match 23.9%; Score 32; DB 5; Length 26;
Best Local Similarity 54.5%; Pred. No. 80;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RGFELIOMDF 11
DB 16 RGMWLLSFDY 26

RESULT 7

US-09-183-217-8
Sequence 8, Application US/09183217A
Patent No. 6153194
GENERAL INFORMATION:
APPLICANT: Skare, Jonathan T.
APPLICANT: Shang, Ellen S.
APPLICANT: Champion, Cheryl I.
APPLICANT: Blanco, David R.
APPLICANT: Miller, James N.
APPLICANT: Lovett, Michael A.
APPLICANT: Mizabekov, Tajib A.
APPLICANT: Kagan, Bruce L.
APPLICANT: Tempst, Paul
APPLICANT: Foley, Denise M.
TITLE OF INVENTION: BORRELIA BURGDOFFERI OUTER MEMBRANE PROTEINS
FILE REFERENCE: UC Case No. 6153194 96-059-3/Skare et al.
CURRENT APPLICATION NUMBER: US/09/183,217A
CURRENT FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 08/787,367
PRIOR FILING DATE: 1997-01-22
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 23
TYPE: PRY
ORGANISM: Borrelia burgdorferi
US-09-183-217-8

Query Match 23.1%; Score 31; DB 4; Length 23;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

OY 1 RGFELIOM-DFG 12
DB 4 KNYTLIOMGTDFG 17

RESULT 8

US-08-199-508-2
Sequence 2, Application US/08199508
Patent No. 5717058
GENERAL INFORMATION:
APPLICANT: Matthews, Maurea-Ann H.
APPLICANT: Stettler, Gary L.
APPLICANT: Anthony-Gahill, Spencer J.
APPLICANT: Anderson, David C.
TITLE OF INVENTION: Modulators of Gene Expression
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Somatogen, Inc.
STREET: 5797 Central Avenue
CITY: Boulder
STATE: Colorado
ZIP: 80301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.0.1
SOFTWARE: Microsoft Word 5.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,508

FILING DATE: February 18, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/021,536
FILING DATE: February 23, 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5717058ak, Henry P.
REGISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: 121 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-541-3322
TELEFAX: 303-444-3013
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: amino acid
TOPOLOGY: unknown to applicant
MOLECULE TYPE: peptide
HYPOTHETICAL: yes
US-08-199-508-2

Query Match 22.4%; Score 30; DB 1; Length 20;
Best Local Similarity 38.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 11 RGFPEHLVDFLO 23
DB 1 RGFYVVGDCVQ 13

RESULT 9

US-08-851-843A-170
Sequence 170, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:

US-09-128-572-15

Query Match 21.6%; Score 29; DB 4; Length 11;
 Best Local Similarity 62.5%; Pred. No. 88;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 15 EHLVDL 22
 ||:|:
 Db 3 EHLVDL 10

RESULT 14

US-08-399-696-85
 ; Sequence 85, Application US/08399696
 ; Patent No. 575669
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: p53-BINDING POLYPEPTIDES AND
 ; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME
 ; NUMBER OF SEQUENCES: 126
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/399,696
 ; FILING DATE: 02-MAR-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/156,671
 ; FILING DATE: 22-NOV-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William M
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 15522-000710
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 326-2400
 ; TELEFAX: (415) 326-2422
 ; INFORMATION FOR SEQ ID NO: 85:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 19 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 ; US-08-399-696-85

Query Match 21.6%; Score 29; DB 1; Length 19;
 Best Local Similarity 62.5%; Pred. No. 1.7e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 15 EHLVDL 22
 ||:|:
 Db 12 EHLVDL 19

RESULT 15
 US-08-484-530-22
 ; Sequence 22, Application US/08484530
 ; Patent No. 5846740
 ; GENERAL INFORMATION:
 ; APPLICANT: Tobin, Allan J
 ; APPLICANT: Erlander, Mark G
 ; APPLICANT: Kaufman, Daniel L
 ; TITLE OF INVENTION: Cloned Glutamic Acid Decarboxylase
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flenr, Hohnach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco

STATE: CA
 COUNTRY: US
 ZIP: 94111-4187
 COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/484,530
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Treacartin, Richard F.
 ; REGISTRATION NUMBER: 31,801
 ; REFERENCE/DOCKET NUMBER: A-60780-8/RFT/MTK
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-783-1989
 ; TELEFAX: 415-398-3249
 ; INFORMATION FOR SEQ ID NO: 22:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 20 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-484-530-22

Query Match 21.6%; Score 29; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 9 MDGFEHL 18
 :||:|
 Db 9 IDHFMELL 18

Search completed: June 18, 2002, 08:13:27
 Job time: 356 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:16:32 ; Search time 14.14 Seconds
(without alignments)
210.663 Million cell updates/sec

Title: US-09-943-334-2
162
Sequence: 1 CQYIKANSKFIGITFCGPEHLVDVFLQSLIS 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 6607

Minimum DB seq length: 0
Maximum DB seq length: 31

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR_71:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	19.1	23	2	S45030
2	31	19.1	24	2	S11384
3	31	19.1	28	2	D38578
4	30	18.5	20	2	S57286
5	29	17.9	30	2	A34622
6	29	17.9	31	2	A70219
7	28.5	17.6	21	2	A32521
8	28	17.3	21	2	JN0386
9	28	17.3	24	2	PN0163
10	27.5	17.0	27	2	C44308
11	27	16.7	24	2	A24417
12	26	16.0	19	2	T50329
13	26	16.0	22	2	PQ0143
14	26	16.0	26	2	C85947
15	26	16.0	27	2	A28391
16	26	16.0	27	2	S55802
17	26	16.0	27	2	S55801
18	26	16.0	27	2	S52355
19	26	16.0	28	2	S49924
20	26	16.0	30	2	S14062
21	25	15.4	15	2	S71306
22	25	15.4	16	2	T44936
23	25	15.4	22	2	B60475
24	25	15.4	23	2	PC4030
25	25	15.4	25	2	A60502
26	25	15.4	25	2	B24417
27	25	15.4	28	4	T68614
28	25	15.4	30	2	S24979
29	25	15.4	31	2	A32364

30	24.5	15.1	24	2	S69080	GDNF receptor alph
31	24.5	15.1	28	2	S64701	hypothetical prote
32	24.5	15.1	29	2	AB0717	hypothetical prote
33	24.5	14.8	10	2	PT0230	Ig heavy chain CDR
34	24	14.8	14	2	A01250	angiotensin I prec
35	24	14.8	15	2	A60834	angiotensin I prec
36	24	14.8	20	2	A37984	ADP/ATP carrier pr
37	24	14.8	22	2	C46285	formaldehyde dehyd
38	24	14.8	23	2	S51188	aldehyde dehydroge
39	24	14.8	24	2	S10618	superoxide dismuta
40	24	14.8	26	2	JN0665	cytochrome-c oxida
41	24	14.8	26	2	B54257	deoxyriboseide ki
42	24	14.8	30	2	A48299	taurine transpor
43	24	14.8	30	2	E71264	hypothetical prote
44	23.5	14.5	25	2	PH1717	Ig heavy chain V r
45	23	14.2	7	2	S36652	dermorphin (Lys-7)

ALIGNMENTS

RESULT 1
S45030
homeotic protein SPOX H1 - Haliclon sp. (fragment)
C:Species: Haliclon sp.
C:Date: 06-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 15-Oct-1999
C:Accession: S45030
R:Degnan, B.M.; Degnan, S.M.; Gustl, A.; Morse, D.E.
submitted to the EMBL Data Library, May 1994
A:Description: A Hox homeobox gene in sponges.
A:Reference number: S45030
A:Accession: S45030
A:Molecule type: DNA
A:Residues: 1-23 <DEG>
A:Cross-references: EMBL:X79263; NID:q488754; PIDN:CA55850.1; PID:q488755
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 19.1% Score 31; DB 2; Length 23;
Best Local Similarity 35.3% Pred. No. 4.3e+02;
Matches 6; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 7 NSKFIGITFCGPEHL 23
Db 1 SKKYLSTERSHALL 17

RESULT 2

S11384
thymidine phosphorylase (EC 2.4.2.4) - Lactobacillus casei (fragment)
N:Alternate names: pyrimidine phosphorylase
C:Species: Lactobacillus casei
C:Date: 19-Mar-1997 #sequence_revision 26-Feb-1998 #text_change 21-Nov-1998
C:Accession: S11384
R:Avraham, Y.; Grossowicz, N.; Yashpe, J.
Biochim. Biophys. Acta 1040, 287-293, 1990
A:Title: Purification and characterization of uridine and thymidine phosphorylase
A:Reference number: S11383; MUID:90381286
A:Accession: S11384
A:Molecule type: protein
A:Residues: 1-24 <AVR>
A:Experimental source: strain ATCC 7469
A>Note: this protein was shown to possess thymidine phosphorylase activity and not gl
C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C:Keywords: glycosyltransferase; homodimer; pentosyltransferase

Query Match 19.1% Score 31; DB 2; Length 24;
Best Local Similarity 85.7% Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 IGITFCG 17

C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 07-May-1999
 C:Accession: J00386
 R:Yamamoto, K.; Komatsu, K.
 Agric. Biol. Chem. 55: 1459-1466, 1991
 A:Title: Purification and characterization of nitrilase responsible for the enantioselective
 A:Reference number: J00386; MUID:91345837
 A:Accession: J00386
 A:Molecule type: protein
 A:Residues: 1-21 <YAM>
 A:Experimental source: strain AK226
 C:Comment: The enzyme prefers S-(-)-2-(4'-isobutylphenyl)-propanonitrile to R-(+)-2-(4'-
 C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 17.3%; Score 28; DB 2; Length 21;
 Best Local Similarity 45.5%; Pred. No. 1.1e+03;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 4 IKANSKFIGIT 14
 : ||||: |
 Db 1 VSYNSKFLNAT 11

RESULT 9
 PN0163
 glyceralddehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - fungus (Fusarium sporotrichoides)
 C:Species: Fusarium sporotrichoides
 C:Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 22-Apr-1995
 C:Accession: PN0163
 R:Fukaya, N.; Chow, L.P.; Sugitara, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.
 A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
 A:Reference number: PN0160
 A:Accession: PN0163
 A:Molecule type: protein
 A:Residues: 1-24 <FUK>
 C:Superfamily: glyceralddehyde-3-phosphate dehydrogenase
 C:Keywords: oxidoreductase

Query Match 17.3%; Score 28; DB 2; Length 24;
 Best Local Similarity 55.6%; Pred. No. 1.3e+03;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 9 KFIGITFERG 17
 : ||: |
 Db 3 KIVGNGFG 11

RESULT 10
 C44908
 chitinase (EC 3.2.1.14), 47K - Streptomyces olivaceoviridis (fragment)
 C:Species: Streptomyces olivaceoviridis
 C:Date: 01-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
 C:Accession: C44908
 R:Romaguera, A.; Menge, U.; Breves, R.; Diekmann, H.
 J. Bacteriol. 174, 3450-3454, 1992
 A:Title: Chitinases of Streptomyces olivaceoviridis and significance of processing for m
 A:Reference number: M44908; MUID:92276319
 A:Accession: C44908
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-27 <ROM>
 A:Experimental source: ATCC 11238
 A:Note: sequence extracted from NCBI backbone (NCBI:P104591)
 C:Superfamily: Streptomyces chitinase ch140
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 17.0%; Score 27.5; DB 2; Length 27;
 Best Local Similarity 53.8%; Pred. No. 1.7e+03;
 Matches 7; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

OY 6 ANSKFIG-ITERG 17
 : ||: |
 Db 1 ASKVGIVGTFEMG 13

RESULT 11
 A24417
 interphotoreceptor retinoid-binding protein - sheep (fragment)
 N:Alternate names: Interstitial retinol-binding protein
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 21-Nov-1997
 C:Accession: A24417
 R:Feong, S.L.; Cook, R.G.; Alvarez, R.A.; Liou, G.I.; Landers, R.A.; Bridges, C.D.B.
 FEBS Lett. 205, 309-312, 1986
 A:Title: N-terminal sequence homologies in interstitial retinol-binding proteins from
 A:Reference number: A91365; MUID:86301171
 A:Accession: A24417
 A:Molecule type: protein
 A:Residues: 1-24 <FON>
 C:Superfamily: Interphotoreceptor retinoid-binding protein
 C:Keywords: duplication

Query Match 16.7%; Score 27; DB 2; Length 24;
 Best Local Similarity 36.4%; Pred. No. 1.8e+03;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 13 ITERGFEHLL 23
 : ||||: |
 Db 14 LDNYTFEPLML 24

RESULT 12
 T50329
 wd-repeat protein popl. [imported] - fission yeast (Schizosaccharomyces pombe) (fragm
 C:Species: Schizosaccharomyces pombe
 C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
 C:Accession: T50329
 R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Harris, D.
 A:Description: submitted to the EMBL Data Library, February 2000
 A:Reference number: Z25062
 A:Accession: T50329
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-19 <LYN>
 A:Cross-references: EMBL:AL157874; PIDN:CA875991.1; GSPDB:GN00067; SPDB:SPBC1718.01
 A:Experimental source: strain 972h(-); cosmid c1718
 C:Genetics:
 A:Gene: SPBC262.18; SPDB:SPBC1718.01
 A:Map position: 2

Query Match 16.0%; Score 26; DB 2; Length 19;
 Best Local Similarity 35.7%; Pred. No. 2e+03;
 Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 4 IKANSKFIGITERG 17
 : ||: |
 Db 1 LRRNRPWIEVLERG 14

RESULT 13
 P00143
 polygalacturonase (EC 3.2.1.15) P26 - evening primrose (fragment)
 C:Species: Oenothera organeensis (evening primrose)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 06-Dec-1996
 C:Accession: P00143
 R:Brown, S.M.; Crouch, M.L.
 Plant Cell 2, 263-274, 1990
 A:Title: Characterization of a gene family abundantly expressed in Oenothera organs
 A:Reference number: J00992; MUID:93005658
 A:Accession: P00143
 A:Molecule type: mRNA

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:18:17 ; Search time 10.13 Seconds
(without alignments)
118.257 Million cell updates/sec

Title: US-09-943-334-2

Perfect score: 162
Sequence: 1 CQYIKANSKFTIGTEFGPEHLVDLFQSL 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 1969

Minimum DB seq length: 0
Maximum DB seq length: 31

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Swissprot_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32.5	20.1	30	1	OTCX_STAEP
2	31	19.1	23	1	TYPH_LACCA
3	31	19.1	29	1	PK4_DICDI
4	30	18.5	22	1	PSP2_PHYRA
5	29	17.9	30	1	FIBR_PANIN
6	28	17.3	21	1	NR1A_ACISP
7	27.5	17.0	27	1	CH12_STROI
8	27	16.7	24	1	IRBP_SHEEP
9	26	16.0	19	1	NS2_MYCTU
10	26	16.0	28	1	GIN_SCHCO
11	25	15.4	22	1	CR33_LITCE
12	25	15.4	22	1	CR34_LITCE
13	25	15.4	25	1	IRBP_PIG
14	25	15.4	30	1	KAB5_OLDAF
15	24.5	15.1	25	1	AMP3_MELGA
16	24	14.8	11	1	TKC2_CALVO
17	24	14.8	13	1	TEML_RANTE
18	24	14.8	14	1	ANGT_HORSE
19	24	14.8	20	1	TL22_SPIOL
20	24	14.8	24	1	SODC_RANCA
21	24	14.8	26	1	DMS5_PHYBI
22	24	14.8	30	1	CLPA_PINPS
23	24	14.8	30	1	PEFN_NEPOL
24	24	14.8	30	1	Y932_TREPA
25	24	14.8	31	1	PEFL_OENHO
26	23.5	14.5	31	1	PEFL_NEPOL
27	23	14.2	17	1	TRP2_LEUMA
28	23	14.2	18	1	NU21_LITGE
29	23	14.2	18	1	RU24_SERMA
30	23	14.2	19	1	TRP3_LEUMA
31	23	14.2	23	1	COXJ_ONCAT
32	23	14.2	24	1	CCAA-STRTI
33	23	14.2	24	1	COXJ_SHEEP

34	23	14.2	25	1	GBX1_MOUSE	P82976	mus musculus
35	23	14.2	29	1	COXK_SHEEP	O9128	ovis aries
36	23	14.2	30	1	CYH1_VIOHE	P58433	vicia heder
37	22.5	13.9	30	1	Y523_BORBU	O51473	borrelia bu
38	22	13.6	13	1	FARB_ASCSU	P43173	ascaris suu
39	22	13.6	20	1	AMP_FUSNU	P81207	fusobacteri
40	22	13.6	20	1	CAOS_RAT	P19633	rattus norv
41	22	13.6	20	1	DNK_CLOPA	P81341	clostridium
42	22	13.6	21	1	DCMS_PSECA	P19921	pseudomonas
43	22	13.6	24	1	KPYK_CLOPA	P81344	clostridium
44	22	13.6	25	1	AU51_LITRA	P82401	litorea ran
45	22	13.6	25	1	G3P2_JACOR	P80447	jaecius ori

ALIGNMENTS

RESULT	ID	OTCX_STAEP	STANDARD:	PRT:	30 AA.
AC	P81682;				
DT	15-JUL-1999 (Rel. 38, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Probable ornithine carbamoyltransferase (EC 2.1.3.3) (OTCase)				
DE	(Fragment).				
OS	Staphylococcus epidermidis.				
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;				
OC	Bacillus/Staphylococcus group; Staphylococcus.				
OX	NCBI_TaxID=1282;				
RN	[1]				
RP	SEQUENCE.				
RC	STRAIN=AB9.				
RA	Hussein M.S., Herrmann M., Chatawal G.S., Peters G.,				
RT	* 42 kDa protein with broad affinity to bind several plasma and				
RT	ECM-proteins in lithium chloride extract of Staphylococcus				
RT	epidermidis is ornithine carbamoyltransferase.*;				
RL	Submitted (FEB-1999) to the SWISS-PROT data bank.				
CC	- FUNCTION: HAS VITROECRIN AND FIBROECRIN-BINDING ACTIVITY.				
CC	- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine = phosphate				
CC	+ L-citrulline.				
CC	- SUBCELLULAR LOCATION: Cytoplasmic.				
CC	- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.				
DR	InterPro: IPR002029; Carbamyltransf.asor.				
KR	PROSITE: PS00097; CARBAMOYLTRANSFERASE; PARTIAL.				
FT	TRANSFERASE. 30				
FT	NON-TER				
FT	SEQUENCE 30 AA: 3629 MW: A7BEE64FCA87A7D CRC64:				
Query Match	20.1%;	Score 32.5;	DB 1;	Length 30;	
Best Local Similarity	36.0%;	Pred. No. 1.4e+02;			
Matches	9;	Conservative 36;	5;	Mismatches 8;	Indels 3;
					Gaps 1;
OY	7 NSKFIGTEFGPEHLVDLFQSL 31				
	: : : : : : : :				
DB	6 NRSFLLDFSRQ---VEFLTLIS 27				
	: : : : : : : :				
RESULT 2	TYPH_LACCA	STANDARD:	PRT:	23 AA.	
AC	P19663;				
DT	01-FEB-1991 (Rel. 17, Created)				
DT	01-FEB-1991 (Rel. 17, Last sequence update)				
DT	30-MAY-2000 (Rel. 39, Last annotation update)				
DE	Thymidine phosphorylase (EC 2.4.2.4) (TDPhase) (Fragment).				
GN	DEOA.				
OC	Lactobacillus casei.				
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;				
OC	Lactobacillus.				
OX	NCBI_TaxID=1582;				
RN	[1]				

RP SEQUENCE.
 RC STRAIN-ATCC 7469;
 RA MEDLINE-90381286; PubMed-2119230;
 RX Avraham Y., Grossowicz N., Yashpe J.;
 RT "Purification and characterization of uridine and thymidine
 phosphorylase from *Lactobacillus casei*."
 RL Blochm. Biophys. Acta 1040:287-293(1990).
 CC -1- FUNCTION: THE ENZYMES WHICH CATALYZE THE REVERSIBLE PHOSPHORYLOSIS
 OF PYRIMIDINE NUCLEOSIDES ARE INVOLVED IN THE DEGRADATION OF THESE
 COMPOUNDS AND IN THEIR UTILIZATION AS CARBON AND ENERGY SOURCES,
 OR IN THE RESCUE OF PYRIMIDINE BASES FOR NUCLEOTIDE SYNTHESIS.
 CC -1- CATALYTIC ACTIVITY: thymidine + phosphate = thymine + 2-deoxy-D-
 ribose 1-phosphate.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: BELONGS TO THE THYMIDINE/PYRIMIDINE-NUCLEOSIDE
 PHOSPHORYLASES FAMILY.
 CC PIR: S11384; S11384.
 DR HSSP: P00357; 1GPD.
 DR InterPro: IPR000173; GAP_DH.
 DR InterPro: IPR000053; Thymid_phosphls.
 DR Pfam: PF00044; gpdb.1
 DR PROSITE: PS00647; THYMID_PHOSPHORYLASE; PARTIAL.
 DR TRANSFERASE; Glycosyltransferase.
 DR NON_TER 23
 SQ SEQUENCE 23 AA; 2752 MW; 8705C9C4D82C1AD7 CRC64;

Query Match 19.1%; Score 31; DB 1; Length 23;
 Best Local Similarity 85.7%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 11 IGITFEG 17
 |||||
 Db 4 IGITFEG 10

RESULT 3
 ID PK4_DICDI STANDARD; PRT; 29 AA.
 AC P34103;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein kinase 4 (EC 2.7.1.-) (Fragment).
 GN PKGD.
 OS Dictyostelium discoideum (Slime mold).
 CC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 CC NCBI_Taxid=4689;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE-91142122; PubMed-1996312;
 RA Haribabu B., Dotlin R.P.;
 RT "Identification of a protein kinase multigene family of Dictyostelium
 discoideum: molecular cloning and expression of a cDNA encoding a
 developmentally regulated protein kinase."
 RL Proc. Natl. Acad. Sci. U.S.A. 88:1115-1119(1991).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation
 at the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@sib-sib.ch).
 CC EMBL: M59747; AAA33189.1;
 DR PIR: D38578; D38578.
 DR DictyDb: DD05049; PKGD.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; PARTIAL.

DR PROSITE: PS00108; PROTEIN_KINASE_ST; PARTIAL.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 FT NON_TER 1 1
 FT DOMAIN <1 >28 PROTEIN KINASE.
 FT MOD_RES 27 27 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 3358 MW; B12D4F42C4C110DA CRC64;

Query Match 19.1%; Score 31; DB 1; Length 29;
 Best Local Similarity 41.7%; Pred. No. 2.3e+02;
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 11 IGITFEGPEHL 22
 |:-|||:-|
 Db 10 IKLIDFPAKRI 21

RESULT 4
 ID PSP2_PHYPA STANDARD; PRT; 22 AA.
 AC P80661;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Oxygen-evolving enhancer protein 2 (OE2) (22 kDa subunit of oxygen
 evolving system of photosystem II) (Fragments).
 OS Physcomitrella patens (Moss).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 CC Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
 CC NCBI_Taxid=3218;
 RN (1)
 RP SEQUENCE.
 RC TISSUE=Protonema;
 RX MEDLINE-97275459; PubMed-9129336;
 RA Kasten B., Buck F., Nuske J., Reski R.;
 RT "Cytoxinin affects nuclear- and plastome-encoded energy-converting
 plastid enzymes."
 RL Planta 201:261-272(1997).
 CC -1- FUNCTION: MAY BE INVOLVED IN THE REGULATION OF PHOTOSYSTEM II.
 CC -1- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated
 with the photosystem II complex.
 CC -1- INDUCTION: BY LIGHT.
 CC -1- SIMILARITY: BELONGS TO THE PSPB FAMILY.
 CC Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane;
 KW Multigene family.
 KM NON_CONS 15 16
 FT NON_TER 22 22
 SQ SEQUENCE 22 AA; 2316 MW; E1553CC575C54BBI CRC64;

Query Match 18.5%; Score 30; DB 1; Length 22;
 Best Local Similarity 50.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 6 ANSKFTITFEG 17
 |:-|||:-|
 Db 10 AGNGFTXITEYG 21

RESULT 5
 ID F1BR_PANIN STANDARD; PRT; 30 AA.
 AC P22775;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE F1brinogen (Fragment).
 OS Panulirus interruptus (California spiny lobster).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Palinura;

OC	Palinuroidea: Palinuridae; Panulirus.
OX	NCBI_TaxID=6735;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=90179743; PubMed=2310387;
RA	Deoolittle R.F., Riley M.;
RT	"The amino-terminal sequence of lobster fibrinogen reveals common ancestry with vitellogenins.";
RL	Biochem. Biophys. Res. Commun. 167:16-19(1990).
CC	-1- FUNCTION: CLOTTING PROTEIN.
CC	-1- SUBUNIT: HOMODIMER.
CC	-1- SUBCELLULAR LOCATION: Extracellular.
CC	-1- TISSUE SPECIFICITY: SECRETED INTO THE HEMOLYMPH.
CC	-1- SIMILARITY: NO VITELLOGENINS.
DR	PIR: A34622; A34622
KY	Glycoprotein; Lipid-binding; Hemolymph clotting.
FT	NON_TER 30 30
EQ	SEQUENCE 30 AA: 3572 MW: A48C8AAFB1BE0794C CRC64;

```
Query Match      17.9%;   Score 29; DB 1; Length 30;
Best Local Similarity 38.5%;   Pred. No. 4.7e+02;
Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
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RESULT	6			
NRLA	ACISP			
ID	NRLA_ACISP	STANDARD:	PRT:	21 AA.
AC	P33036;			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	01-OCT-1993 (Rel. 27, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	Nitrilase (EC 3.5.5.1) (Fragment).			
OS	Acinetobacter sp. (strain AK226).			
OC	Bacterio: Proteobacteria; gamma subdivision; Moraxellaceae;			
OC	Acinetobacter.			
OX	NCBI_TaxID=472;			
RN	[1]			
RE	SEQUENCE.			
RX	MEDLINE=91345837; PubMed=1369128;			
RA	Yamamoto K., Komatsu K.;			
RT	"Purification and characterization of nitrilase responsible for the			
RT	enantioselective hydrolysis from Acinetobacter sp. AK 226."			
RL	Agric. Biol. Chem. 55:1459-1466(1991)			
CC	-1- FUNCTION: ACTS ON MANY KINDS OF NITRILE COMPOUNDS SUCH AS			
CC	ALIPHATIC, AROMATIC, AND HETEROCYCLIC MONONITRILES OR DINITRILES.			
CC	PREFERS S-(+)-2-(4'-ISOBUTYRPHENYL)-PROPNITRILE TO R-(+)-2-(4'-			
CC	ISOBUTYRPHENYL)-PROPNITRILE AS THE SUBSTRATE.			
CC	-1- CATALYTIC ACTIVITY: A nitrile + H(2)O = a carboxylate + NH(3).			
CC	-1- SIMILARITY: BELONGS TO THE NITRILASE FAMILY.			
DR	PIR: J00386; J00386.			
DR	Interpro: IPR000132: Nitril_Cyn_hydrolase.			
DR	PROSITE: PS00920: NITRIL_CHT_1; PARTIAL.			
DR	PROSITE: PS00921; NITRIL_CHT_2; PARTIAL.			
KM	Hydrolase.			
FT	NON_TER	21	21	
SEQUENCE	21 AA; 2223 MW; 5FA7A1C41EAC619B CRC64;			

```

Query Match      17.3%; Score 28; DB 1; Length 2;
Best Local Similarity 45.5%;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
OY      4 IKANSKRFIGIT 14
        :      ||||: 1
Db      1 VSYNSKRFLEAAT 11
Result  7

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ID	CHIT1_STROI	STANDARD:	PRT:	27 AA.
AC	P29116;			
DT	01-DEC-1992 (Rel. 24, Created)			
DT	01-DEC-1992 (Rel. 24, Last sequence update)			
DT	01-DEC-1992 (Rel. 24, Last annotation update)			
DE	Chitinase 47 kDa (EC 3.2.1.14) (Fragment).			
OS	Streptomyces olivaceoviridis (Streptomyces corchorus11).			
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteriales;			
OC	Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.			
OX	NCBI_Taxid=1921;			
RN	[1]			
RP	SEQUENCE.			
RC	STRAIN=ATCC 11238;			
RX	MEDLINE=92276319; PubMed=1592803;			
RA	Romaguera A., Menge U., Breves R., Diekmann H.;			
RT	"Chitinases of Streptomyces olivaceoviridis and significance of			
RT	processing for multiplicity."			
RL	J. Bacteriol. 174:3450-3454(1992).			
CC	-1- FUNCTION: ABLE TO CLEAVE CHITIN OLIGOMERS FROM N-3 TO 6.			
CC	-1- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-			
CC	acetyl-D-glucosamine polymers of chitin.			
CC	-1- SUBUNIT: HOMODIMER.			
CC	-1- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL			
CC	HYDROLASES).			
DR	PIR: C44908; C44908.			
DR	InterPro: IPR001579; Chitinase_2.			
DR	InterPro: IPR001223; Glyco_hydro_18.			
DR	Pfam: PF00704; Glyco_hydro_18; 1.			
DR	PROSITE: PS01093; CHITINASE_18; PARTIAL.			
KW	Hydrolase; Glycosidase; Chitin degradation.			
FT	NON_TER 27			
SEQUENCE	27 AA: 3172 MW; E9549DSE273DFEE9 CRC64;			

```

Query Match      17.0%  Score 27.5; DB 1.7; Length 27;
      Local Similarity 53.8%; Pred. No. 7.1e+07;
Matches 7; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

OY      6 ANSKFIC-ITFEG 17
      1 1 1 1 1 1
Db      1 AGSKVGYETWEG 13

RESULT SHEEP
IRBP_SHEEP 8
ID IRBP_SHEEP STANDARD: PRT: 24 AA.
P12663;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Interphotoreceptor retinoid-binding protein (IRBP) (Interstitial
  retinol-binding protein) (Fragment).
DE GN RBP3.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Kumlantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RX MEDLINE=86301171; PubMed=3743780;
RA Fong S.L., Cook R.G., Alvarez R.A., Llou G.I., Landers R.A.,
  Bridges C.D.B.;
  "N-terminal sequence homologies in interstitial retinol-binding
  proteins from 10 vertebrate species."
RL FEBS Lett. 205:309-312(1986).
RT -I- FUNCTION: IRBP SHOTLES 11-CIS AND ALL TRANS RETINOIDS BETWEEN
  THE RETINOL ISOMERASE IN THE PIGMENT EPITHELIUM AND THE VISUAL
  PIGMENTS IN THE PHOTORECEPTOR CELLS OF THE RETINA.
CC -I- SUBCELLULAR LOCATION: INTERPHOTORECEPTOR MATRIX THAT PERMEATES
  THE SPACE BETWEEN THE RETINA AND THE CONTIGUOUS LAYER OF PIGMENT
  EPITHELIUM CELLS.
CC

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PIR: A24417; A24417.
 DR Vitamin A; Transport.
 KW NON_TER 24
 SO SEQUENCE 24 AA; 2799 MW; 02DEBE61A8E4523 CRC64;

Query Match 16.7%; Score 27; DB 1; Length 24;
 Best Local Similarity 36.4%; Pred. No. 7.5e+02;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 13 ITERGFEHL 23
 : : 11111:
 DB 14 LDNTFENLM 24

RESULT 9
 NS2_MYCTU STANDARD; PRT; 19 AA.

AC P81136; 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 30 kDa non-secretory protein 2 (Fragment).
 OS Mycobacterium tuberculosis.
 CC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 CC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]

RP SEQUENCE.
 RC STRAIN=H37RV;
 RA Prasad H.K., Annapurna P.S.;
 RL Submitted (DEC-1997) to the SWISS-PROT data bank.
 CC -1 SIMILARITY: STRONG, TO THE N-TERMINALS OF C.ELEGANS F20A1.4
 CC AND H.INFLUENZAE HI0967.

-1 CAUTION: We are unable to find this protein in the translation of
 the genome of strain H37RV.

CC NON_TER 19
 FT SEQUENCE 19 AA; 2211 MW; A8C1854BF1F70 CRC64;

Query Match 16.0%; Score 26; DB 1; Length 19;
 Best Local Similarity 57.1%; Pred. No. 8.2e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 12 GITERGF 18
 : : 1111
 DB 10 GVAEPF 16

RESULT 10
 GUN_SCHCO STANDARD; PRT; 28 AA.

AC P81190; 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Endoglucanase (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase)
 DE (Fragment).
 OS Schizophyllum commune (Bracket fungus).
 CC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 CC Stereales; Schizophyllaceae; Schizophyllum.
 OX NCBI_TaxID=5334;
 RN [1]

RP SEQUENCE.
 RC MEDLINE=97459758; PubMed=9315718;
 RA Clarke A.J., Drummelsmith J., Yaguchi M.;

*Identification of the catalytic nucleophile in the cellulase from
 Schizophyllum commune and assignment of the enzyme to Family 5,
 subfamily 5 of the glycosidases.*

RT FEBS Lett. 414:359-361(1997).
 CC -1 CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 linkages in cellulose.
 CC -1 SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor

CC (Probable).
 CC -1 SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL
 CC HYDROLASES).
 DR InterPro: IPR001547; Glyco_hydro_F5.
 DR PROSITE: PS00659; GLYCOSYL_HYDROL_F5; PARTIAL.
 KW Cellulose degradation; Hydrolase; Glycosidase; Zymogen; Membrane;
 FT Lipo-protein.
 FT ACT_SITE 20
 FT NON_TER 28
 SO SEQUENCE 28 AA; 2937 MW; B3F1C0C99C9950BE CRC64;

Query Match 16.0%; Score 26; DB 1; Length 28;
 Best Local Similarity 38.5%; Pred. No. 1.2e+03;
 Matches 5; Conservative 6; Mismatches 0; Indels 2; Gaps 1;

OY 2 OIKANSK--FIG 12
 : : 11111: 1:1
 DB 7 EWLKANNORFLG 19

RESULT 11
 CR33_LITCE STANDARD; PRT; 22 AA.

AC P56240; 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Caerin 3.3.
 OS Litoria caerulea (Green tree frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 CC Litoria.
 OX NCBI_TaxID=30344;

RP [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Parotoid gland;
 RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. The structures of the caerins from
 RT Litoria caerulea.";

RL J. Chem. Res. 138:910-936(1993).

CC -1 FUNCTION: ANTIBACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL
 CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN
 CC DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY

CC -1 TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
 CC GLANDS.

CC -1 MASS SPECTROMETRY: MW=2424; METHOD=FAE.

KW Antibiotic; Amphibian skin; Amidation.
 FT MOD_RES 22
 FT SEQUENCE 22 AA; 2427 MW; 1D440B2200DA367C CRC64;

Query Match 15.4%; Score 25; DB 1; Length 22;
 Best Local Similarity 54.5%; Pred. No. 1.4e+03;
 Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 5 KANSKFIGITE 15
 : : 111111
 DB 9 KANELVSGIVE 19

RESULT 12
 CR34_LITCE STANDARD; PRT; 22 AA.

AC P56241; 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Caerin 3.4.

OS Litoria caerulea (Green tree frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 CC Litoria.

OX NCBI_TaxID-30344;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE-pancreatic gland;
 RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. The structures of the caerins from
 RT *Litoria caerulea*."
 RL J. Chem. Res. 138:910-936(1993).
 CC -1- FUNCTION: ANTI-BACTERIAL PEPTIDE, THAT ADOPTS AN ALPHA HELICAL
 CC CONFORMATION WHICH CAN DISRUPT BACTERIAL MEMBRANES. EACH CAERIN
 CC DISPLAYS A DIFFERENT ANTIMICROBIAL SPECIFICITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PANCREATOID AND/OR ROSTRAL
 CC GLANDS.
 CC -1- MASS SPECTROMETRY: MW-2452; METHOD-FAB.
 CC Antibiotic; Amphibian skin; Amidation.
 FT MOD.RES 22 22
 SO SEQUENCE 22 AA: 2455 MW: 3AB40B2200D43663 CRC64;

Query Match 15.4%; Score 25; DB 1; Length 22;
 Best Local Similarity 54.5%; Pred. No. 1.4e+03;
 Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 5 KANSKFIGITE 15
 Db 9 KANELVSGIVE 19

RESULT 13
 IRBP_PIG STANDARD; PRT: 25 AA.
 ID IRBP_PIG
 AC P12662;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Interphotoreceptor retinoid-binding protein (IRBP) (Interstitial
 DE retinoid-binding protein) (fragment).
 GN RBP3.
 OS *Sus scrofa* (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus
 OX NCBI_TaxID-9823;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-86301171; PubMed-3743780;
 RA Fong S.L., Cook R.G., Alvarez R.A., Liou G.I., Landers E.A.,
 RA Bridges C.D.B.;
 RT "N-terminal sequence homologues in interstitial retinol-binding
 RT proteins from 10 vertebrate species.";
 RL FEBS Lett. 205:309-312(1986).
 CC -1- FUNCTION: IRBP SHUTTLES 11-CIS AND ALL TRANS RETINOIDS BETWEEN
 CC THE RETINOL ISOMERASE IN THE PIGMENT EPITHELIUM AND THE VISUAL
 CC PIGMENTS IN THE PHOTORECEPTOR CELLS OF THE RETINA.
 CC -1- SUBCELLULAR LOCATION: INTERPHOTORECEPTOR MATRIX THAT PERMEATES
 CC THE SPACE BETWEEN THE RETINA AND THE CONTIGUOUS LAYER OF PIGMENT
 CC EPITHELIUM CELLS.
 CC PIR: B24417; B24417.
 DR Vitamin A: Transport.
 KM VITAMIN A: Transport.
 FT NON-TER 25
 SO SEQUENCE 25 AA: 2813 MW: 4E751DFA160231B7 CRC64;

Query Match 15.4%; Score 25; DB 1; Length 25;
 Best Local Similarity 36.4%; Pred. No. 1.6e+03;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 13 ITFEGFPHLL 23
 Db 14 LDNYTFPESIM 24

RESULT 14
 KABS_OLDAR

ID KABS_OLDAR STANDARD; PRT: 30 AA.
 AC P58456;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Kalata B5.
 OS Oldenlandia affinis.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Gentianales; Rubiaceae; Rubioidae;
 OC Spectaceae; Oldenlandia.
 OX NCBI_TaxID-60225;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-20069951; PubMed-10600388;
 RA Craik D.J., Daly N.L., Bond T., Waite C.;
 RT "Plant cyclotides: a unique family of cyclic and knotted proteins that
 RT defines the cyclic cysteine knot structural motif."
 RL J. Mol. Biol. 294:1327-1336(1999).
 CC -1- FUNCTION: Probably participates in a plant defense mechanism.
 CC -1- PTM: This is a cyclic peptide.
 CC -1- CAUTION: This peptide is cyclic, its sequence was chosen to start
 CC at the position shown below by similarity to Oak1 (kalata B1)
 CC whose DNA sequence is known.
 CC Multigene family.
 FT DISULFID 4 20
 FT DISULFID 8 27
 FT DISULFID 13 27
 SO SEQUENCE 30 AA: 3044 MW: CDA3C52FC0EB7A3 CRC64;

Query Match 15.4%; Score 25; DB 1; Length 30;
 Best Local Similarity 50.0%; Pred. No. 1.9e+03;
 Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 COTIKANSKFIG 12
 Db 8 CVYIPICISGIVG 19

RESULT 15
 AMP3_MELGA STANDARD; PRT: 25 AA.
 ID AMP3_MELGA
 AC P80393;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Antimicrobial peptide TFP3 (Turkey heterophil peptide 3) (Fragment).
 OS *Meleagris gallopavo* (Common turkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagrids.
 OX NCBI_TaxID-9103;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-95053386; PubMed-7964174;
 RA Evans E.W., Beach G.G., Wunderlich J., Harmon B.G.;
 RT "Isolation of antimicrobial peptides from avian heterophils.";
 RL J. Leukoc. Biol. 56:661-665(1994).
 CC -1- FUNCTION: BACTERICIDAL ACTIVITY; INHIBITS STAPHYLOCOCCUS AUREUS.
 KM Antibiotic.
 FT NON-TER 25
 SO SEQUENCE 25 AA: 2592 MW: 4AAB9AC193874035 CRC64;

Query Match 15.1%; Score 24.5; DB 1; Length 25;
 Best Local Similarity 46.2%; Pred. No. 1.8e+03;
 Matches 6; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

OY 12 GTFEGFPHLL 23
 Db 6 GTCHFGCPSHLL 18

Wed Jun 19 10:20:12 2002

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Search completed: June 18, 2002, 08:21:34
Job time: 197 sec

Db 12 PTRHLYSEFOS 22

RESULT 2
09GJ4 PRELIMINARY; PRT; 28 AA.

AC 09GJ4;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MHC CLASS II B ANTIGEN (FRAGMENT).
GN GAC-D.
OS Gasterosteus aculeatus (three spined stickleback).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
OC Gasterosteidae; Gasterosteus.
OX NCBI_TaxID=69293;
RN [1]
RP SEQUENCE FROM N.A.
RA Bluz T.;
RT "SSCP analysis of MHC genes in the stickleback.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF249305; AAF98328.1; -.
FT NON_TER 1 1
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3131 MW; DF7A5AC51F1B6798 CRC64;

Query Match 21.0%; Score 34; DB 7; Length 28;
Best Local Similarity 62.5%; Pred. No. 4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 FIGITERG 17
Db 1 FVGFTERG 8

RESULT 3
P70861 PRELIMINARY; PRT; 21 AA.

AC P70861;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE THDF (FRAGMENT).
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=212;
RX MEDLINE=97312006; PubMed=9168617;
RA Ge Y., Old I.G., Glrons I.S., Charon N.W.;
RT "The flag motility operon of Borrelia burgdorferi is initiated by a
sigma 70-like promoter.";
RL Microbiology 143:1681-1690(1997).
DR EMBL: U62901; AAB62742.1; -.
FT NON_TER 21 21
SQ SEQUENCE 21 AA; 2432 MW; F33E1EC548BD5B33 CRC64;

Query Match 19.8%; Score 32; DB 2; Length 21;
Best Local Similarity 66.7%; Pred. No. 5.7e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 15 ERGFEHLL 23
Db 8 EFDFFGILL 16

RESULT 4
Q9R495

ID Q9R495 PRELIMINARY; PRT; 23 AA.
AC Q9R495;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE 40 KDA STREPTOCOCCAL GROUP A SURFACE GLYCERALDEHYDE-3-PHOSPHATE
DE DEHYDROGENASE HOMOLOG (FRAGMENT).
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE.
RX MEDLINE=96355859; PubMed=8751897;
RA Kolberg J., Sletten K.;
RT "Monoclonal antibodies that recognize a common pneumococcal protein
with similarities to streptococcal group A surface glyceraldehyde-3-
phosphate dehydrogenase.";
RL Infect. Immun. 64:3544-3547(1996).
CC -1- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + ORTHOPHOSPHATE
+ NAD(+) = 1,3-DIPHOSPHATEGLYCERATE + NADH.
CC -1- PATHWAY: FIRST STEP IN THE SECOND PHASE OF GLYCOLYSIS.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
DEHYDROGENASE FAMILY.
DR InterPro: IPR000173; GAP_DH.
DR Pfam: PF00044; gpdh. 1.
KM Glycolysis; NAD: Oxidoreductase.
SQ SEQUENCE 23 AA; 2391 MW; 5F023652B2A0ABD4 CRC64;

Query Match 19.8%; Score 32; DB 2; Length 23;
Best Local Similarity 35.0%; Pred. No. 6.3e+02;
Matches 7; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 11 IGITRGFEHLLVDFLOSL 30
Db 4 VGINFGXIGXLAFLDXIONV 23

RESULT 5
Q9ZG27 PRELIMINARY; PRT; 30 AA.

AC Q9ZG27;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE UDP-N-ACETYLMORAXATE ALANINE LIGASE (FRAGMENT).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=L2 434B;
RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;
RT "Gene identification of Chlamydia trachomatis by random DNA
sequencing.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF087346; AAD04119.1; -.
KM Ligase.
FT NON_TER 1 1
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3352 MW; D01C685DE67A1A55 CRC64;

Query Match 19.8%; Score 32; DB 2; Length 30;
Best Local Similarity 36.4%; Pred. No. 8.3e+02;
Matches 8; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 10 FIGITRGFEHLLVDFLOSL 31
Db 2 FLGNOEHITPGAVVYSSIS 23

RESULT	6			
Q9TRR6		PRELIMINARY;	PRT;	19 AA.
ID	Q9TRR6			
AC	Q9TRR6			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, last annotation update)			
DE	CALCYCLIN-ASSOCIATED PROTEIN, CAP50-CA2+/PHOSPHOLIPID-BINDING PROTEIN			
DE	1-14 FRAGMENT.			
OS	Oryctolagus cuniculus (Rabbit).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.			
OX	NCBI_TaxID=9986;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=92250478; PubMed=1533622;			
RA	Tokumitsu H., Mizutani A., Minami H., Kobayashi R., Hiatake H.;			
RT	"A calyculin-associated protein is a newly identified member of the			
RT	Ca2+/phospholipid-binding proteins, annexin family."			
U	J. Biol. Chem. 267:8919-8924(1992).			
SO	SEQUENCE			
	19 AA; 2018 MW; 9A54062504B8522E CRC64;			

Query Match	19.1%	Score 31	DB 6	Length 19
Best Local Similarity	43.8%	Pred. No. 7.2e+02		
Matches 7; Conservative		2; Mismatches 7;	Indels 0;	Gaps 0

```
QY      16 FGPEHLLVDFLQSL$ 31
      || | :: | | |
Db      2 FGTDEQAIDXLGSR$ 17
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SEQ	SEQUENCE	23 AA:	2681 MW:	FB394DEDC85BEB60	CRC64:
Q25161	RESULT 7				
AC	Q25161.	PRELIMINARY:	PRT:	23 AA.	
DT	01-NOV-1996	(TREMBLrel. 01.	Created)		
DT	01-NOV-1996	(TREMBLrel. 01.	Last sequence update)		
DT	01-MAY-1999	(TREMBLrel. 10.	Last annotation update)		
DE	SPOXHI PROTEIN (FRAGMENT).				
GN	SPOX HL.				
OS	Halictona sp.				
OC	Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha				
OC	Haplosterida; Chalinidae; Halictona.				
OX	NCBI_TaxID=34490;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=95337605; PubMed=7721087;				
RA	Degnan B.M., Degnan S.M., Giusti A., Morse D.E.;				
RT	"A. box/hom homeobox gene in sponges."				
RL	Gene 155:175-178(1995).				
DR	EMBL; X79263; CAA55850.1; -.				
FT	NON_TER	1			
FT	NON_TER	23			
FT	NON_TER	23			

Query Match	19.1%	Score 31;	DB 5;	Length 23;
Best Similarity	35.3%	Pred. NO.	8.9e+02;	
Matches	6;	Conservative	4;	Mismatches 7;
				Indels 0;
				Gaps 0

```
QY      7  NSKFIGITEFGFPEHLL 23
        : 1:::11 11
Db      1  SKKYLSTERSHIAHLL 17
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RESULT	8	
Q9GJP6		
ID	Q9GJP6	PRELIMINARY;
AC	Q9GJP6;	PRT;
DT	01-MAR-2001	28 AA
	(TREMBLrel, 16, Created)	

DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE MHC CLASS II B ANTIGEN (FRAGMENT).
GN GAA-C-D.
OS *Gasterosteus aculeatus* (three spined stickleback).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorpha; Gasterosteiformes;
OC *Gasterosteidae*; *Gasterosteus*.
OX NCBI_TaxID=69293;
RN [1]
RP SEQUENCE FROM N.A.
RA Binz T.;
RT *SSCP analysis of MHC genes in the stickleback.*;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF249303; AAF98326.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 28 AA; 3214 MW; 5BA44726E62179F4 CRC64;

Query Match	19.1%	Score 31:	DB 7:	Length 28:
Best Local	Similarity 50.0%	Pred. No.	1.1e+03:	
Matches 4:	Conservative	3:	Mismatches 1:	Indels 0:
				Gaps 0:

QY	10	FIGITEFG	17
	:	:	
Db	1	YVGFTETG	8

RESULT	9	
Q02800		
ID	Q02800	PRELIMINARY;
		PRT;
		30 AA

DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, last annotation update)
 DE HYPOTHETICAL PROTEIN IN PH14 PROMOTER (FRAGMENT).
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=93163057; PubMed=7679386;
 RA Tan H., Chater K. F.;
 RT "Two developmentally controlled promoters of Streptomyces coelicolor
 RT A3(2) that resemble the major class of motility-related promoters in
 RT other bacteria".
 RL J. Bacteriol. 175:933-940(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Bruton C.J.;
 RL Submitted (OCT-1992) to the EMBL/Genbank/DBJ databases.
 EMBL: X68791; CAA48685.1; -.
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 30 AA: 3217 MW: 67545FD68BFB12A9 CRC64;

Query Match	19.1%	Score 31	DB 2	Length 30
Best Similarity	70.0%	Pred. No. 1.2e+03		
Matches	7	Mismatches	1	Indels 0
				Gaps 0

QY	22	LIVDFLOSL	31
		: :	
Db	8	LIVDWLASLA	17

RESULT 10
Q9R4I6

ID 09R416 PRELIMINARY; PRT; 30 AA.
AC 09R416;
DT 01-MAY-2000 (TREMBLREL. 13, Created)
DT 01-MAY-2000 (TREMBLREL. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLREL. 13, Last annotation update)
DE ARGININE DEIMINASE (EC 3.5.3.6) (FRAGMENT).
OS Mycoplasma arginini.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2094;
RN [1]
RP SEQUENCE.
RX MEDLINE=96042668; PubMed=7591961;
RA Takaku H., Matsumoto M., Misawa S., Miyazaki K.;
RT "Anti-tumor activity of arginine deiminase from Mycoplasma argini and
its growth-inhibitory mechanism.";
RL Jpn. J. Cancer Res. 86:840-846(1995).
SQ SEQUENCE 30 AA; 3389 MW; 66DA98752F6D6694 CRC64;

Query Match 18.8%; Score 30.5; DB 2; Length 30;
Best Local Similarity 47.6%; Pred. No. 1.4e+03;
Matches 10; Conservative 3; Mismatches 5; Indels 3; Gaps 1;

OY 7 NSKFIGI---TERGFPHLLV 24
Db 4 DSKFKGIHVSEIGLESLV 24

RESULT 11
09ZAA4 PRELIMINARY; PRT; 26 AA.
AC 09ZAA4;
DT 01-MAY-1999 (TREMBLREL. 10, Created)
DT 01-MAY-1999 (TREMBLREL. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLREL. 10, Last annotation update)
DE UVRA (FRAGMENT).
GN UVRA.
OS Rhodobacter capsulatus (Rhodospseudomonas capsulata).
OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
OC Rhodobacter.
OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=750;
RX MEDLINE=99142327; PubMed=9987839;
RA Labazi M., del Rey A., Fernandez de Henestrosa A.R., Barbe J.;
RT "A consensus sequence for the Rhodospirillaceae SOS operators.";
RL FEMS Microbiol. Lett. 171:37-42(1999).
DR EMBL; AF060210; AAC67504.1; -.
FT NON_TER 26
SQ SEQUENCE 26 AA; 2915 MW; C026355E10E534A CRC64;

Query Match 18.5%; Score 30; DB 2; Length 26;
Best Local Similarity 38.5%; Pred. No. 1.4e+03;
Matches 10; Conservative 3; Mismatches 11; Indels 2; Gaps 1;

OY 6 ANSKFIGITEFGPHEHLVDFLOSLS 31
Db 2 AEQKFEYR--GAREHNKGFSAIS 25

RESULT 12
037180 PRELIMINARY; PRT; 27 AA.
AC 037180;
DT 01-JAN-1998 (TREMBLREL. 05, Created)
DT 01-JAN-1998 (TREMBLREL. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)
DE ENVELOPE PROTEIN 2 (FRAGMENT).
GN E2.
OS Hepatitis C virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10;
RX MEDLINE=98105815; PubMed=9445070;
RA Navas S., Martin J., Quiroga J.A., Castillo I., Carreno V.;
RT "Genetic diversity and tissue compartmentalization of the hepatitis C
virus genome in blood mononuclear cells, liver, and serum from chronic
hepatitis C patients.";
RL J. Virol. 72:1640-1646(1998).
DR EMBL; AF018289; AAC03570.1; -.
FT NON_TER 1
FT NON_TER 27
SQ SEQUENCE 27 AA; 2600 MW; 9B84D51B2E58BBD8 CRC64;

Query Match 18.5%; Score 30; DB 12; Length 27;
Best Local Similarity 46.2%; Pred. No. 1.5e+03;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 5 KANSKFIGITFEG 17
Db 11 QATSKFVGSSTOG 23

RESULT 13
093JY7 PRELIMINARY; PRT; 28 AA.
AC 093JY7;
DT 01-DEC-2001 (TREMBLREL. 19, Created)
DT 01-DEC-2001 (TREMBLREL. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLREL. 19, Last annotation update)
DE DNA-DIRECTED RNA POLYMERASE (FRAGMENT).
GN RPOB.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PATIENT NO.30;
RA Cheruvu M.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PATIENT NO.30;
RX MEDLINE=21367865; PubMed=11474030;
RA Mani C., Selvakumar N., Narayanan S., Narayanan P.R.;
RT "Mutations in the rpoB gene of multidrug-resistant Mycobacterium
tuberculosis clinical isolates from India.";
RL J. Clin. Microbiol. 39:2987-2990(2001).
DR EMBL; AJ297926; CAC50347.1; -.
KW DNA-directed RNA polymerase.
FT NON_TER 1
FT NON_TER 28
SQ SEQUENCE 28 AA; 3071 MW; 678638BED9D9D446 CRC64;

Query Match 18.5%; Score 30; DB 2; Length 28;
Best Local Similarity 38.5%; Pred. No. 1.6e+03;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 2 QYKANSKFIGIT 14
Db 7 QPMKQNNPLSGLT 19

RESULT 14
09DVT7 PRELIMINARY; PRT; 28 AA.
AC 09DVT7;

DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE TAX (FRAGMENT).
 GN PX.
 OS Human T-cell lymphotropic virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
 OX NCBI_TaxID=11908;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATL258;
 RA Furukawa Y., Kubota R., Tara M., Izumo S., Osame M.;
 RT "Existence of escape mutation in HTLV-I tax the developemnt of adult
 RL T-cell leukemia.";
 RL Immunology 97:987-993(2001).
 DR EMBL: AB045431; BAB20130.1; -.
 FT NON_TER 1
 SQ SEQUENCE 28 AA; 3196 MW; 875436AB89BD5A4E CRC64;

Query Match 18.5%; Score 30; DB 15; Length 28;
 Best Local Similarity 38.5%; Pred. NO. 1.6e+03;
 Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 16 FGPEHLVDFIQ 28
 ||:|::|:
 Db 11 FGYPYVFGDCVQ 23

RESULT 15
 Q9R4I5 PRELIMINARY; PRT; 30 AA.
 AC Q9R4I5;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE ARGININE DEIMINASE (EC 3.5.3.6) (FRAGMENT).
 OS Mycoplasma hominis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Molllicutes;
 OC Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2098;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96042668; PubMed=7591961;
 RA Takaku H., Matsunoto M., Misawa S., Miyazaki K.;
 RT "Anti-tumor activity of arginine deiminase from Mycoplasma argini and
 RL its growth-inhibitory mechanism.";
 RL Jpn. J. Cancer Res. 86:840-846(1995).
 SQ SEQUENCE 30 AA; 3389 MW; 93DC43752F6D6022 CRC64;

Query Match 18.2%; Score 29.5; DB 2; Length 30;
 Best Local Similarity 47.6%; Pred. NO. 2e+03;
 Matches 10; Conservative 3; Mismatches 5; Indels 3; Gaps 1;

QY 7 NSKFIGI---TEGPEHLV 24
 :||| || :| | :||
 Db 4 DSKFNGIHVSEIGLETVLV 24

Search completed: June 18, 2002, 08:21:18
 Job time: 196 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:15:42 ; Search time 29.28 Seconds
(without alignments)
117.599 Million cell updates/sec

Title: US-09-943-334-2
Perfect score: 162
Sequence: 1 CQYIKANSKFEIGTEFGPEHLVDFLQSLIS 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 281105

Minimum DB seq length: 0
Maximum DB seq length: 31

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	162	100.0	31	17	AAW06129 Anti-cholesteryl e
2	162	100.0	31	20	AAW02470 Fusion of a tetanu
3	85	52.5	22	20	AAV13815 Rabbit CERP immuno
4	85	52.5	22	20	AAV13821 Human CERP immuno
5	85	52.5	26	17	AAW06128 Human CERP immuno
6	85	52.5	26	20	AAV13801 Human CERP immuno
7	85	52.5	26	21	AAV91228 Human cholesteryl
8	83	51.2	16	21	AAV91229 Human cholesteryl
9	81	50.0	22	20	AAV13809 Rabbit CERP immuno
10	81	50.0	26	20	AAV13802 Rabbit CERP immuno
11	81	50.0	26	21	AAV91231 Human cholesteryl

12	79	48.8	16	21	AAV91230 Human cholesteryl
13	76	46.9	29	16	AAW83561 IGE CH4 region con
14	76	46.9	31	21	AAV82632 Tetanus toxoid T c
15	73	45.1	28	20	AAV53552 Lipopeptide #3. S
16	73	45.1	29	20	AAV53551 Lipopeptide #2. S
17	71.5	44.1	27	15	AAW62701 LHRH-containing im
18	70	43.2	14	11	AAW6309 Tetanus toxin epit
19	70	43.2	14	14	AAW83497 Tetanus toxin epit
20	70	43.2	14	14	AAW46509 Tetanus toxoid res
21	70	43.2	14	16	AAW878918 Tetanus toxoid 830
22	70	43.2	14	16	AAW75943 T helper epitope f
23	70	43.2	14	16	AAW70910 Tetanus toxoid 830
24	70	43.2	14	16	AAW74160 Antigenic peptide
25	70	43.2	14	17	AAW03003 Carrier peptide fo
26	70	43.2	14	18	AAW35437 T-cell stimulatory
27	70	43.2	14	19	AAW50108 Pan DR binding pep
28	70	43.2	14	20	AAV26601 Tetanus toxin-deri
29	70	43.2	14	20	AAV33251 Peptide derived fr
30	70	43.2	14	21	AAV93035 HLA class II bindi
31	70	43.2	14	21	AAV99127 HLA class II bindi
32	70	43.2	14	21	AAV99277 CD4+ T cell epitop
33	70	43.2	14	21	AAV49261 Vaccine related M
34	70	43.2	14	22	AAW99514 Human Leukocyte an
35	70	43.2	14	22	AAW06292 Tetanus toxoid pep
36	70	43.2	14	22	AAW89705 Tetanus toxoid pro
37	70	43.2	14	22	AAW62427 Tetanus toxoid 830
38	70	43.2	14	22	AAW84516 Human Leukocyte an
39	70	43.2	14	22	AAW84532 Tetanus toxoid 830
40	70	43.2	14	22	AAW88268 Human Leukocyte an
41	70	43.2	14	22	AAW88284 Human Leukocyte an
42	70	43.2	14	22	AAW89365 Tetanus toxoid 830
43	70	43.2	14	22	AAW89380 Human Leukocyte an
44	70	43.2	14	22	AAW84432 Amino acid sequenc
45	70	43.2	14	22	AAW98456 Tetanus toxoid pep

ALIGNMENTS

AAW06129	1	RESULT	1
ID	AAW06129	standard; Peptide: 31 AA.	
XX	AC	AAW06129;	
XX	XX		
DT	07-FEB-1997	(first entry)	
XX	DE	Anti-cholesteryl ester transfer peptide vaccine.	
XX	KW	Cholesteryl ester transfer protein; CERP; antigen; vaccine;	
KW	cardiovascular disease; atherosclerosis.		
XX	OS	Synthetic.	
XX	PH	Key	Location/Qualifiers
FT	Misc-difference	1	/note="C-terminal Cys residue is present for use in linking the peptide to itself or other molecules"
FT	Region	2..15	/label="T-cell epitope comprises amino acids 16..31"
FT	Region	16..31	/label="B-cell epitope comprises the C-terminal 16 amino acids of human CERP (Claim 5)"
FT	Region	16..31	/note="B-cell epitope comprises the C-terminal 16 amino acids of human CERP (Claim 5)"
PN	WO9634888-A1.		
XX	07-NOV-1996.		
PD	01-MAY-1996;	96WO-US06147.	
XX			
PF			

XX 01-MAY-1995; 95US-0432483.
 PR (TCEL-) T CELL SCI INC.
 PA
 XX
 PI Rittershaus CW, Thomas LJ;
 XX
 DR WPI; 1996-506103/50.
 XX
 PT Cholesteryl ester transfer protein B cell epitope linked to T cell
 PT epitope - used to generate vaccine to regulate CERP activity for
 PT decreasing the risk of developing a cardiovascular disease e.g.
 PT atherosclerosis
 XX
 PS Claim 8; Page 41-42; 72pp; English.
 XX
 CC A synthetic peptide vaccine comprises an immunogenic helper T-cell
 CC epitope of tetanus toxoid protein covalently linked to the
 CC C-terminal B-cell epitope of human cholesteryl ester transfer
 CC protein (CERP) (see also AA060127) that is involved in a neutral
 CC lipid binding or a transfer activity of CERP. The vaccine elicits
 CC an immune response against endogenous CERP activity, and is used to
 CC treat or prevent a cardiovascular disease, such as atherosclerosis.
 XX
 SQ Sequence 31 AA;

Query Match 100.0%; Score 162; DB 17; Length 31;
 Best Local Similarity 100.0%; Pred. No. 4.6e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 COYIKANSKFTGTERGPEPHLLVDFLOSL 31
 Db 1 cgyikanskftgtergpephllvdflosls 31

RESULT 2

AA02470
 ID AAY02470 standard; protein; 31 AA.

XX
 AC AAY02470;

DT 14-JUL-1999 (first entry)

XX Fusion of a tetanus toxoid fragment and C-terminal of human CERP.

XX Vaccine; antibody; endogenous; cholesteryl ester transfer protein; CERP;

KW high-density lipoprotein-associated cholesterol; metabolism;

KW low-density lipoprotein-associated cholesterol; atherosclerotic lesion;

KW cholesterol; atherosclerosis; heart disease.

XX Synthetic.

OS
 XX
 PN WO9920302-A1.

PD 29-APR-1999.

PF 20-OCT-1998; 98WO-US22145.

XX 20-OCT-1997; 97US-0954643.

PA (AVANT-) AVANT IMMUNOTHERAPEUTICS INC.

PI Rittershaus CW, Thomas LJ;

XX WPI; 1999-302645/25.

DR Vaccine against cholesteryl ester transfer protein

XX Disclosure; Page 55; 61pp; English.

CC The specification describes a vaccine that promotes the production of
 CC antibodies that bind endogenous cholesteryl ester transfer protein

CC (CERP). The vaccines (and equivalent plasmid-based vaccines) are
 CC used to increase the ratio of circulating high-density lipoprotein
 CC (HDL)-associated cholesterol to low-density lipoprotein (LDL) associated
 CC cholesterol; to decrease the level of endogenous CERP activity in humans
 CC or other animals; to alter metabolism of LDL-associated cholesterol, for
 CC inhibiting development of atherosclerotic lesions; to lower circulating
 CC levels of LDL and total cholesterol; and to treat or prevent
 CC atherosclerosis (or more generally heart disease). The present sequence
 CC was used in the course of the invention.
 XX
 SQ Sequence 31 AA;

Query Match 100.0%; Score 162; DB 20; Length 31;
 Best Local Similarity 100.0%; Pred. No. 4.6e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 COYIKANSKFTGTERGPEPHLLVDFLOSL 31
 Db 1 cgyikanskftgtergpephllvdflosls 31

RESULT 3

AA13815
 ID AAY13815 standard; peptide; 22 AA.

XX
 AC AAY13815;

DT 08-JUL-1999 (first entry)

XX Rabbit CERP immunogenic fragment.

KW CERP; cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;

KW antibody production; cholesteryl ester transfer; therapy;

KW high density lipoprotein; HDL cholesterol concentration;

KW pro-atherogenic dyslipoproteinaemia.

XX Oryctolagus sp.

OS
 XX
 PN WO9915655-A1.

PD 01-APR-1999.

PF 17-SEP-1998; 98WO-US19366.

XX 19-SEP-1997; 97US-0934367.

PA (MONS) MONSANTO CO.

PI Glenn K, Needleman P;

XX WPI; 1999-276984/23.

DR New recombinant DNA vaccines

XX Disclosure; Page 75; 99pp; English.

CC This sequence represents an immunogenic fragment of the rabbit

CC cholesteryl ester transferase protein (CERP).

CC The invention relates to recombinant DNA vaccines that contain DNA

CC encoding CERP, which can be used for producing antibodies to lessen the

CC transfer of cholesteryl esters from high density lipoprotein (HDL). The

CC method can provide an autogenic immunological process for lessening the

CC transfer of cholesteryl esters from HDL particles and for increasing the

CC HDL cholesterol concentration of a mammal whose blood also contains

CC CERP. The method may be useful in treating human pro-atherogenic

CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The

CC method can have an effect that lasts for months as compared to the

CC short-term effects of the small molecule drugs now available.
 XX
 SQ Sequence 22 AA;

PN W09915655-A1.
XX
XX 01-APR-1999.
XX
XX 17-SEP-1998; 98WO-US19366.
XX
XX 19-SEP-1997; 97US-0934367.
XX
XX (MONS) MONSANTO CO.
XX
XX Glenn K, Needleman P;
XX
XX WPI. 1999-276984/23.
XX
XX
XX New recombinant DNA vaccines
XX
XX
XX Claim 15; Page 85; 99pp; English.
XX
XX This sequence represents an immunogenic fragment of the rabbit
XX
XX cholesteryl ester transferase protein (CETP).
XX
XX The invention relates to recombinant DNA vaccines that contain DNA
XX
XX encoding CETP, which can be used for producing antibodies to lessen the
XX
XX transfer of cholesteryl esters from high density lipoprotein (HDL). The
XX
XX method can provide an autogenic immunological process for lessening the
XX
XX transfer of cholesteryl esters from HDL particles and for increasing the
XX
XX HDL cholesterol concentration of a mammal whose blood also contains
XX
XX CETP. The method may be useful in treating human pro-atherogenic
XX
XX dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
XX
XX method can have an effect that lasts for months as compared to the
XX
XX short-term effects of the small molecule drugs now available.
XX
XX
XX Sequence 26 AA:
SO
Query Match 52.5%; Score 85; DB 20; Length 26;
Best Local Similarity 94.1%; Pred. No. 3.4e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 15 ERGFEHLVDFLOSLS 31
Db 10 dfgfephlvdflois 26
RESULT 7
AA91228
ID AA91228 standard; peptide: 26 AA.
XX
XX AA91228;
XX
XX 22-MAY-2000 (first entry)
XX
XX
XX Human cholesteryl transport protein (CETP) peptide, SEQ ID NO:106.
XX
XX
XX Promiscuous T-cell epitope; measles virus F protein; MVE;
XX
XX hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
XX
XX interleukin-6; growth promoting hormone; LHRH; contraceptive; anticancer;
XX
XX somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; PMDV;
XX
XX foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
XX
XX Plasmodium falciparum; circumsporozoite; antimalarial; CETP;
XX
XX cholesteryl ester transport protein; anti-arteriosclerotic.
XX
XX
XX Homo sapiens.
XX
XX
XX W09966957-A2.
XX
XX
XX 29-DEC-1999.
XX
XX 21-JUN-1999; 99WO-US13975.
XX
XX 20-JUN-1998; 98US-0100412.
XX
XX (UNBT-) UNITED BIOMEDICAL INC.
XX

PI Wang CY;
XX
XX DR WPI: 2000-160564/14.
XX
XX
XX New artificial T helper cell epitope and derived immunogens with target
XX
XX antigenic site, for immunization against e.g. malaria, arteriosclerosis
XX
XX or human immune deficiency virus -
XX
XX
XX Claim 10; Page 49; 129pp; English.
XX
XX
XX The invention relates to novel promiscuous T helper cell epitopes (Th),
XX
XX and immunogenic peptides comprising the Th epitopes of the invention
XX
XX along with B cell epitopes. The Th epitopes and peptide immunogens
XX
XX containing them, are used to induce a T helper cell response,
XX
XX specifically against Plasmodium falciparum, cholesteryl ester transport
XX
XX protein (CETP) or HIV epitopes, but more generally against any pathogen,
XX
XX peptide immunogens may be used for prevention and/or treatment of
XX
XX infections (HIV, foot-and-mouth disease or malaria); for cancer
XX
XX immunotherapy; for inhibition of the action of interleukin hormone
XX
XX releasing hormone (LHRH) for contraception, treatment of hormone-
XX
XX dependent cancer, prevention of boar taint in meat, and
XX
XX immunocastration); for promoting the growth of animals; or for
XX
XX treating allergies or arteriosclerosis. Incorporation of a promiscuous
XX
XX Th (functional in genetically diverse subjects) into an immunogen
XX
XX improves capacity to induce a strong T helper cell mediated immune
XX
XX response, resulting in production of antibodies against a target
XX
XX antigen. Th can replace carrier proteins and pathogen-derived T helper
XX
XX epitopes. Sequence AA91121 represents a promiscuous T helper epitope
XX
XX from the measles virus F (MVE) protein and sequences AA91122-Y91142,
XX
XX AA91226 and AA91245-Y91246 represent synthetic Th epitopes based on the
XX
XX MVE Th epitope. Sequence AA91143 represents a promiscuous Th epitope
XX
XX from hepatitis B virus (HBV) surface antigen, and sequences
XX
XX AA91144-Y91155 are synthetic epitopes derived from this HBV epitope.
XX
XX AA91156-Y91196, AA91227 and AA91242-Y91244 are antigenic peptides
XX
XX comprising an LHRH sequence joined to a promiscuous Th epitope. AA91197
XX
XX is the LHRH target antigenic peptide used in these LHRH antigenic
XX
XX peptides. AA91200 is somatostatin, and AA91201-Y91207 are antigenic
XX
XX peptides comprising somatostatin and a Th epitope. Somatostatin
XX
XX immunogens may be used to promote growth in livestock. AA91208 is a
XX
XX human CD4 CDR2-like domain antigenic site, and AA91209-Y90211 are MVE Th
XX
XX epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
XX
XX infection of T cells. AA90212 is a modified version of a human IGE
XX
XX (immunoglobulin E) CH3 domain, and AA90213-Y90219 are Th epitope/IgE CH3
XX
XX antigenic peptides which may be used in the treatment of allergies.
XX
XX AA91220 is a peptide derived from foot and mouth disease virus (FMDV)
XX
XX VP1 capsid protein and AA91221-Y91222 comprise this peptide and a Th
XX
XX epitope. AA91223 is a Plasmodium falciparum circumsporozoite (CS) target
XX
XX antigen, and AA91224-Y91225 comprise the CS antigen and an MVE Th
XX
XX epitope and may be used in a malaria vaccine. AA91228-Y91231 represent
XX
XX CETP-derived peptides and AA91232-Y91241 are immunogens comprising a
XX
XX CETP peptide and a Th epitope which may be used to prevent or treat
XX
XX arteriosclerosis and cardiovascular disease. AA91247 and AA91252-Y91257
XX
XX are HIV-1 neutralising B-cell epitopes, and AA91248-Y91251 and
XX
XX AA91258-Y91273 are antigenic peptides comprising MVE Th and HIV-1 B-cell
XX
XX epitope which may be used as a component in an anti-HIV-1 vaccine.
XX
XX AA91198 and AA91199 are respectively an immunostimulatory invasin
XX
XX protein epitope from Yersinia species, and hinge spacer peptide, both of
XX
XX which may optionally be used in the antigenic peptides of the invention.
XX
XX Note: Sequence AA91227 is also designated SEQ ID NO:106 in the
XX
XX specification.
XX
XX
XX Sequence 26 AA:
SO
Query Match 52.5%; Score 85; DB 21; Length 26;
Best Local Similarity 94.1%; Pred. No. 3.4e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 15 ERGFEHLVDFLOSLS 31
Db 10 dfgfephlvdflois 26

RESULT 8
 AA91229
 ID AA91229 standard; peptide: 16 AA.
 XX
 AC AA91229;
 XX
 DT 22-MAY-2000 (first entry)
 XX
 DE Human cholesterol transport protein (CETP) peptide, SEQ ID NO:107.
 XX
 KM Promastis T-cell epitope; measles virus F protein; MVF;
 KM hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KM interleukin hormone releasing hormone; LHRH; contraceptive; anticancer;
 KM somatostatin; growth promotion; CD4 receptor; HIV-T; antitumor; FMDV;
 KM foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 KM Plasmodium falciparum; circumsporozoite; antimalarial; CETP;
 KM cholesterol ester transport protein; anti-arteriosclerotic.
 XX
 OS Homo sapiens.
 XX
 PN MO9966957-A2.
 XX
 PD 29-DEC-1999.
 XX
 PF 21-JUN-1999; 99WO-US13975.
 XX
 PR 20-JUN-1998; 98US-0100412.
 XX
 PA (UNBI-) UNITED BIOMEDICAL INC.
 XX
 PI Wang CY;
 XX
 DR WPI: 2000-160564/14.
 XX
 PT New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus -
 XX
 PS Claim 10: Page 50; 129pp; English.
 XX
 CC The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesterol ester transport
 CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of interleukin hormone-
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunosuppression); for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AA91121 represents a promiscuous T helper epitope
 CC from the measles virus F (MVF) protein and sequences AA91122-Y91142,
 CC AA91126 and AA91245-Y91246 represent synthetic Th epitopes based on the
 CC MVF Th epitope. Sequence AA91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AA91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AA91156-Y91196, AA91227 and AA91242-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AA91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AA91200 is somatostatin, and AA91201-Y91207 are antigenic
 CC peptides comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AA91208 is a
 CC human CD4 CDR2-like domain antigenic site, and AA91209-Y91211 are MVH Th
 CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV

CC Infection of T cells. AA90212 is a modified version of a human IGE
 CC (immunoglobulin E) CH3 domain, and AA90213-Y90219 are Th epitope/IgE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AA91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VP1 capsid protein and AA91221-Y91222 comprise this peptide and a Th
 CC epitope. AA91223 is a Plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AA91224-Y91225 comprise the CS antigen and an MVF Th
 CC epitope, and may be used in a malaria vaccine. AA91228-Y91231 represent
 CC CETP-derived peptides and AA91232-Y91241 are immunogens comprising a
 CC CETP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AA91247 and AA91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AA91248-Y91251 and
 CC AA91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AA91198 and AA91199 are respectively an immunostimulatory invasion
 CC protein epitope from Yersinia species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.
 XX
 SO Sequence 16 AA;
 XX
 Query Match 51.2%; Score 83; DB 21; Length 16;
 Best Local Similarity 100.0%; Pred. No. 4e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 16 FGPEHLLVDFLOSTS 31
 Db 1 fgiPehllvdfllqsls 16
 XX
 RESULT 9
 AA913809
 ID AA913809 standard; peptide: 22 AA.
 XX
 AC AA913809;
 XX
 DT 08-JUL-1999 (first entry)
 XX
 DE Rabbit CETP immunogenic fragment.
 XX
 KM CETP: cholesterol-ester transfer protein; recombinant DNA vaccine; HDL;
 KM antibody production; cholesterol ester transfer; therapy;
 KM high density lipoprotein; HDL cholesterol concentration;
 KM pro-atherogenic dyslipoproteinaemia.
 XX
 OS Oryctolagus sp.
 XX
 PN MO9915655-A1.
 XX
 PD 01-APR-1999.
 XX
 PF 17-SEP-1998; 98WO-US19366.
 XX
 PR 19-SEP-1997; 97US-0934367.
 XX
 PA (MONS) MONSANTO CO.
 XX
 PI Glenn K, Needleman P;
 XX
 DR WPI: 1999-276984/23.
 XX
 PT New recombinant DNA vaccines
 PS Example 1: Page 73; 99pp; English.
 XX
 CC This sequence represents an immunogenic fragment of the rabbit
 CC cholesterol ester transferase protein (CETP).
 CC The invention relates to recombinant DNA vaccines that contain DNA
 CC encoding CETP, which can be used for producing antibodies to lessen the
 CC transfer of cholesterol esters from high density lipoprotein (HDL). The
 CC method can provide an autogenous immunological process for lessening the
 CC transfer of cholesterol esters from HDL particles and for increasing the

CC HDL cholesterol concentration of a mammal whose blood also contains
 CC CERP. The method may be useful in treating human pro-atherogenic
 CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
 CC method can have an effect that lasts for months as compared to the
 CC short-term effects of the small molecule drugs now available.
 XX
 SQ Sequence 22 AA;

Query Match 50.0%; Score 81; DB 20; Length 22;
 Best Local Similarity 88.2%; Pred. NO. 1.2e-05;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 15 EFGPEHLVDFLOSL 31
 :||||:|||||||
 Db 6 dfgfpxhllvdflqsls 22

RESULT 10

AAV13802
 ID AAV13802 standard; peptide; 26 AA.

AAV13802;

08-JUL-1999 (first entry)

Rabbit CERP immunogenic fragment.

CERP; cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;
 antibody production; cholesteryl ester transfer; therapy;
 high density lipoprotein; HDL cholesterol concentration;
 pro-atherogenic dyslipoproteinaemia.

Oryctolagus sp.

WO9915655-A1.

01-APR-1999.

17-SEP-1998; 98WO-US19366.

19-SEP-1997; 97US-0934367.

(MONS) MONSANTO CO.

Glenn K, Needleman P;

WPI; 1999-276984/23.

New recombinant DNA vaccines

Claim 15; Page 94; 99pp; English.

This sequence represents an immunogenic fragment of the rabbit
 cholesteryl ester transferase protein (CERP).
 The invention relates to recombinant DNA vaccines that contain DNA
 encoding CERP, which can be used for producing antibodies to lessen the
 transfer of cholesteryl esters from high density lipoprotein (HDL). The
 method can provide an autogenic immunological process for lessening the
 transfer of cholesteryl esters from HDL particles and for increasing the
 HDL cholesterol concentration of a mammal whose blood also contains
 CERP. The method may be useful in treating human pro-atherogenic
 CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
 CC method can have an effect that lasts for months as compared to the
 CC short-term effects of the small molecule drugs now available.

Sequence 26 AA;

Query Match 50.0%; Score 81; DB 20; Length 26;
 Best Local Similarity 88.2%; Pred. NO. 1.4e-05;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 15 EFGPEHLVDFLOSL 31
 :||||:|||||||
 Db 10 dfgfpxhllvdflqsls 26

RESULT 11

AAV91231
 ID AAV91231 standard; peptide; 26 AA.

AAV91231;

22-MAY-2000 (first entry)

Human cholesteryl transport protein (CERP) peptide, SEQ ID NO:109.

Promiscuous T-cell epitope; measles virus F protein; MVF;
 hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
 somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMOV;
 foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 Plasmodium falciparum; circumsporozoite; antimalarial; CERP;
 cholesteryl ester transport protein; anti-arteriosclerotic.

Homo sapiens.

WO9966957-A2.

29-DEC-1999.

21-JUN-1999; 99WO-US13975.

20-JUN-1998; 98US-0100412.

(UNBI-) UNITED BIOMEDICAL INC.

Wang CY;

WPI; 2000-160564/14.

New artificial T helper cell epitope and derived immunogens with target
 antigenic site, for immunization against e.g. malaria, arteriosclerosis
 or human immune deficiency virus

Claim 10; Page 62; 129pp; English.

The invention relates to novel promiscuous T helper cell epitopes (Th),
 and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesteryl ester transport
 CC protein (CERP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of luteinising hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunosuppression; for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAV91227 represents a promiscuous T helper epitope
 CC from the measles virus F (MVF) protein and sequences AAV9122-Y91142,
 CC AAV91226 and AAV91245-Y91246 represent synthetic Th epitopes based on the
 CC MVF Th epitope. Sequence AAV91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AAV91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AAV91156-Y91196, AAV91227 and AAV91242-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAV91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAV91200 is somatostatin, and AAV91201-Y91207 are antigenic

peptides comprising somatostatin and a Th epitope. Somatostatin immunogens may be used to promote growth in livestock. AAY91208 is a human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVA Th epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV infection of T cells. AAY90212 is a modified version of a human IGE (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IGE CH3 antigenic peptides which may be used in the treatment of allergies. AAY91220 is a peptide derived from foot and mouth disease virus (FMDV) VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th epitope. AAY91223 is a plasmodium falciparum circumsporozoite (CS) target antigen, and AAY91224-Y91225 comprise the CS antigen and an MVA Th epitope and may be used in a malaria vaccine. AAY91226-Y91231 represent CERP-derived peptides and AAY91232-Y91241 are immunogens comprising a CERP peptide and a Th epitope which may be used to prevent or treat arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and AAY91258-Y91273 are antigenic peptides comprising MVA Th and HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1 vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory Invasin protein epitope from Yersinia species, and hinge spacer peptide, both of which may optionally be used in the antigenic peptides of the invention.

Sequence 26 AA:

Query Match 50.0%; Score 81; DB 21; Length 26;
Best Local Similarity 88.2%; Pred. No. 1.4e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

15 EFGPEHLVDFLOSLS 31
:||||:|||||||
Db 10 dfgfphkhlvdflqsls 26

RESULT 12

AAY91230
ID AAY91230 standard; peptide; 16 AA.

AC AAY91230;

22-MAY-2000 (first entry)

Human cholesterol transport protein (CERP) peptide, SEQ ID NO:108.

Promiscuous T-cell epitope; measles virus F protein; MVA;
hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
somatostatin; growth promotion; CD4 receptor; HIV-1, antiviral; FMDV;
foot and mouth disease virus; immunoglobulin E; Ige; anti-allergic;
plasmodium falciparum; circumsporozoite; antimalarial; CERP;
cholesterol ester transport protein; anti-arteriosclerotic.

Homo sapiens.

MO9966957-A2.

29-DEC-1999.

21-JUN-1999; 99MO-US13975.

20-JUN-1998; 98US-0100412.

(UNBI-) UNITED BIOMEDICAL INC.

Wang CY;

WPI; 2000-160564/14.

New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis or human immune deficiency virus

PS Claim 10; Page 62; 129pp; English.

The invention relates to novel promiscuous T helper cell epitopes (Th), and immunogenic peptides comprising the Th epitopes of the invention along with B cell epitopes. The Th epitopes and peptide immunogens containing them, are used to induce a T helper cell response, specifically against plasmodium falciparum, cholesterol ester transport protein (CERP) or HIV epitopes, but more generally against any pathogen, immunoreactive self-antigen or tumour antigen. The Th epitopes and peptide immunogens may be used for prevention and/or treatment of infections (HIV, foot-and-mouth disease or malaria); for cancer immunotherapy; for inhibition of the action of luteinising hormone releasing hormone (LHRH) for contraception, treatment of hormone-dependent cancer, prevention of bear taint in meat, and immunocastration); for promoting the growth of animals; or for treating allergies or arteriosclerosis. Incorporation of a promiscuous Th (functional in genetically diverse subjects) into an immunogen improves capacity to induce a strong T helper cell-mediated immune response, resulting in production of antibodies against a target antigen. Th can replace carrier proteins and pathogen-derived T helper epitopes. Sequence AAY91121 represents a promiscuous T helper epitope from the measles virus F (WVF) protein and sequences AAY91122-Y91142, AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the MVA Th epitope. Sequence AAY91143 represents a promiscuous Th epitope from hepatitis B virus (HBV) surface antigen, and sequences AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope. AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197 is the LHRH target antigenic peptide used in these LHRH antigenic peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic peptides comprising somatostatin and a Th epitope. Somatostatin immunogens may be used to promote growth in livestock. AAY91208 is a human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVA Th epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV infection of T cells. AAY90212 is a modified version of a human IGE (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IGE CH3 antigenic peptides which may be used in the treatment of allergies. AAY91220 is a peptide derived from foot and mouth disease virus (FMDV) VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th epitope. AAY91223 is a plasmodium falciparum circumsporozoite (CS) target antigen, and AAY91224-Y91225 comprise the CS antigen and an MVA Th epitope and may be used in a malaria vaccine. AAY91226-Y91231 represent CERP-derived peptides and AAY91232-Y91241 are immunogens comprising a CERP peptide and a Th epitope which may be used to prevent or treat arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and AAY91258-Y91273 are antigenic peptides comprising MVA Th and HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1 vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory Invasin protein epitope from Yersinia species, and hinge spacer peptide, both of which may optionally be used in the antigenic peptides of the invention.

Sequence 16 AA:

Query Match 48.8%; Score 79; DB 21; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.7e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

16 EFGPEHLVDFLOSLS 31
||||:|||||||
Db 1 fdfphkhlvdflqsls 16

RESULT 13

AAR83561
ID AAR83561 standard; peptide; 29 AA.

AAR83561;

13-JUN-1996 (first entry)

DE IGE CH4 region contg. peptide immunogen for treating allergies.
 XX IGE; CH4; immunoglobulin; epsilon; immunogen; helper T cell; epitope;
 KW vaccine; allergy; antibody; constant heavy chain.
 XX Synthetic.
 OS WO9526365-A1.
 PN 05-OCT-1995.
 XX 24-MAR-1995; 95WO-0503741.
 XX 25-OCT-1994; 94US-0328912.
 PR 28-MAR-1994; 94US-0218461.
 XX (UNBI-) UNITED BIOMEDICAL INC.
 XX Wang CY;
 PI WPI; 1995-351297/45.
 DR Synthetic peptide-based immunogen contg. IGE CH4 peptide and helper
 XX T cell epitope - useful for eliciting antibody prodn. for allergy
 PT treatment
 PS Claim 5; Page 68-69; 87pp; English.
 XX AAR83592-R82600 and AAR83560-R83581 are peptide immunogens that are
 CC useful in vaccines for treating allergic reactions. In the immunogens,
 CC an IGE CH4 peptide is attached C-terminally to a series of amino acids
 CC including a helper T cell epitope. The immunogen may also opt. contain
 CC a fatty acid or fatty acid derivative, an invasins domain or alpha-NH2.
 CC The immunogen produces high titres of antibodies to the effector site
 CC in human IGE heavy chain (the CH4 domain peptide) which inhibit mast
 CC cell activation and reduce allergen-induced IGE prodn. The immunogens
 CC may be used in either a radially branching multimeric form or a
 CC linearly arranged monomeric form.
 CC
 SO Sequence 29 AA;
 Query Match 46.9%; Score 76; DB 16; Length 29;
 Best Local Similarity 93.8%; Pred. No. 9.7e-05;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 OYIKANSKFGITTEFG 17
 Db 3 qyikanskfigitelg 18
 RESULT 14
 AAY82632
 ID AAY82632 standard; peptide; 31 AA.
 XX AAY82632;
 AC 07-AUG-2000 (first entry)
 DT Tetanus toxoid T cell epitope and der pII B cell epitope peptide.
 DE
 XX T cell epitope; B cell epitope; allergy; allergen; antigenic;
 KW anti-allergic; antiallergic; antiinflammatory; dermatological;
 KW immunosuppressive; vaccine; rhinitis; sinusitis; bronchial asthma;
 KW atopic dermatitis; acute urticaria; chronic urticaria;
 KW gastro-intestinal syndrome; food allergen; oro-pharyngeal syndrome;
 KW anaphylactic reaction; drug hypersensitivity; allergic reaction.
 XX
 XX Dermatophagoides pteronyssinus.
 OS Clostridium tetani.
 OS Synthetic.
 XX W0200006694-A2.
 PN

XX 10-FEB-2000.
 PD 20-JUL-1999; 99WO-BE00092.
 XX 30-JUL-1998; 98EP-0870167.
 XX (UNIO) UCB SA.
 XX Saint-Remy J, Jacquemin M;
 PI WPI; 2000-422470/36.
 DR New compound for prevention and treatment of allergies comprises at
 XX least one allergen antigenic determinant recognized by a B cell and at
 PT least one antigenic determinant which does not trigger T cell
 PT activation -
 XX Claim 8; Page 35; 50pp; English.
 XX The present invention describes a compound (I) for the prevention and/or
 CC treatment of allergy. The compound comprises at least one allergen
 CC antigenic determinant (I) recognised by a B cell or an antibody secreted
 CC by a B cell of a non-atopic individual and at least one antigenic
 CC determinant (II) different from the allergen that triggers T cell
 CC activation. (I) has antiallergic, antiallergic, antiinflammatory,
 CC dermatological and immunosuppressive activities, and can be used in a
 CC vaccine. (II) may be used in a pharmaceutical or cosmetic medicament to
 CC treat and/or prevent allergies or a disease of allergic origin,
 CC especially hypersensitivities. These include rhinitis, sinusitis,
 CC bronchial asthma, atopic dermatitis, some forms of acute and chronic
 CC urticaria, gastro-intestinal syndromes associated with the ingestion of
 CC food allergens, oro-pharyngeal syndrome, anaphylactic reactions
 CC associated with drug hypersensitivities and/or a mixture of these. The
 CC use of (I) in the treatment of allergic conditions avoids the need for
 CC drug treatment, which often causes undesirable side-effects. Also, prior
 CC art drug therapies alleviate symptoms, but do not influence their
 CC causes, however (I) actually combats the cause of an allergic reaction.
 CC The present sequence represents a specifically claimed compound peptide
 CC sequence from the present invention.
 CC
 SO Sequence 31 AA;
 Query Match 46.9%; Score 76; DB 21; Length 31;
 Best Local Similarity 93.8%; Pred. No. 0.0001;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 OYIKANSKFGITTEFG 17
 Db 1 qyikanskfigitelg 16
 RESULT 15
 AAY53552
 ID AAY53552 standard; Protein; 28 AA.
 XX AAY53552;
 AC 18-JAN-2000 (first entry)
 DT Lipopeptide #3.
 DE
 XX Lipopeptide; epitope; cytotoxic T lymphocyte; CTL; lipid; spacer; p53;
 KW electrical charge; hydrophilicity; vaccine; immune response; HIV; HBV;
 KW human immunodeficiency virus; hepatitis B virus; papilloma virus;
 KW melanoma; malaria; parasite.
 XX
 XX Synthetic.
 OS Homo sapiens.
 OS
 XX Key location/Qualifiers
 FH Modified-site 1
 FT

/note- "contains palmitoyl residue attached at the N-terminus and on the epsilon carbon of the side chain"

FR2776926-A1.

08-OCT-1999.

07-APR-1998; 98FR-0004323.

07-APR-1998; 98FR-0004323.

(INRM) INSERM INST NAT SANTE & RECH MEDICALE.

(CNRS) CNRS CENT NAT RECH SCI.

(INSP) INST PASTEUR LILLE.

Le Gal FA, Gulliet JG, Gahery SH, Gras MH, Melnyk O, Tartar A;

WPI; 1999-58313/50.

New lipopeptide containing lipid regions and two epitopes, all separated by peptide spacers that impart hydrophilicity, useful in vaccines

Example 1; Page 9; 35pp; French.

The invention relates to the generation of a lipopeptide comprising at least one auxiliary T epitope, at least one cytotoxic T lymphocyte (CTL) epitope and at least one lipid residue with (1) the epitopes and lipid portion and (11) the epitopes, being separated independently by peptide spacers. These spacers comprise sequences of amino acids which carry an overall electrical charge in neutral media to ensure that the lipopeptide is hydrophilic. This peptide represents an example of them the N-terminal end of the molecule and 2 epitopes separated by the spacer residues Ser-Ser and Ala-Ala-Ala. Peptides AAV5301-Y53549 represent CC peptide epitopes used in the generation of the lipopeptides. These are used in therapeutic or prophylactic compositions and vaccines to induce specific immune responses against human immunodeficiency, hepatitis B or papilloma viruses; p53 of melanoma or the malaria parasite.

Sequence 28 AA;

Query Match 45.1%; Score 73; DB 20; Length 28;

Best Local Similarity 93.8%; Pred. No. 0.00027;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2 QYIKANGKFGITEFG 17

3 QYIKANGKFGITEFG 18

Search completed: June 18, 2002, 08:17:57
Job time: 135 sec

GenCore version 4.5
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OW protein - protein search, using sw model

Run on: June 18, 2002, 08:16:47 ; Search time 102.33 Seconds
(without alignments)
106.008 Million cell updates/sec

Title: US-09-943-334-2
Perfect score: 162
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 2213444

Minimum DB seq length: 0
Maximum DB seq length: 31

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	162	100.0	31 8 US-08-432-483-2	Sequence 2, Appl1
2	162	100.0	31 8 US-08-432-483A-2	Sequence 2, Appl1
3	162	100.0	31 13 US-08-945-289-2	Sequence 2, Appl1
4	162	100.0	31 13 US-08-954-643-7	Sequence 7, Appl1
5	162	100.0	31 19 US-09-529-762-7	Sequence 7, Appl1
6	162	100.0	31 23 US-09-943-334-2	Sequence 2, Appl1
7	162	100.0	31 23 US-09-943-348-2	Sequence 2, Appl1

8	85	52.5	22 11 US-08-785-997-10	Sequence 10, Appl1
9	85	52.5	22 11 US-08-785-997-34	Sequence 34, Appl1
10	85	52.5	22 11 US-08-788-882-10	Sequence 10, Appl1
11	85	52.5	22 11 US-08-788-882-34	Sequence 34, Appl1
12	85	52.5	22 13 US-08-934-367-10	Sequence 10, Appl1
13	85	52.5	22 13 US-08-934-367-34	Sequence 34, Appl1
14	85	52.5	22 17 US-09-386-591-10	Sequence 10, Appl1
15	85	52.5	22 17 US-09-386-591-34	Sequence 34, Appl1
16	85	52.5	22 17 US-09-387-340-10	Sequence 10, Appl1
17	85	52.5	22 17 US-09-387-340-34	Sequence 34, Appl1
18	85	52.5	26 1 PCT-US99-139758-106	Sequence 106, App
19	85	52.5	26 8 US-08-432-483-1	Sequence 1, Appl1
20	85	52.5	26 11 US-08-785-997-29	Sequence 29, Appl1
21	85	52.5	26 11 US-08-788-882-29	Sequence 29, Appl1
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25	85	52.5	26 17 US-09-387-340-29	Sequence 29, Appl1
26	85	52.5	26 21 US-09-701-588-106	Sequence 106, App
27	85	52.5	26 23 US-09-943-334-1	Sequence 1, Appl1
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37	81	50.0	26 11 US-08-785-997-50	Sequence 50, Appl1
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39	81	50.0	26 13 US-08-934-367-50	Sequence 50, Appl1
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43	81	50.0	16 1 PCT-US99-139758-108	Sequence 108, App
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ALIGNMENTS

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RESULT 1
US-08-432-483-2
; Sequence 32, Application US/08432483
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; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles, W.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
; TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Banner & Allegretti, Ltd.
; STREET: Ten South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-7407
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/432,483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Leon R. Yankwich
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: 95,179(TCS-95179)
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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL:
; ANTI-SENSE:
; FEATURE:
; NAME/KEY:
; LOCATION:
; US-08-432-483A-2

Query Match 100.0%; Score 162; DB 8; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 COYIKANSKFIGITRGFPFHLVDFLOSL 31

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; Sequence 2, Application US/08432483A
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
; TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Wilcoff, Ltd.
; STREET: Ten South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-7407
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/432,483A
; FILING DATE: 1-May-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Leon R. Yankwich
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: 95,179(TCS-95179)
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL:
; ANTI-SENSE:
; FEATURE:
; NAME/KEY:
; LOCATION:
; US-08-432-483A-2

Query Match 100.0%; Score 162; DB 8; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 COYIKANSKFIGITRGFPFHLVDFLOSL 31

RESULT 3
; Sequence 2, Application US/08945289
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; APPLICANT: Thomas, Lawrence J.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
; TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/945,289
; FILING DATE: October 17, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/432,483
; FILING DATE: May 1, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Leon R. Yankwich
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: TCS-411.1P US
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
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; MOLECULE TYPE: peptide
; HYPOTHEICAL:
; ANTI-SENSE:
; FEATURE:
; NAME/KEY:
; LOCATION:
; US-08-945-289-2

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Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 COYIKANSKFIGITRGFPFHLVDFLOSL 31
Db 1 COYIKANSKFIGITRGFPFHLVDFLOSL 31

RESULT 4
; Sequence 7, Application US/08954643
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; APPLICANT: Thomas, Lawrence J.
; TITLE OF INVENTION: XENOGENEIC CHOLESTERYL ESTER
; TITLE OF INVENTION: TRANSFER PROTEIN (CETP) FOR MODULATION OF CETP ACTIVITY
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: MA
; US-08-954-643-7
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COUNTRY: U.S.A.
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,643
FILING DATE: concurrently herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: TCS-420.0 US
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-954-643-7

Query Match 100.0%; Score 162; DB 13; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 COYIKANSKFITGTFEGFPEHLVDFLOSL 31
DB 1 COYIKANSKFITGTFEGFPEHLVDFLOSL 31

RESULT 5
US-09-529-762-7
; Sequence 7, Application US/09529762
; GENERAL INFORMATION:
; APPLICANT: AVANT Immunotherapeutics, Inc.
; APPLICANT: Rittershaus, Charles
; APPLICANT: Thomas, Lawrence
; TITLE OF INVENTION: Xenogeneic Cholesteryl Ester Transfer Protein (CETP) for
; FILE REFERENCE: sequence listing for TCS-420.1 PCT
; CURRENT APPLICATION NUMBER: US/09/529,762
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: USSN 08/954,643
; PRIOR FILING DATE: 1997-10-20
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn ver. 2.1
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; LENGTH: 31
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; OTHER INFORMATION: Description of Artificial Sequence: synthetic
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; OTHER INFORMATION: linked to human CETP C-terminus
US-09-529-762-7

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Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-09-943-334-2
; Sequence 2, Application US/09943334
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; APPLICANT: Thomas, Lawrence J.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVI
; FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
; CURRENT APPLICATION NUMBER: US/09/943,334
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 08/432,483
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: PCT/US96/06147
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/945,289
; PRIOR FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: vaccine peptide of the invention
US-09-943-334-2

Query Match 100.0%; Score 162; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 COYIKANSKFITGTFEGFPEHLVDFLOSL 31
DB 1 COYIKANSKFITGTFEGFPEHLVDFLOSL 31

RESULT 7
US-09-943-548-2
; Sequence 2, Application US/09943548
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; APPLICANT: Thomas, Lawrence J.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVI
; FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
; CURRENT APPLICATION NUMBER: US/09/943,548
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 08/432,483
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: PCT/US96/06147
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/945,289
; PRIOR FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: vaccine peptide of the invention
US-09-943-548-2

Query Match 100.0%; Score 162; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 4e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 COYIKANSKFITGTFEGFPEHLVDFLOSL 31
DB 1 COYIKANSKFITGTFEGFPEHLVDFLOSL 31

RESULT 8
US-08-785-997-10

Sequence 10, Application US/08785997
GENERAL INFORMATION:
ATTORNEY/AGENT INFORMATION:
APPLICANT: Needleman, Philip
TITLE OF INVENTION: An Immunological Process for Increasing
the HDL Cholesterol Concentration
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,997
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gamsen Ph.D., Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-101.0 6018/68346
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1500
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-785-997-10

Query Match 52.5%; Score 85; DB 11; Length 22;
Best Local Similarity 94.1%; Pred. No. 1.9e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 15 EFGPEHLVDFLOSL 31
DB 6 DFGPEHLVDFLOSL 22

RESULT 9
US-08-785-997-34
Sequence 34, Application US/08785997
GENERAL INFORMATION:
ATTORNEY/AGENT INFORMATION:
APPLICANT: Needleman, Philip
TITLE OF INVENTION: An Immunological Process for Increasing
the HDL Cholesterol Concentration
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,997
FILING DATE:

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gamsen Ph.D., Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-101.0 6018/68346
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1501
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-785-997-34

Query Match 52.5%; Score 85; DB 11; Length 22;
Best Local Similarity 94.1%; Pred. No. 1.9e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 15 EFGPEHLVDFLOSL 31
DB 6 DFGPEHLVDFLOSL 22

RESULT 10
US-08-788-882-10
Sequence 10, Application US/08788882
GENERAL INFORMATION:
ATTORNEY/AGENT INFORMATION:
APPLICANT: Needleman, Philip
TITLE OF INVENTION: An Immunological Process and Constructs
for Increasing the HDL Cholesterol Concentration
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,882
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gamsen, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1501
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-788-882-10

Query Match 52.5%; Score 85; DB 11; Length 22;
Best Local Similarity 94.1%; Pred. No. 1.9e-05;

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 EFGFPEHLVDFLOSL 31
:|||||
DB 6 DFGFPEHLVDFLOSL 22

RESULT 11

US-08-788-882-34
; Sequence 34, Application US/08788882
; GENERAL INFORMATION:
; APPLICANT: Needleman, Philip
; APPLICANT: Glenn, Kevin
; APPLICANT: Krul, Elaine
; APPLICANT: Gamsen, Edward P.
; TITLE OF INVENTION: An Immunological Process and Constructs
; TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 120 South Riverside Plaza, 22nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,882
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamsen, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)655-1500
; TELEFAX: (312)655-1501
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-788-882-34

Query Match 52.5%; Score 85; DB 11; Length 22;
Best Local Similarity 94.1%; Pred. No. 1.9e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 EFGFPEHLVDFLOSL 31
:|||||
DB 6 DFGFPEHLVDFLOSL 22

RESULT 12

US-08-934-367-10
; Sequence 10, Application US/08934367
; GENERAL INFORMATION:
; APPLICANT: Needleman, Philip
; APPLICANT: Glenn, Kevin
; TITLE OF INVENTION: An Immunological Process and Constructs
; TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration by DNA
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 120 South Riverside Plaza, 22nd Floor

CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,367
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gamsen Ph.D., Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1500
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-367-10

Query Match 52.5%; Score 85; DB 13; Length 22;
Best Local Similarity 94.1%; Pred. No. 1.9e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 EFGFPEHLVDFLOSL 31
:|||||
DB 6 DFGFPEHLVDFLOSL 22

RESULT 13
US-08-934-367-34
; Sequence 34, Application US/08934367
; GENERAL INFORMATION:
; APPLICANT: Needleman, Philip
; APPLICANT: Glenn, Kevin
; TITLE OF INVENTION: An Immunological Process and Constructs
; TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration by DNA
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 120 South Riverside Plaza, 22nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,367
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamsen Ph.D., Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)655-1500
; TELEFAX: (312)655-1501
; INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-367-34

Query Match 52.5%; Score 85; DB 13; Length 22;
Best Local Similarity 94.1%; Pred. No. 1.9e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 EFGFPEHLVDLQSL 31
:|||||
DB 6 DFGFPEHLVDLQSL 22

RESULT 14
US-09-386-591-10
; Sequence 10, Application US/09386591

GENERAL INFORMATION:
APPLICANT: Needleman, Philip
TITLE OF INVENTION: An Immunological Process and Constructs
TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration by DNA
TITLE OF INVENTION: Vaccination
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/386,591
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gamson Ph.D., Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1501
TELEFAX: (312)655-1500
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-386-591-10

Query Match 52.5%; Score 85; DB 17; Length 22;
Best Local Similarity 94.1%; Pred. No. 1.9e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 EFGFPEHLVDLQSL 31
:|||||
DB 6 DFGFPEHLVDLQSL 22

RESULT * 15
US-09-386-591-34
; Sequence 34, Application US/09386591

GENERAL INFORMATION:
APPLICANT: Needleman, Philip
TITLE OF INVENTION: An Immunological Process and Constructs
TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration by DNA
TITLE OF INVENTION: Vaccination
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/386,591
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gamson Ph.D., Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1500
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-386-591-34

Query Match 52.5%; Score 85; DB 17; Length 22;
Best Local Similarity 94.1%; Pred. No. 1.9e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 EFGFPEHLVDLQSL 31
:|||||
DB 6 DFGFPEHLVDLQSL 22

Search completed: June 18, 2002, 08:20:26
Job time: 219 sec

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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:17:22 ; Search time 13.61 Seconds
(without alignments)
192.857 Million cell updates/sec

Title: US-09-943-334-2
Perfect score: 162
Sequence: 1 CQYKANSKRIGTFEGFPEHLVDLQSLIS 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 257105 seqs, 84670655 residues

Total number of hits satisfying chosen parameters: 46494

Minimum DB seq length: 0
Maximum DB seq length: 31

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/1/paa/PCF_NEW_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	78.5	48.5	24 6 US-10-128-711-110	Sequence 110, App
2	71.5	44.1	27 6 US-10-076-674-7	Sequence 7, Appl
3	71.5	44.1	27 6 US-10-076-674A-7	Sequence 7, Appl
4	70	43.2	14 5 US-09-707-738-5	Sequence 5, Appl
5	70	43.2	14 5 US-09-543-608A-38	Sequence 38, Appl
6	70	43.2	14 5 US-09-709-774-5	Sequence 5, Appl
7	70	43.2	14 5 US-09-942-052-710	Sequence 710, App
8	70	43.2	14 5 US-09-748-714B-1	Sequence 1, Appl
9	70	43.2	14 6 US-10-128-711-95	Sequence 95, Appl
10	70	43.2	14 6 US-10-001-469-1403	Sequence 1403, Ap
11	70	43.2	15 5 US-09-413-186A-11	Sequence 11, Appl
12	70	43.2	17 1 PCF-US02-10293-3	Sequence 3, Appl
13	70	43.2	25 5 US-09-413-186A-14	Sequence 14, Appl
14	70	43.2	25 5 US-09-413-186A-15	Sequence 15, Appl
15	70	43.2	25 5 US-09-413-186A-16	Sequence 16, Appl
16	70	43.2	27 6 US-10-128-711-111	Sequence 111, App
17	70	43.2	27 6 US-10-128-711-112	Sequence 112, App
18	53	32.7	11 5 US-09-523-033A-3	Sequence 3, Appl
19	34	21.0	21 1 PCF-US02-09257-427	Sequence 427, App
20	34	21.0	21 1 PCF-US02-09370-671	Sequence 671, App
21	34	21.0	21 6 US-10-105-299-5439	Sequence 5439, Ap
22	32	19.8	22 5 US-09-453-834-133	Sequence 133, App
23	32	19.8	22 5 US-09-453-841-133	Sequence 133, App
24	32	19.8	22 6 US-10-099-574A-133	Sequence 133, App
25	32	19.8	22 6 US-10-147-849-133	Sequence 133, App
26	32	19.8	22 6 US-10-147-993-133	Sequence 133, App

27	31	19.1	21 5 US-09-924-941-15	Sequence 15, Appl
28	31	19.1	31 5 US-09-956-206A-32	Sequence 32, Appl
29	30	18.5	9 6 US-10-014-340-19	Sequence 19, Appl
30	30	18.5	12 5 US-09-862-179A-20	Sequence 20, Appl
31	30	18.5	12 5 US-09-652-169-13	Sequence 13, Appl
32	30	18.5	12 5 US-09-945-166A-3	Sequence 3, Appl
33	30	18.5	12 5 US-09-575-580B-32	Sequence 32, Appl
34	30	18.5	12 5 US-09-936-035-14	Sequence 14, Appl
35	30	18.5	12 6 US-10-145-415-68	Sequence 68, Appl
36	30	18.5	16 5 US-09-050-359B-136	Sequence 136, App
37	30	18.5	16 5 US-09-069-827A-136	Sequence 136, App
38	30	18.5	20 6 US-10-043-487-403	Sequence 403, App
39	30	18.5	27 6 US-10-105-299-4415	Sequence 4415, App
40	29.5	18.2	20 5 US-09-656-417-2	Sequence 2, Appl
41	29.5	18.2	28 5 US-09-636-596C-27	Sequence 27, Appl
42	29.5	18.2	31 6 US-10-004-860-1163	Sequence 1163, App
43	29	17.9	11 6 US-10-105-232-72	Sequence 72, Appl
44	29	17.9	21 6 US-10-105-299-4564	Sequence 4564, App
45	29	17.9	5 US-09-242-772-120	Sequence 120, App

ALIGNMENTS

RESULT 1
US-10-128-711-110
: Sequence 110, Application US/10128711
: GENERAL INFORMATION:
: APPLICANT: VITIELLO, Maria A.
: CHESTNUT, Robert W.
: SETTE, Alessandro D.
: CELIS, Esteban
: GRAY, Howard
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
: CTL IMMUNITY
: NUMBER OF SEQUENCES: 153
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Townsend and Townsend Kourie and Crew
: STREET: Stewart Street Tower, One Market Plaza
: CITY: San Francisco
: STATE: California
: COUNTRY: US
: ZIP: 94105-1493
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/128, 711
: FILING DATE: 22-Apr-2002
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/197, 484
: FILING DATE: 16-FEB-1994
: APPLICATION NUMBER: US 07/935, 811
: FILING DATE: 26-AUG-1992
: APPLICATION NUMBER: US 07/874, 491
: FILING DATE: 27-APR-1992
: APPLICATION NUMBER: US 07/827, 682
: FILING DATE: 29-JAN-1992
: APPLICATION NUMBER: US 07/749, 568
: FILING DATE: 26-AUG-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Parmelee, Steven W.
: REGISTRATION NUMBER: 31,990
: REFERENCE/DOCKET NUMBER: 14137-26-4
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 467-9600
: TELEFAX: (206) 623-6793
: INFORMATION FOR SEQ ID NO: 110:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 24 amino acids

TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 110:
US-10-128-711-110

Query Match 48.5%; Score 78.5; DB 6; Length 24;
Best Local Similarity 65.5%; Pred. No. 1.8e-05;
Matches 19; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

OY 2 QYIKANSKFIGITEFGPEHLVDFQSL 30
DB 1 QYIKANSKFIGITEF-----LPSDFEPSV 24

RESULT 2
US-10-076-674-7
Sequence 7, Application US/10076674
GENERAL INFORMATION:
APPLICANT: Sokoll, Kenneth K.
TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
FILE REFERENCE: Immunogen Delivery System
CURRENT APPLICATION NUMBER: US/10/076,674
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 27
TYPE: PRT
ORGANISM: Human
US-10-076-674-7

Query Match 44.1%; Score 71.5; DB 6; Length 27;
Best Local Similarity 80.0%; Pred. No. 0.00024;
Matches 16; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

OY 2 QYIKANSKFIGITEFGPEH 21
DB 3 QYIKANSKFIGITEL---EH 19

RESULT 3
US-10-076-674A-7
Sequence 7, Application US/10076674A
GENERAL INFORMATION:
APPLICANT: Sokoll, Kenneth K.
TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
FILE REFERENCE: Immunogen Delivery System
CURRENT APPLICATION NUMBER: US/10/076,674A
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 27
TYPE: PRT
ORGANISM: Human
US-10-076-674A-7

Query Match 44.1%; Score 71.5; DB 6; Length 27;
Best Local Similarity 80.0%; Pred. No. 0.00024;
Matches 16; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

OY 2 QYIKANSKFIGITEFGPEH 21
DB 3 QYIKANSKFIGITEL---EH 19

RESULT 4
US-09-707-738-5

Sequence 5, Application US/09707738
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Gaeta, Federico
APPLICANT: Grey, Howard M.
APPLICANT: Sidney, John
APPLICANT: Alexander, Jeffery L.
TITLE OF INVENTION: Induction of Immune Response Against
FILE REFERENCE: 018623-006250US
CURRENT APPLICATION NUMBER: US/09/707,738
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 08/121,101
PRIOR FILING DATE: 1993-09-14
PRIOR APPLICATION NUMBER: US 08/305,871
PRIOR FILING DATE: 1994-09-14
PRIOR APPLICATION NUMBER: US 08/485,218
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 60/010,510
PRIOR FILING DATE: 1996-01-24
PRIOR APPLICATION NUMBER: US 08/788,822
PRIOR FILING DATE: 1997-01-23
PRIOR APPLICATION NUMBER: US 09/310,462
PRIOR FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Tet Tox 830-843, T-helper epitope from tetanus
US-09-707-738-5

Query Match 43.2%; Score 70; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 QYIKANSKFIGITE 15
DB 1 QYIKANSKFIGITE 14

RESULT 5
US-09-543-608A-38
Sequence 38, Application US/09543608A
GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Celis, Esteban
APPLICANT: Keogh, Elissa A.
APPLICANT: Chesnut, Robert
APPLICANT: Epiimmune Inc.
TITLE OF INVENTION: HLA Class I A2 Tumor Associated Antigen
FILE REFERENCE: 018623-015710US
CURRENT APPLICATION NUMBER: US/09/543,608A
CURRENT FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 38
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: tetanus toxoid positions 830-843, standard peptide
US-09-543-608A-38


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Query Match          43.2%; Score 70; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYKANSKFIGITE 15
DB 1 QYKANSKFIGITE 14

RESULT 6
US-09-709-774-5
; Sequence 5, Application US/09709774
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Gaeta, Federico
; APPLICANT: Grey, Howard M.
; APPLICANT: Sidney, John
; APPLICANT: Alexander, Jeffery L.
; APPLICANT: Eplimmune Inc.
; TITLE OF INVENTION: Alteration of Immune Response Using Pan DR-Binding
; FILE REFERENCE: 018623-006240US
; CURRENT APPLICATION NUMBER: US/09/709,774
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 08/121,101
; PRIOR FILING DATE: 1993-09-14
; PRIOR APPLICATION NUMBER: US 08/305,871
; PRIOR FILING DATE: 1994-09-14
; PRIOR APPLICATION NUMBER: US 60/010,510
; PRIOR FILING DATE: 1996-01-24
; PRIOR APPLICATION NUMBER: US 08/788,822
; PRIOR FILING DATE: 1997-01-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Tet Tox 830-843
US-09-709-774-5

Query Match          43.2%; Score 70; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYKANSKFIGITE 15
DB 1 QYKANSKFIGITE 14

RESULT 7
US-09-942-052-710
; Sequence 710, Application US/09942052
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afari, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Chailita-Bid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 710
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Tetanus toxoid
US-09-942-052-710

Query Match          43.2%; Score 70; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYKANSKFIGITE 15
DB 1 QYKANSKFIGITE 14

RESULT 8
US-09-260-714B-1
; Sequence 1, Application US/09260714B
; GENERAL INFORMATION:
; APPLICANT: Eplimmune Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chesnut, Robert
; APPLICANT: Sidney, John
; TITLE OF INVENTION: PEPTIDES WITH INCREASED BINDING AFFINITY
; FILE REFERENCE: FOR HLA A3 SUPERTYPE MOLECULES
; CURRENT APPLICATION NUMBER: US/09/260,714B
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Tetanus toxoid
US-09-260-714B-1

Query Match          43.2%; Score 70; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYKANSKFIGITE 15
DB 1 QYKANSKFIGITE 14

RESULT 9
US-10-128-711-95
; Sequence 95, Application US/10128711
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Esteban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend Kourile and Crew
; STREET: Stewart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/128,711
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..14
; OTHER INFORMATION: /note="Tetanus toxoid 830-843"
;
; US-10-128-711-95
;
Query Match          43.2%; Score 70; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 QYKANSKFQIGTE 15
        |||111111111111
Db       1 QYKANSKFQIGTE 14

RESULT 10
US-10-001-469-1403
; Sequence 1403, Application US/10001469
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AVA
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: SAFERAN, DOUGLAS
; APPLICANT: HUBERT, RENE
; APPLICANT: FARIS, MARY
; APPLICANT: CHALITA-EID, PIA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; FILE REFERENCE: 101P311 USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20024.20
; CURRENT APPLICATION NUMBER: US/10/001,469
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/157,902
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/291,118
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/680,728
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 2888
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1403
; LENGTH: 14
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; TYPE: PRT
; ORGANISM: Clostridium sp.
; US-10-001-469-1403

Query Match          43.2%; Score 70; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 QYKANSKFQIGTE 15
        |||111111111111
Db       1 QYKANSKFQIGTE 14

RESULT 11
US-09-413-186A-11
; Sequence 11, Application US/09413186A
; GENERAL INFORMATION:
; APPLICANT: Steinaa, Lucilla
; APPLICANT: Mouritsen, Soren
; APPLICANT: Gautam, Anand
; APPLICANT: Haaning, Jesper
; APPLICANT: Dalum, Iben
; APPLICANT: Birk, Peter
; APPLICANT: Leach, Dana
; APPLICANT: Nielsen, Klaus
; APPLICANT: Karlsson, Gunilla
; TITLE OF INVENTION: NOVEL METHODS FOR THERAPEUTIC VACCINATION
; FILE REFERENCE: 3631-0115P
; CURRENT APPLICATION NUMBER: US/09/413,186A
; CURRENT FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/105,011
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: PA 1998 01261
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Clostridium tetani
; US-09-413-186A-11

Query Match          43.2%; Score 70; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 QYKANSKFQIGTE 15
        |||111111111111
Db       1 QYKANSKFQIGTE 14

RESULT 12
PCT-US02-10293-3
; Sequence 3, Application PC/WUS0210293
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: Immunogenic peptide composition as vaccines for the
; FILE REFERENCE: 1151-4167
; CURRENT APPLICATION NUMBER: PCT/US02/10293
; CURRENT FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Clostridium tetani
; PCT-US02-10293-3

Query Match          43.2%; Score 70; DB 1; Length 17;
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Best Local Similarity 100.0%; Pred. No. 0.00024;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QYKANSKFIGITE 15
 Db 3 QYKANSKFIGITE 16

RESULT 13
 US-09-413-186A-14
 ; Sequence 14, Application US/09413186A
 ; GENERAL INFORMATION:
 ; APPLICANT: Steinnae, Lucilla
 ; APPLICANT: Mouritsen, Soren
 ; APPLICANT: Gautam, Anand
 ; APPLICANT: Haaning, Jesper
 ; APPLICANT: Dalum, Iben
 ; APPLICANT: Birk, Peter
 ; APPLICANT: Leach, Dana
 ; APPLICANT: Nielsen, Klaus
 ; APPLICANT: Karlsson, Gunilla
 ; TITLE OF INVENTION: NOVEL METHODS FOR THERAPEUTIC VACCINATION
 ; FILE REFERENCE: 3631-0115P
 ; CURRENT APPLICATION NUMBER: US/09/413,186A
 ; CURRENT FILING DATE: 1999-10-05
 ; PRIOR FILING DATE: 1998-10-20
 ; PRIOR APPLICATION NUMBER: PA 1998 01261
 ; PRIOR FILING DATE: 1998-10-05
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 14
 ; LENGTH: 25
 ; TYPE: PRF
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Fusion of tetanus toxoid epitope and PSM
 US-09-413-186A-14

Query Match 43.2%; Score 70; DB 5; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.00037;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QYKANSKFIGITE 15
 Db 6 QYKANSKFIGITE 19

RESULT 14
 US-09-413-186A-15
 ; Sequence 15, Application US/09413186A
 ; GENERAL INFORMATION:
 ; APPLICANT: Steinnae, Lucilla
 ; APPLICANT: Mouritsen, Soren
 ; APPLICANT: Gautam, Anand
 ; APPLICANT: Haaning, Jesper
 ; APPLICANT: Dalum, Iben
 ; APPLICANT: Birk, Peter
 ; APPLICANT: Leach, Dana
 ; APPLICANT: Nielsen, Klaus
 ; APPLICANT: Karlsson, Gunilla
 ; TITLE OF INVENTION: NOVEL METHODS FOR THERAPEUTIC VACCINATION
 ; FILE REFERENCE: 3631-0115P
 ; CURRENT APPLICATION NUMBER: US/09/413,186A
 ; CURRENT FILING DATE: 1999-10-05
 ; PRIOR FILING DATE: 1998-10-20
 ; PRIOR APPLICATION NUMBER: PA 1998 01261
 ; PRIOR FILING DATE: 1998-10-05
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 15

; LENGTH: 25
 ; TYPE: PRF
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Fusion of tetanus toxoid epitope and PSM
 US-09-413-186A-15

Query Match 43.2%; Score 70; DB 5; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.00037;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QYKANSKFIGITE 15
 Db 6 QYKANSKFIGITE 19

RESULT 15
 US-09-413-186A-16
 ; Sequence 16, Application US/09413186A
 ; GENERAL INFORMATION:
 ; APPLICANT: Steinnae, Lucilla
 ; APPLICANT: Mouritsen, Soren
 ; APPLICANT: Gautam, Anand
 ; APPLICANT: Haaning, Jesper
 ; APPLICANT: Dalum, Iben
 ; APPLICANT: Birk, Peter
 ; APPLICANT: Leach, Dana
 ; APPLICANT: Nielsen, Klaus
 ; APPLICANT: Karlsson, Gunilla
 ; TITLE OF INVENTION: NOVEL METHODS FOR THERAPEUTIC VACCINATION
 ; FILE REFERENCE: 3631-0115P
 ; CURRENT APPLICATION NUMBER: US/09/413,186A
 ; CURRENT FILING DATE: 1999-10-05
 ; PRIOR FILING DATE: 1998-10-20
 ; PRIOR APPLICATION NUMBER: PA 1998 01261
 ; PRIOR FILING DATE: 1998-10-05
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 16
 ; LENGTH: 25
 ; TYPE: PRF
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Fusion of tetanus toxoid epitope and PSM
 US-09-413-186A-16

Query Match 43.2%; Score 70; DB 5; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.00037;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QYKANSKFIGITE 15
 Db 6 QYKANSKFIGITE 19

Search completed: June 18, 2002, 08:20:46
 Job time: 204 sec

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OM protein - protein search, using sw model

Run on: June 18, 2002, 08:16:02 ; Search time 12.95 Seconds
(without alignments)
58.471 Million cell updates/sec

Title: US-09-943-334-2
Perfect score: 162
Sequence: 1 COYIKANSKFIGITEFGFPEHLVDFLOSLIS 31

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 145535

Minimum DB seq length: 0
Maximum DB seq length: 31

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA: *
1: /cg2_6/prodata/2/1aa/5A.COMB.pep: *
2: /cg2_6/prodata/2/1aa/5B.COMB.pep: *
3: /cg2_6/prodata/2/1aa/6A.COMB.pep: *
4: /cg2_6/prodata/2/1aa/6B.COMB.pep: *
5: /cg2_6/prodata/2/1aa/PCTUS.COMB.pep: *
6: /cg2_6/prodata/2/1aa/backfilest1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78.5	48.5	24	5	PCT-US92-07218-25
2	78.5	48.5	24	5	PCT-US95-02121-110
3	78.5	48.5	27	5	PCT-US92-07218-32
4	71.5	44.1	27	1	US-08-446-692-13
5	71.5	44.1	27	2	US-08-488-351A-13
6	70	43.2	14	1	US-08-186-266-5
7	70	43.2	14	1	US-08-305-871A-5
8	70	43.2	14	1	US-08-661-167A-18
9	70	43.2	14	2	US-08-817-933A-9
10	70	43.2	14	5	PCT-US92-07218-15
11	70	43.2	14	5	PCT-US92-07218-30
12	70	43.2	14	5	PCT-US95-02121-95
13	70	43.2	15	2	US-08-319-704-10
14	70	43.2	15	2	US-08-661-052-6
15	70	43.2	15	2	US-08-460-502-7
16	70	43.2	15	4	US-09-046-373-2
17	70	43.2	15	4	US-09-188-082-6
18	70	43.2	15	5	PCT-US93-11703-69
19	70	43.2	16	4	US-09-248-588-55
20	70	43.2	17	1	US-08-446-692-4
21	70	43.2	17	1	US-08-488-351A-4
22	70	43.2	17	3	US-09-100-409A-40
23	70	43.2	17	5	PCT-US95-08596-23
24	70	43.2	17	5	PCT-US95-13841-7
25	70	43.2	24	5	PCT-US92-07218-31
26	70	43.2	27	5	PCT-US92-07218-26
27	70	43.2	27	5	PCT-US92-07218-27

28	70	43.2	27	5	PCT-US92-07218-28	Sequence 28, Appl
29	70	43.2	27	5	PCT-US95-02121-111	Sequence 111, App
30	70	43.2	27	5	PCT-US95-02121-112	Sequence 112, App
31	70	43.2	29	3	US-09-075-257A-13	Sequence 13, Appl
32	70	43.2	29	3	US-09-075-257A-14	Sequence 14, Appl
33	70	43.2	29	4	US-09-534-639-13	Sequence 13, Appl
34	70	43.2	29	4	US-09-534-639-14	Sequence 14, Appl
35	70	43.2	30	5	PCT-US92-07218-29	Sequence 29, Appl
36	70	43.2	31	5	PCT-US93-11703-63	Sequence 63, Appl
37	66	40.7	14	4	US-09-082-279B-510	Sequence 510, App
38	66	40.7	14	4	US-09-315-304B-510	Sequence 510, App
39	65	40.1	13	1	US-08-787-547-42	Sequence 42, Appl
40	65	40.1	15	2	US-08-661-052-9	Sequence 9, Appl1
41	65	40.1	15	4	US-09-188-082-9	Sequence 9, Appl1
42	64	39.5	19	1	US-08-787-547-41	Sequence 41, Appl
43	60	37.0	13	5	PCT-US94-10257A-26	Sequence 26, Appl
44	36	22.2	15	2	US-08-671-094B-7	Sequence 7, Appl1
45	36	22.2	17	1	US-08-311-307B-8	Sequence 8, Appl1

ALIGNMENTS

RESULT 1
PCT-US92-07218-25
Sequence 25, Application PC/RUS9207218
GENERAL INFORMATION:
APPLICANT: Vitellio, Maria A.
APPLICANT: Chesnut, Robert W.
TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS CTL
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESS: Townsend and Townsend
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07218
FILING DATE: 19920826
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14137-26-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US92-07218-25

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,692
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-446-692-13

Query Match 44.1%; Score 71.5; DB 1; Length 27;
Best Local Similarity 80.0%; Pred. No. 3.7e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

Oy 2 OYKANSKFIGITEFGPEH 21
Db 3 OYKANSKFIGITEL--EH 19

RESULT 5
US-08-488-351A-13
Sequence 13, Application US/08488351A
Patent No. 5843446
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang YI
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,351A
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,692
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/229,275
FILING DATE: 14-APR-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,166
FILING DATE: 27-APR-1992
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-488-351A-13

Query Match 44.1%; Score 71.5; DB 2; Length 27;
Best Local Similarity 80.0%; Pred. No. 3.7e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

Oy 2 OYKANSKFIGITEFGPEH 21
Db 3 OYKANSKFIGITEL--EH 19

RESULT 6
US-08-186-266-5
Sequence 5, Application US/08186266
Patent No. 5662907
GENERAL INFORMATION:
APPLICANT: KUBO, Ralph T.
APPLICANT: GREY, Howard M.
APPLICANT: SETTE, Alessandro
APPLICANT: CELIS, Esteban
TITLE OF INVENTION: INDUCTION OF ANTI-TUMOR CYTOTOXIC
TITLE OF INVENTION: T LYMPHOCYTES IN HUMANS USING
TITLE OF INVENTION: SYNTHETIC PEPTIDE EPITOPES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/186,266
FILING DATE: 25-JAN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/159,339
FILING DATE: 29-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14137-50-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043

```
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..14
; OTHER INFORMATION: /note="Tetanus toxin at positions
; OTHER INFORMATION: 830-843."
US-08-186-266-5

Query Match          43.2%; Score 70; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYKANSKFIGITE 15
DB 1 QYKANSKFIGITE 14

RESULT 7
US-08-305-871A-5
; Sequence 5, Application US/08305871A
; Patent No. 5736142
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Gaeta, Federico
; APPLICANT: Sidney, Howard M.
; APPLICANT: Sidney, John
; APPLICANT: Alexander, Jeffrey L.
; TITLE OF INVENTION: Alteration of Immune Response Using Pan
; TITLE OF INVENTION: DR-Binding Peptides
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/305,871A
; FILING DATE: 14-SEP-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/121,101
; FILING DATE: 14-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-0062-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-08-305-871A-5

Query Match          43.2%; Score 70; DB 1; Length 14;
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Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYKANSKFIGITE 15
DB 1 QYKANSKFIGITE 14

RESULT 8
US-08-465-167A-18
; Sequence 18, Application US/08465167A
; Patent No. 5750395
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Sette, Alessandro D.
; APPLICANT: Sidney, John C.
; TITLE OF INVENTION: DNA ENCODING MAGE-1 C-TERMINAL
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES (as amended)
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 98111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,167A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/103,623
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-60-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-465-167A-18

Query Match          43.2%; Score 70; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QYKANSKFIGITE 15
DB 1 QYKANSKFIGITE 14

RESULT 9
US-08-817-933A-9
; Sequence 9, Application US/08817933A
; Patent No. 5945104
; GENERAL INFORMATION:
; APPLICANT: STANWORTH, DENIS R.
; APPLICANT: LEWIN, IAN V.
; TITLE OF INVENTION: PEPTIDES FOR ANTI-ALLERGY TREATMENT
```


NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye
STREET: 1100 No. 5945104th Glabe Road, 8th Floor
CITY: Arlington
STATE: Virginia
COUNTRY: US
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/917,933A
FILING DATE: 27-JUN-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9422294.0
FILING DATE: 04-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C.
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 179-23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4005
TELEFAX: (703) 816-4100
TELEX: N/A
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-817-933A-9

Query Match 43.2%; Score 70; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OYIKANSKFIGITE 15
Db 1 OYIKANSKFIGITE 14

RESULT 10
PCT-US92-07218-15
Sequence 15, Application PC/TUS9207218
GENERAL INFORMATION:
APPLICANT: Vitellio, Maria A.
APPLICANT: Chesnut, Robert W.
TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS CTL
TITLE OF INVENTION: EPTOPES
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07218
FILING DATE: 19920826
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14137-26-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US92-07218-15

Query Match 43.2%; Score 70; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OYIKANSKFIGITE 15
Db 1 OYIKANSKFIGITE 14

RESULT 11
PCT-US92-07218-30
Sequence 30, Application PC/TUS9207218
GENERAL INFORMATION:
APPLICANT: Vitellio, Maria A.
APPLICANT: Chesnut, Robert W.
TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS CTL
TITLE OF INVENTION: EPTOPES
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07218
FILING DATE: 19920826
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14137-26-3
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-07218-30

Query Match 43.2%; Score 70; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OYIKANSKFIGITE 15
|
Db 1 OYIKANSKFIGITE 14

RESULT 12
PCT-US95-02121-95
; Sequence 95, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02121
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,484
; FILING DATE: 16-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..14
; OTHER INFORMATION: /note- "tetanus toxoid 830-843"
PCT-US95-02121-95

Query Match 43.2%; Score 70; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OYIKANSKFIGITE 15
|
Db 1 OYIKANSKFIGITE 14

RESULT 13
US-08-319-704-10
; Sequence 10, Application US/08319704
; Patent No. 5814617
; GENERAL INFORMATION:
; APPLICANT: Hoffman, Stephen L.
; APPLICANT: Charoenvit, Yupin L.
; APPLICANT: Hedstrom, Richard C.
; APPLICANT: Doolan, Denise L.
; TITLE OF INVENTION: Protective 17 kDa Malaria Hepatic and
; TITLE OF INVENTION: Erythrocytic Stage Immunogen and Gene
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Naval Medical R & D Command
; STREET: Bldg 1, T-12, 8901 Wisconsin Avenue
; CITY: Bethesda
; STATE: Maryland
; COUNTRY: U.S.A
; ZIP: 20889-5606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/319,704
; FILING DATE: 07-OCT-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: A. David Spevack
; REGISTRATION NUMBER: 24,743
; REFERENCE/DOCKET NUMBER: 75,206
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 295-6759
; TELEFAX: (301) 295-1022
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-319-704-10

Query Match 43.2%; Score 70; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 OYIKANSKFIGITE 15
|
Db 1 OYIKANSKFIGITE 14

RESULT 14
US-08-661-052-6
; Sequence 6, Application US/08661052
; Patent No. 5837243
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED

```

: TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
: NUMBER OF SEQUENCES: 16
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LAHIVE & COCKFIELD
: STREET: 60 State Street, Suite 510
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02109-1875
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/661,052
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/484,172
: FILING DATE: 07-JUNE-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Arnold, Beth E.
: REGISTRATION NUMBER: 35,430
: REFERENCE/DOCKET NUMBER: MXI-043CP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617)227-7400
: TELEFAX: (617)227-5941
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FRAGMENT TYPE: internal
: US-08-661-052-6

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Query Match 43.2%; Score 70; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 2 QYKANSKFIGITE 15
Db 1 QYKANSKFIGITE 14

```

```

RESULT 15
US-08-460-502-7
: Sequence 7, Application US/08460502
: Patent No. 5843464
: GENERAL INFORMATION:
: APPLICANT: Bakaletz, Lauren O.
: APPLICANT: Kaumaya, Parvin T.
: TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Calfee, Halter and Griswold
: STREET: 800 Superior Avenue
: CITY: Cleveland
: STATE: OHIO
: COUNTRY: U.S.A.
: ZIP: 44114-2688
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/460,502
: FILING DATE:
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Golrick, Mary E.

```

```

: REGISTRATION NUMBER: 34,829
: REFERENCE/DOCKET NUMBER: 22727/00120
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (216) 622-8458
: TELEFAX: (216) 241-0816
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-460-502-7

```

```

Query Match 43.2%; Score 70; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 2 QYKANSKFIGITE 15
Db 1 QYKANSKFIGITE 14

```

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Search completed: June 18, 2002, 08:18:16
Job time: 134 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 19, 2002, 11:06:16 ; Search time 14.7 seconds
(without alignments)
169.954 Million cell updates/sec

Title: US-09-943-334-1

Perfect score: 26

Sequence: 1 RDGFLLLQMDGFPFPHLLVDFLOSL 26

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database :

PIR-71:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	26	100.0	493	2	A53176	cholesteryl ester
2	26	100.0	493	2	A26941	cholesteryl ester
3	25	96.2	289	2	A38700	cholesteryl ester
4	11	42.3	497	2	I46692	cholesteryl ester
5	7	26.9	263	2	F86278	hypothetical prote
6	7	26.9	280	2	D84015	maltose/maltodextr
7	7	26.9	378	2	AH3635	c-di-GMP phosphodi
8	7	26.9	405	2	F86314	protein F2H15.16 f
9	7	26.9	547	2	E82422	anaerobic glycerol
10	7	26.9	825	2	T00818	hypothetical prote
11	7	26.9	903	2	T26743	hypothetical prote
12	7	26.9	961	1	P2XR4U	outer capsid prote
13	7	26.9	961	1	P2XR8A	outer capsid prote
14	7	26.9	961	1	A60017	outer capsid prote
15	7	26.9	1300	2	T00317	probable serine pr
16	6	23.1	96	2	F90932	hypothetical prote
17	6	23.1	96	2	D64931	hypothetical prote
18	6	23.1	115	2	T44558	hypothetical prote
19	6	23.1	130	2	H70454	conserved hypotnet
20	6	23.1	144	2	E11298	hypothetical prote
21	6	23.1	156	2	E84861	hypothetical prote
22	6	23.1	163	2	G90437	hypothetical prote
23	6	23.1	167	2	A95366	NADH dehydrogenase
24	6	23.1	189	2	IVH04B	interferon alpha-1
25	6	23.1	189	2	I52347	interferon alpha-M
26	6	23.1	204	1	S76652	hypothetical prote
27	6	23.1	210	2	F87455	transcription regu
28	6	23.1	214	2	S70734	adenylylate kinase (
29	6	23.1	214	2	AC0378	adenylylate kinase (

30	6	23.1	234	1	D69093	DNA repair protein
31	6	23.1	235	2	AC1368	amino acid ABC tra
32	6	23.1	241	2	T35437	hypothetical prote
33	6	23.1	260	2	C64005	enoyl-[acyl-carrie
34	6	23.1	268	2	T46631	phospholipid biosy
35	6	23.1	269	2	G69845	enoyl-[acyl-carrie
36	6	23.1	275	2	D89902	conserved hypotnet
37	6	23.1	279	2	T35791	probable transmemb
38	6	23.1	283	2	E70038	maltodextrin trans
39	6	23.1	283	2	E83902	maltose/maltodextr
40	6	23.1	283	2	E80105	probable maltodext
41	6	23.1	285	2	T10069	membrane associate
42	6	23.1	286	2	G83211	conserved hypotnet
43	6	23.1	298	2	B83823	endonuclease IV BR
44	6	23.1	303	2	H89881	hypothetical prote
45	6	23.1	313	2	F90026	hypothetical prote
46	6	23.1	333	2	H69679	involved in fatty
47	6	23.1	393	2	H90440	musonate cyclisom
48	6	23.1	394	2	G90114	type IIS restricti
49	6	23.1	397	2	G64703	probable type II r
50	6	23.1	406	2	G71816	hypothetical prote
51	6	23.1	414	2	T19912	probable oxidoredu
52	6	23.1	416	2	T37023	hypothetical prote
53	6	23.1	419	2	T08683	hypothetical prote
54	6	23.1	422	2	A49837	clathrin-associate
55	6	23.1	425	2	T23603	hypothetical prote
56	6	23.1	472	2	AD2284	hypothetical prote
57	6	23.1	489	2	T10334	late expression fa
58	6	23.1	490	2	T41806	LEF-9 orf62 - Bomb
59	6	23.1	491	1	ITRUA2	alpha-2-antiplasmi
60	6	23.1	496	2	T30412	late expression fa
					cytochrome P450 2D	late expression fa
					tubulin delta chain	probable membrane
					peptide transpor	myo-inositol cat
					hypothetical prote	hypothetical prote
					probable replicati	probable replicati
					mis protein [limpo	hypothetical prote
					hypothetical prote	chitin synthase (E
					P-type ATPase - 91	protein F3566.2 [1
					hypothetical prote	

ALIGNMENTS

RESULT 1
A53176
cholesteryl ester transfer protein - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 12-May-1994 #sequence, revision 12-May-1994 #text_change 07-May-1999
R:Accession: A53176
R:Paper, M.E.; Rehberg, E.F.; Marotti, K.R.; Melchior, G.W.
Arterioscler. Thromb. 11, 1759-1771, 1991
A:Title: Molecular cloning, sequence, and expression of cynomolgus monkey cholesteryl
asma high density lipoprotein levels
A:Reference number: A53176; MUID:92031355
A:Accession: A53176
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-493 <PAP>
A:Cross-references: GB:M66343

Query Match 100.0%; Score 26; DB 2; Length 493;
Best Local Similarity 100.0%; Pred. No. 5.5e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 26.9%: Score 7; DB 2: Length 280;
Best Local Similarity 100.0%: Pred. No. 8.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFLIOM 9
|||||
DB 112 GFLIOM 118

RESULT 7
A:3635
c-di-GMP phosphodiesterase A [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:Accession: A83635
R:DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Ios, T.; Ivanova,
.; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A>Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A:Reference number: A83252; PMID:11756688
A:Accession: A83635
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-378 <KUR>
A:Cross-references: GB:AE008918; PIDN:AAL54251.1; PID:q17985224; GSPDB:GN00191
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BME11009
A:Map position: 11

Query Match 26.9%: Score 7; DB 2: Length 378;
Best Local Similarity 100.0%: Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLL 7
|||||
DB 241 RDGFLL 247

RESULT 8
F66314
protein F2H15.16 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: F66314
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lures, J.S.; Maiti, R.; Marzilli,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: F66314
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-405 <STO>
A:Cross-references: GB:AE005172; NID:g9665071; PIDN:AAF97273.1; GSPDB:GN00141
C:Genetics:
A:Gene: F2H15.16
A:Map position: 1

Query Match 26.9%: Score 7; DB 2: Length 405;
Best Local Similarity 100.0%: Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 VDFLOSL 25
|||||
DB 37 VDFLOSL 43

RESULT 9
E82422
anaerobic glycerol-3-phosphate dehydrogenase, chain A VCA0747 [imported] - Vibrio cho
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: E82422
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Glinn, M.L.; Dodson, R.
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers
L., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A>Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833
A:Accession: E82422
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-547 <HEI>
A:Cross-references: GB:AE004403; GB:AE003853; NID:g9658159; PIDN:AAF96645.1; GSPDB:GN
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VCA0747
A:Map position: 2
C:Superfamily: glycerol-3-phosphate dehydrogenase (aerobic)

Query Match 26.9%: Score 7; DB 2: Length 547;
Best Local Similarity 100.0%: Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HLVDL 22
|||||
DB 495 HLVDL 501

RESULT 10
T00818
hypothetical protein Atg41620 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein T326.14
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 23-Mar-2001
C:Accession: T00818; A84844
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; K
submitted to the EMBL Data Library, November 1997
A:Description: Arabidopsis thaliana chromosome II BAC T326 genomic sequence.
A:Reference number: Z14163
A:Accession: T00818
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-825 <ROU>
A:Cross-references: EMBL:AC002510; NID:g2618683; PID:g2618698
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanhaken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: A84844
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-825 <STO>
A:Cross-references: GB:AE002093; NID:g2618698; PID:AA84345.1; GSPDB:GN00139
C:Genetics:
A:Gene: Atg41620; T326.14
A:Map position: 2
A:Introns: 43/3; 74/2; 96/3; 116/3; 146/3; 234/3; 266/3; 311/3; 329/3; 368/3; 669/3;
A>Note: T326.14
C:Superfamily: Arabidopsis thaliana hypothetical protein Atg41620

Query Match 26.9%; Score 7; DB 2; Length 825;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DFIQSL 26
Db 155 DFIQSL 161

RESULT 11

T26743

hypothetical protein Y39A1A.15c - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T26743

R:Wall, M.

Submitted to the EMBL Data Library, September 1998

A:Reference number: Z20257

A:Accession: T26743

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-903 <MIL>

A:Cross-references: EMBL:AL031633; PIDN:CAA21032.1; GSPDB:GN00021; CESP:Y39A1A.15c

C:Experimental source: clone Y39A1A

C:Genetics: CESP:Y39A1A.15c

A:Map position: 3

A:Introns: 33/3; 63/1; 139/3; 185/1; 382/3; 424/2; 798/3; 852/3

Query Match 26.9%; Score 7; DB 2; Length 903;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LTVDFLQ 23
Db 7 LTVDFLQ 13

RESULT 12

P2XR4U

outer capsid protein VP2 - bluetongue virus (serotype 1, strain Australia)

C:Species: bluetongue virus

C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999

C:Accession: S03654; J50322

R:Yamaguchi, S.; Fukusho, A.; Roy, P.

Nucleic Acids Res. 16, 2725, 1988

A:Title: Complete sequence of VP2 gene of the bluetongue virus serotype 1 (BTW-1).

A:Reference number: S03654; MUID:88203217

A:Accession: S03654

A:Molecule type: genomic RNA

A:Residues: 1-961 <YAM>

R:Gould, A.R.

Virus Res. 9, 145-158, 1988

A:Title: Conserved and non-conserved regions of the outer coat protein, VP2, of the Aust

0.

A:Reference number: J50322; MUID:88180013

A:Accession: J50322

A:Molecule type: genomic RNA

A:Residues: 1-12, 'V', 14-71, 'V', 73-185, 'LTV', 189-199, 'D', 201-350, 'F', 352-556, 'D', 558-749,

A:Cross-references: GB:M21844; NID:9323187; PIDN:AAA42844.1; PID:9323188

C:Genetics:

A:Map position: segment 2

C:Superfamily: bluetongue virus VP2 protein

C:Keywords: capsid protein

Db 12 GFPEHLL 18
|||||||

RESULT 13

P2XRSA

outer capsid protein VP2 - bluetongue virus (serotype 1, strain South Africa)

C:Species: bluetongue virus

C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 07-May-1999

C:Accession: A60014; B60014

R:Made-Evans, A.M.; Mertens, P.P.C.

Virus Res. 15, 213-230, 1990

A:Title: Expression of the outer capsid protein, VP2, from a full length cDNA clone o

a comparison of the nucleic acid sequence of this segment with those of other seroty

A:Reference number: A60014; MUID:90261331

A:Accession: A60014

A:Molecule type: mRNA

A:Residues: 1-961 <MAL>

A:Accession: B60014

A:Molecule type: protein

A:Residues: 322-346;492-503 <MA2>

C:Genetics:

A:Map position: segment 2

C:Superfamily: bluetongue virus VP2 protein

C:Keywords: capsid protein; glycoprotein; transmembrane protein

F:66-682/Domain: transmembrane #status predicted <TMN>

F:303,432/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 26.9%; Score 7; DB 1; Length 961;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GFPEHLL 18
Db 12 GFPEHLL 18

RESULT 14

A60017

outer capsid protein VP2 - bluetongue virus (serotype 1, strain South Africa-VACC)

C:Species: bluetongue virus

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999

C:Accession: A60017

R:Gould, A.R.; Pritchard, L.I.

Virus Res. 17, 31-52, 1990

A:Title: Relationships amongst bluetongue viruses revealed by comparisons of capsid a

A:Reference number: A60017; MUID:91021485

A:Accession: A60017

A:Molecule type: genomic RNA

A:Residues: 1-961 <GOU>

A:Cross-references: GB:X55800; NID:g297132; PIDN:CAA39322.1; PID:g297133

C:Genetics:

A:Map position: segment 2

C:Superfamily: bluetongue virus VP2 protein

C:Keywords: capsid protein; glycoprotein; membrane protein

F:303,432/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 26.9%; Score 7; DB 1; Length 961;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GFPEHLL 18
Db 12 GFPEHLL 18

RESULT 15

T00317

probable serine proteinase espP, extracellular - Escherichia coli plasmid p0157

N:Alternate names: putative exoprotein-precursor

C:Species: Escherichia coli


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C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 08-Dec-2000
C/Accession: T00317; T42120
R/Makino, K.; Ishii, K.; Yasunaga, T.; Hattori, M.; Yokoyama, K.; Yatsudo, H.C.; Kubota, S.; Shinagawa, H.
DNA Res. 5, 1-9, 1998
A/Title: Complete nucleotide sequences of 93-kb and 3.3-kb plasmids of an enterohemorrhagic E. coli O157:H7
A/Reference number: Z14127; MUID:98290540
A/Accession: T00317
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1300 <MAX>
A/Cross-references: EMBL:AB011549; NID:94589740; PIDN:BA031835.1; PID:93337077
A/Experimental source: strain EHEC O157:H7, substrain RMD 0509952
R/Burland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
Nucleic Acids Res. 26, 4196-4204, 1998
A/Title: The complete DNA sequence and analysis of the large virulence plasmid of Escherichia coli O157:H7
A/Reference number: Z22068; MUID:98391744
A/Accession: T42120
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1300 <MAX>
A/Cross-references: EMBL:AF074613; PIDN:AACT0088.1
A/Experimental source: strain EDL933, serotype O157:H7
C/Genetics:
A:Gene: espP
A:Genome: plasmid pO157
C:Superfamily: IGA-specific metalloendopeptidase
C:Keywords: serine proteinase

Query Match      26.9%; Score 7; DB 2; Length 1300;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LVDPLQ 23
|||||
DB 933 LVDPLQ 939

RESULT 16
P090932
hypothetical protein ECs2430 [imported] - Escherichia coli (strain O157:H7, substrain RMD 0509952)
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C/Accession: P090932
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic islands
A/Reference number: A99629; MUID:21156231; PMID:11258796
A/Accession: F90932
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-96 <MAX>
A/Cross-references: GB:BA000007; PIDN:BA035853.1; PID:913361897; GSPDB:GN00154
A/Experimental source: strain O157:H7, substrain RMD 0509952
C/Genetics:
A:Gene: ECs2430

Query Match      23.1%; Score 6; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLL 6
|||||
DB 32 RDGFLL 37

RESULT 17
D64931
hypothetical protein b1724 - Escherichia coli
C/Species: Escherichia coli

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C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999
C/Accession: D64931
R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; MUID:97426617
A/Accession: D64931
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-96 <BLAT>
A/Cross-references: GB:AE000267; GB:U00096; NID:q1788011; PIDN:AACT4794.1; PID:q17880
A/Experimental source: strain K-12, substrain MG1655

Query Match      23.1%; Score 6; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLL 6
|||||
DB 32 RDGFLL 37

RESULT 18
T44558
hypothetical protein PRF29 [imported] - Pseudomonas aeruginosa
C/Species: Pseudomonas aeruginosa
C/Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 31-Dec-2000
C/Accession: T44558; C83565
R/Nakayama, K.; Takashima, K.; Ishihara, H.; Shimizu, T.; Kageyama, M.; Kanaya, S.; submitted to the EMBL Data Library, August 1999
A/Description: Genetic relationship between bacteriophages and bacteriophages.
A/Reference number: Z22790
A/Accession: T44558
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-115 <NAK>
A/Cross-references: EMBL:AB030825; PIDN:BA083173.1
A/Experimental source: strain PA01
R/Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Adam, S.; Van, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapid, K.; L.; Lory, S.; Olson, M.V.
Nature 400, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A/Reference number: A82950; MUID:20437337
A/Accession: C83565
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-115 <STO>
A/Cross-references: GB:AE004499; GB:AE004091; NID:99946508; PIDN:AA04023.1; GSPDB:GN
A/Experimental source: strain PA01
C/Genetics:
A:Gene: PA0634
C:Superfamily: Pseudomonas aeruginosa hypothetical protein PRF29

Query Match      23.1%; Score 6; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFLLQ 8
|||||
DB 96 GFLLQ 101

RESULT 19
H70454
conserved hypothetical protein aq_1797 - Aquifex aeolicus
C/Species: Aquifex aeolicus
C/Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C/Accession: H70454
R/Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;

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V. Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666
A:Accession: H70454
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-130 <ADP>
A:Cross-references: GB:AE000756; NID:g2994076; PIDN:AAC07630.1; PID:g2984091; GB:AE00065
A:Experimental source: strain VF5
C:Genetics:
A:Gene: eq_1797

Query Match 23.1%; Score 6; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 L1VDFL 22
| | | | |
DB 80 L1VDFL 85

RESULT 20

hypothetical protein TP0638 - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
C:Accession: E71298
R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwilt
reyn, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uitterback, T.; McDo
Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770
A:Accession: E71298
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-144 <COI>
A:Cross-references: GB:AE001239; GB:AE000520; NID:g3322937; PIDN:AAC65625.1; PID:g332295
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0638
C:Superfamily: syphilis spirochete hypothetical protein TP0638

Query Match 23.1%; Score 6; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 L1VDFL 22
| | | | |
DB 71 L1VDFL 76

RESULT 21

hypothetical protein At2g43060 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: E84861
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umeyama, T.; Tallon, L.
eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: E84861
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-156 <STO>
A:Cross-references: GB:AE002093; NID:g4531440; PIDN:AAD2125.1; GSPDB:GN00139
C:Genetics:

A:Gene: At2g43060
A:Map position: 2

Query Match 23.1%; Score 6; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 FLOSLS 26
| | | | |
DB 22 FLOSLS 27

RESULT 22

hypothetical protein cutC-2 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C:Accession: G90437
R:She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweyer, M.J.; Ch
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder
arrett, R.A.; Ragan, M.A.; Sengen, C.W.; Van der Oost, J.
Submitted to Genbank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: G90437
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-163 <KUR>
A:Cross-references: GB:AE006641; NID:g13815949; PIDN:AAK42758.1; GSPDB:GN00155
A:Genetics:
A:Gene: cutC-2
C:Superfamily: isouquinoline 1-oxidoreductase alpha chain; ferredoxin [2Fe-2S] homolog
C:Keywords: 2Fe-2S; metalloprotein
F:48,53,56,68/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted

Query Match 23.1%; Score 6; DB 2; Length 163;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 L1VDFL 22
| | | | |
DB 30 L1VDFL 35

RESULT 23

NADH dehydrogenase (ubiquinone) (bc 1.6.5.3) chain B Nuor2 - Sinorhizobium meliloti (C)
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C:Accession: A95366
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; B
; Kallman, S.; Keating, D.H.; Palm, C.; Beck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: A95366
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-167 <KUR>
A:Cross-references: GB:AE006469; PIDN:AAK65491.1; PID:g14523963; GSPDB:GN00165
A:Experimental source: strain 1021, megaplasmid pSYMA
R:Galibert, F.; Flatau, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl
pela, D.; Chailu, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kallman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,
A:Title: The composite genome of the legume symbiont sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:

A:Gene: nuob2
A:Genome: plasmid
C:Superfamily: psbG protein
C:Keywords: oxidoreductase; NAD

Query Match 23.1% Score 6; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 GFLIIO 8
Db 142 GFLIIO 147

RESULT 24
Interferon alpha-I-4b precursor - human
IVH04B
N:Alternate names: HuIFN-alpha-I-4b; type I interferon
C:Species: Homo sapiens (man)
C>Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 18-Jun-1999
C:Accession: E23753
R:Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes, J.R.; Hochstadt, J.; Kov
J. Mol. Biol. 185, 227-260, 1985
A:Title: Structural relationship of human Interferon alpha genes and pseudogenes.
A:Reference number: A92916; MUID:86037205
A:Accession: E23753
A:Molecule type: DNA
A:Residues: 1-189 <HENC>
A:Cross-references: GB:X02955; NID:g32656; PIDN:CAA26701.1; PID:g758078
C:Gene: GDB:IFN1E
C:Genetics:
A:Cross-references: GDB:119328; OMIM:147660
A:Map position: 9g22-9p22
C:Superfamily: interferon alpha
C:Keywords: antiviral
F:1-23/Domain: signal sequence #status predicted <Sig>
F:24-189/product: Interferon alpha-I-4b #status predicted <Mat>
F:24-122,52-162/Disulfide Bonds: #status predicted

Query Match 23.1% Score 6; DB 1; Length 183;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 DECFPE 15
Db 58 DECFPE 63

RESULT 25
Interferon alpha-M1 precursor - human
I52347
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C:Accession: I52347
R:Linane, A.W.; Bellbarz, M.W.; McMullen, G.L.; Macreadle, J.G.; Murphy, M.; Nisbet, I.
Biochem. Int. 8, 725-732, 1984
A:Title: Nucleotide sequence and expression in E. coli of a human Interferon-alpha gene
A:Reference number: I52347; MUID:84307815
A:Accession: I52347
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-189 <RES>
A:Cross-references: GB:M27318; NID:g184617; PIDN:AAA52726.1; PID:g306909
C:Genetics:
A:Gene: IFN1
C:Superfamily: Interferon alpha

Query Match 23.1% Score 6; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 DECFPE 15
Db 58 DECFPE 63

RESULT 26
S76652
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: S76652
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
s.
A:Reference number: S74322; MUID:97061201
A:Accession: S76652
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-204 <KAN>
A:Cross-references: EMBL:D64004; GB:AB01339; NID:g1001701; PID:g1001758
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: Bacillus subtilis conserved hypothetical protein ydgE

Query Match 23.1% Score 6; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 17 LVYDFL 22
Db 23 LVYDFL 28

RESULT 27
F87455
transcription regulator, TetR family [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: F87455
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Duxin, A.S.; Gwin, M.L.; Haft, D.H.; Ko
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A67249; MUID:21173698; PMID:11259647
A:Accession: F87455
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-210 <STO>
A:Cross-references: GB:AE005673; NID:g13423072; PIDN:AAK23642.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC1664

Query Match 23.1% Score 6; DB 2; Length 210;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 19 VDFIQS 24
Db 182 VDFIQS 187

RESULT 28
S70734
adenylate kinase (EC 2.7.4.3) - Yersinia enterocolitica
N:Alternate names: ATP-AMP transphosphorylase
C:Species: Yersinia enterocolitica
C>Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999

C:Accession: S70734; S51258
R:Skurikh, M.; Venho, R.; Toivanen, P.; Al-Hendy, A.
Mol. Microbiol. 17, 575-594, 1995
A:Title: A novel locus of *Yersinia enterocolitica* serotype O:3 involved in lipopolysacch
A:Reference number: S70734; MIMD:96100456
A:Accession: S70734
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-214 <SKU>
A:Cross-references: EMBL:247767; NID:9633689; PIDN:CAA87696.1; PID:9633690
A:Experimental source: strain 6471/76 serotype O:3
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
C:Genetics:
A:Gene: adk
C:Function:
A:Description: catalyzes reversible phosphorylation of AMP with ATP to form two ADP
A:Note: magnesium required
C:Superfamily: adenylate kinase
C:Keywords: ATP; P-loop; phosphotransferase
F:7-14/Region: nucleotide-binding motif A (P-loop) #status atypical
F:80-85/Region: nucleotide-binding motif B #status atypical
F:126/Active site: His #status predicted

Query Match 23.1%; Score 6; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLL 6
|||||
Db 78 RDGFLL 83

RESULT 29
AG0378
adenylate kinase (EC 2.7.4.3) [imported] - *Yersinia pestis* (strain CO92)
C:Species: *Yersinia pestis*
C:Date: 02-Nov-2001 #sequence-revision 02-Nov-2001 #text-change 27-Nov-2001
C:Accession: AG0378
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tlball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G.;
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,
Nature 413, 523-527, 2001
A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A:Reference number: AB0001; MIMD:21470413; PMID:11586360
A:Accession: AG0378
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-214 <KUR>
A:Cross-references: GB:AL590842; PIDN:CA092354.1; PID:915981059; GSPDB:GN00175
C:Genetics:
A:Gene: adk
C:Superfamily: adenylate kinase
C:Keywords: phosphotransferase

Query Match 23.1%; Score 6; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLL 6
|||||
Db 78 RDGFLL 83

RESULT 30
D69093
DNA repair protein Rad51 homolog - *Methanobacterium thermoautotrophicum* (strain Delta H)
C:Species: *Methanobacterium thermoautotrophicum*
C:Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text-change 10-Sep-1999
C:Accession: D69093
R:Smith, D.R.; Doucette-Stamm, L.A.; Delonghery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadatore, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jivanli, N.

kl, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of *Methanobacterium thermoautotrophicum* Delta H: fu
A:Reference number: A69000; MIMD:98037514
A:Accession: D69093
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-234 <MTB>
A:Cross-references: GB:AE000927; GB:AE000666; NID:92622822; PIDN:AA86165.1; PID:9262
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH1693
C:Superfamily: *Methanococcus* DNA repair protein Rad51

Query Match 23.1%; Score 6; DB 1; Length 234;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FLLLOM 9
|||||
Db 150 FLLLOM 155

RESULT 31
AC1368
amino acid ABC transporter (permease) homolog lmo2347 [imported] - *Listeria monocytog*
C:Species: *Listeria monocytogenes*
C:Date: 27-Nov-2001 #sequence-revision 27-Nov-2001 #text-change 14-Dec-2001
C:Accession: AC1368
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bjoec
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlian, K.D.; Fahrl,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.;
ok, C.; Schluter, T.; Simoes, N.; Tiller, A.; Vazquez-Boland, J.A.; Voss, H.; Wenla
A:Title: Comparative genomics of *Listeria species*.
A:Reference number: AB1077; MIMD:21537279; PMID:11679669
A:Accession: AC1368
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-235 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CAD00425.1; PID:916411835; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo2347
C:Superfamily: histidine permease protein M

Query Match 23.1%; Score 6; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LNVDFL 22
|||||
Db 80 LNVDFL 85

RESULT 32
T35437
hypothetical protein SC6A9.06 SC6A9.06 - *Streptomyces coelicolor*
C:Species: *Streptomyces coelicolor*
C:Date: 05-Nov-1999 #sequence-revision 05-Nov-1999 #text-change 17-Mar-2000
C:Accession: T35437
R:Murphy, L.; Harris, D.; Parkhill, J.; Barrett, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, July 1998
A:Reference number: Z21578
A:Accession: T35437
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-241 <MUR>
A:Cross-references: EMBL:AL031035; PIDN:CAA19891.1; GSPDB:GN00070; SCOEDB:SC6A9.06
A:Experimental source: strain A3(2)

Query Match 23.1%; Score 6; DB 2;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 L1VDFL 22
|||||
DB 114 L1VDFL 119

RESULT 37

T35791
probable transmembrane sugar transport protein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
C:Accession: T35791
R:Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1998
A:Reference number: Z21570
A:Accession: T35791
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-279 <SEF>
A:Cross-references: EMBL:AL031013; PIDN:CAA19796.1; GSPDB:GN00070; SCOPDB:SC8A6.24
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOPDB:SC8A6.24
C:Superfamily: maltose transport protein malG

Query Match 23.1%; Score 6; DB 2; Length 279;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFLILQ 8
|||||
DB 261 GFLILQ 266

RESULT 38

E70038
maltodextrin transport system permease homolog yvfM - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: E70038
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertet
C.; Bron, S.; Brouillet, S.; Brunsch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrati, E.
Nature 350, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koester, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A:Authors: Lauber, J.; Lazarovic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel
Reiger, M.; Rivoita, C.; Kocha, E.; Koche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Tepstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Dancin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A65580; MUID:98044033
A:Accession: E70038
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-283 <KUN>
A:Cross-references: GB:Z99121; GB:AL009126; NID:92635827; PIDN:CAB1541.1; PID:g2635927
A:Experimental source: strain 168
C:Genetics:
A:Gene: yvfM
C:Superfamily: maltose transport protein malG

Query Match 23.1%; Score 6; DB 2; Length 283;

Best Local Similarity 100.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 FLLILQ 9
|||||
DB 116 FLLILQ 121

RESULT 39

E83902
maltose/maltodextrin transport system (permease) BH2021 [imported] - Bacillus halodur
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: E83902
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujl, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: E83902
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-283 <STO>
A:Cross-references: GB:AP001514; GB:BA000004; NID:910174613; PIDN:BA805740.1; GSPDB:G
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH2021
C:Superfamily: maltose transport protein malG

Query Match 23.1%; Score 6; DB 2; Length 283;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 FLLILQ 9
|||||
DB 116 FLLILQ 121

RESULT 40

AB0105
probable maltodextrin permease protein YPO0854 [imported] - Yersinia pestis (strain C
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C:Accession: AB0105
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, R.M.; Davis, P.; Dougan, G
ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB00001; MUID:21470413; PMID:11586360
A:Accession: AB0105
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-283 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC89701.1; PID:g15978928; GSPDB:GN00175
C:Genetics:
A:Gene: YPO0854
C:Superfamily: maltose transport protein malG

Query Match 23.1%; Score 6; DB 2; Length 283;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 FLLILQ 9
|||||
DB 116 FLLILQ 121

RESULT 41

T10069
membrane associated protein - Methylophilus methylotrophus
C:Species: Methylophilus methylotrophus

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C/Accession: T10069
R:Chistoserdov, A.Y.; McIntire, W.S.; Mathews, F.S.; Lidstrom, M.E.
J. Bacteriol. 176, 4073-4080, 1994
A>Title: Organization of the methylamine utilization (mau) genes in *Methylobacillus methyl*
A/Reference number: Z16936; MUID:94292427
A/Accession: T10069
A>Status: preliminary; translated from GB/EMBL/DDAJ
A/Molecule type: DNA
A/Residues: 1-285 <CHT>
A/Cross-references: EMBL:L26407; NID:9561931; PIDN:AB46947.1; PID:9556330
C/Experimental source: strain W3A1
C/Genetics:
A:Gene: mauF

Query Match 23.1%; Score 6; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGFLL 7
DB 268 DGFLL 273

RESULT 42
G83211
conserved hypothetical protein PA3474 [imported] - *Pseudomonas aeruginosa* (strain PA01)
C/Species: *Pseudomonas aeruginosa*
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C/Accession: G83211
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapidig, K.; Llm,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A>Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
A/Reference number: A82930; MUID:20437337
A/Accession: G83211
A>Status: preliminary
A/Molecule type: DNA
A/Residues: 1-286 <STO>
A/Cross-references: GB:AE004768; GB:AE004091; NID:9949611; PIDN:AA06862.1; GSPDB:GN001
A/Experimental source: strain PA01
C/Genetics:
A:Gene: PA3474

Query Match 23.1%; Score 6; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFLLQ 8
DB 139 GFLLQ 144

RESULT 43
B83823
endonuclease IV BH1386 [imported] - *Bacillus halodurans* (strain C-125)
C/Species: *Bacillus halodurans*
C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C/Accession: B83823
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hir
Nucleic Acids Res. 28, 4317-4331, 2000
A>Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
A/Reference number: AB9650; MUID:2051582; PMID:11058132
A/Accession: B83823
A>Status: preliminary
A/Molecule type: DNA
A/Residues: 1-298 <STO>
A/Cross-references: GB:AP001511; GB:BA000004; NID:910173727; PIDN:BA05105.1; GSPDB:GN00
C/Experimental source: strain C-125
C/Genetics:

A:Gene: BH1386
C:Superfamily: deoxyribonuclease IV (phage T4-induced)

Query Match 23.1%; Score 6; DB 2; Length 298;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 VDFLOS 24
DB 90 VDFLOS 95

RESULT 44
H89881
hypothetical protein SA0964 [imported] - *Staphylococcus aureus* (strain N315)
C/Species: *Staphylococcus aureus*
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C/Accession: H89881
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A>Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A/Reference number: AB9758; MUID:21311952; PMID:11418146
A/Accession: H89881
A>Status: preliminary
A/Molecule type: DNA
A/Residues: 1-303 <CUR>
A/Cross-references: GB:BA000018; PID:913700916; PIDN:BA042212.1; GSPDB:GN00149
A/Experimental source: strain N315
C/Genetics:
A:Gene: SA0964
C:Superfamily: cytochrome caa3 oxidase ctaa

Query Match 23.1%; Score 6; DB 2; Length 303;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFLLQ 8
DB 100 GFLLQ 105

RESULT 45
F90026
hypothetical protein SA2078 [imported] - *Staphylococcus aureus* (strain N315)
C/Species: *Staphylococcus aureus*
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C/Accession: F90026
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A>Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A/Reference number: AB9758; MUID:21311952; PMID:11418146
A/Accession: F90026
A>Status: preliminary
A/Molecule type: DNA
A/Residues: 1-313 <CUR>
A/Cross-references: GB:BA000018; PID:913702083; PIDN:BA043375.1; GSPDB:GN00149
A/Experimental source: strain N315
C/Genetics:
A:Gene: SA2078

Query Match 23.1%; Score 6; DB 2; Length 313;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 FLLQ 9
DB 11111

Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557
A:Accession: G71816
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-406 <ARN>
A:Cross-references: GB:AE001559; GB:AE001439; NID:g4155974; PIDN:AAD06939.1; PID:g415597
A:Experimental source: strain J99
C:Genetics:
A:Gene: jhp1364

Query Match 23.1%; Score 6; DB 2; Length 406;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 LQOMDF 11
DB 276 LQOMDF 281

Search completed: June 19, 2002, 11:08:20
Job time: 124 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 19, 2002, 11:08:01 ; Search time 10.35 Seconds
(without alignments)
97.267 Million cell updates/sec

Title: US-09-943-334-1

Perfect score: 26

Sequence: 1 RDGFLLQMDFGFPHLLVDFLQSLIS 26

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size: 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database: SwissProt_40:*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	493	1	CETP_HUMAN
2	26	100.0	493	1	CETP_MACRA
3	25	96.2	289	1	CETP_MESAU
4	11	42.3	497	1	CETP_RABIT
5	7	26.9	421	1	SNAA_STRPR
6	7	26.9	825	1	Y240_ARATH
7	7	26.9	961	1	VP2_BRVIA
8	7	26.9	961	1	VP2_BRVIS
9	7	26.9	961	1	VP2_BRVIV
10	6	23.1	96	1	VP2_BRVIV
11	6	23.1	144	1	YDIZ_ECOLI
12	6	23.1	153	1	MAUF_METPL
13	6	23.1	167	1	NUB2_RHIME
14	6	23.1	189	1	INNA4_HUMAN
15	6	23.1	214	1	KAD_YEREN
16	6	23.1	214	1	KAD_YEREP
17	6	23.1	234	1	RADB_METPL
18	6	23.1	258	1	FABI_BACSU
19	6	23.1	269	1	CYST_MESVI
20	6	23.1	285	1	MAUF_METME
21	6	23.1	286	1	Y774_PSEAE
22	6	23.1	295	1	TF_RAT
23	6	23.1	298	1	END4_BACHD
24	6	23.1	333	1	PLSX_BACSU
25	6	23.1	410	1	AUP1_MOUSE
26	6	23.1	422	1	AP47_CAEEL
27	6	23.1	423	1	AIM2_HUMAN
28	6	23.1	423	1	AIM2_MOUSE
29	6	23.1	443	1	MT17_KLUDA
30	6	23.1	489	1	LEF9_NPYOP
31	6	23.1	491	1	AZAP_HUMAN
32	6	23.1	499	1	CPDF_CANRA
33	6	23.1	516	1	LEF9_NPVAC

34	6	23.1	628	1	HCYF_EURCA	09nf15 eurytelma c
35	6	23.1	715	1	ORC3_MOUSE	091x30 mus musculus
36	6	23.1	892	1	MIS5_SCHPO	P49721 schizosacch
37	6	23.1	911	1	CHSG_ASPFU	P34267 aspergillus
38	6	23.1	1058	1	PMAL1_DICDI	P54679 dictyostell
39	6	23.1	1188	1	YEC5_YEAST	P39991 saccharomyc
40	6	23.1	1246	1	YMW2_CAEEL	P34504 caenorhabdi
41	6	23.1	1451	1	SPT6_YEAST	P33615 saccharomyc
42	6	23.1	1636	1	YN37_YEAST	P48553 saccharomyc
43	6	23.1	1877	1	PKK3_RAT	P41413 rattus norv
44	6	23.1	1956	1	ATX1_PLAFA	P04956 plasmodium
45	6	23.1	4563	1	APB_HUMAN	P04114 homo sapien
46	6	19.2	32	1	PETM_PORPU	P51275 porphyra pu
47	5	19.2	45	1	Y5K6_SSV1	P20198 sulfolobus
48	5	19.2	48	1	ATPB_HANMI	P48882 hansenula w
49	5	19.2	63	1	TAC1_BOVIN	P01000 bos taurus
50	5	19.2	74	1	YCS5_HABIN	P44141 haemophilus
51	5	19.2	84	1	VE5_HPV51	P26553 human papil
52	5	19.2	91	1	YVBE_VACCV	P20545 vaccinia vl
53	5	19.2	104	1	DSVC_DESVH	P45573 desulfovibr
54	5	19.2	114	1	CON2_TURCB	P05336 tupatia glis
55	5	19.2	117	1	KV5H_MOUSE	P01641 mus musculu
56	5	19.2	119	1	Y128_STNP6	P05677 synecococc
57	5	19.2	130	1	KV5G_MOUSE	P01639 mus musculu
58	5	19.2	130	1	YQJF_ECOLI	P42619 escherichia
59	5	19.2	131	1	FRDC_ECOLI	P03805 escherichia
60	5	19.2	134	1	YQBL_BACSU	P45928 bacillus su
61	5	19.2	139	1	FXSA_SERMA	P37148 serratia ma
62	5	19.2	140	1	ANF_CHICK	P18908 gallus gall
63	5	19.2	143	1	MK_HUMAN	P21741 homo sapien
64	5	19.2	146	1	AP4A_HUMAN	P50583 homo sapien
65	5	19.2	146	1	AP4A_MOUSE	P56380 mus musculu
66	5	19.2	146	1	AP4A_PIG	P50554 sus scrofa
67	5	19.2	148	1	LYC1_RAT	P00627 rattus norv
68	5	19.2	148	1	LYC2_RAT	P00627 rattus norv
69	5	19.2	150	1	YMEI_STRLN	P55049 streptomyce
70	5	19.2	151	1	DTD_LACIA	O9c192 lactococcus
71	5	19.2	156	1	CYNS_ECO57	P58704 escherichia
72	5	19.2	156	1	CYNS_ECOLI	P00816 escherichia
73	5	19.2	157	1	YTZF_BACSU	O32068 bacillus su
74	5	19.2	159	1	COAD_STRCO	O9zbd1 streptomyce
75	5	19.2	161	1	COAD_AQUAE	O66614 aquiflex aeo

ALIGNMENTS

RESULT 1	CETP_HUMAN	STANDARD:	PRT: 493 AA.
ID	P11597: 013987: 013988:		
AC	P11597: 013987: 013988:		
DT	01-OCT-1989 (Rel. 12, Created)		
DT	01-OCT-1989 (Rel. 12, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Cholesteryl ester transfer protein precursor (Lipid transfer protein 1).		
DE	CETP.		
GN	Homo sapiens (Human).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.		
RX	MEDLINE=87258172: Pubmed=3600759:		
RA	Drayna D., Jarnagin A.S., McLean J., Henzel W., Kohr W., Fielding C.,		
RT	Laun R.,		
RF	"Cloning and sequencing of human cholesteryl ester transfer protein		
RL	cDNA.",		
RL	Nature 327:632-634(1987).		
RP	[2]		
RX	SEQUENCE FROM N.A.,		
RX	MEDLINE=90241928: Pubmed=23347701;		
RA	Agellon L.B., Quinet E.M., Gillette T.G., Drayna D.T., Brown M.L.,		

RA Tall A.R.;
 RT "Organisation of the human cholesteryl ester transfer protein gene";
 RL Biochemistry 29:1372-1376(1990).
 RN [3]
 RP SEQUENCE OF 1-15 FROM N.A.
 RX MEDLINE-97112972; PubMed8943225;
 RA Oliveira C.F.O., Chouinard R.A., Agellon L.B., Bruce C., Ma L.,
 Walsh A., Breslow J.L., Tall A.R.;
 RT "Human cholesteryl ester transfer protein gene proximal promoter
 RT contains dietary cholesterol positive responsive elements and mediates
 RT expression in small intestine and periphery while predominant liver
 RT and spleen expression is controlled by 5'-distal sequences. Cis-acting
 RT sequences mapped in transgenic mice";
 RL J. Biol. Chem. 271:31831-31838(1996).
 RN [4]
 RP SEQUENCE OF 1-27 FROM N.A.
 RX MEDLINE-97473500; PubMed9332354;
 RA Williams S., Hayes L., Eisenboss L., Williams A., Andre C.,
 Abramson R., Thompson J.F., Milos P.M.;
 RT "Sequencing of the cholesteryl ester transfer protein 5' regulatory
 RT region using artificial transposons";
 RL Gene 197:101-107(1997).
 RN [5]
 RP SEQUENCE OF 9-493 FROM N.A.
 RC TISSUE-Liver;
 RA Dinchuk J.E., Hart J.T., Mirak D.O.;
 RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP VARIANT GLY-459.
 RX MEDLINE-94013514; PubMed8408659;
 RA Takahashi K., Jiang X.-C., Sakai N., Yamashita S., Hirano K., Bjorjo H.,
 Yamazaki H., Kusunoki J., Miura T., Kussie P., Matsuzawa Y., Saito Y.,
 Tall A.;
 RT "A missense mutation in the cholesteryl ester transfer protein gene
 RT with possible dominant effects on plasma high density lipoproteins";
 RL J. Clin. Invest. 92:2060-2064(1993)
 CC -1- FUNCTION: CETP IS AN EXTREMELY HYDROPHOBIC PROTEIN INVOLVED IN THE
 CC TRANSFER OF INSOLUBLE CHOLESTERYL ESTERS IN THE REVERSE TRANSPORT
 CC OF CHOLESTEROL.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED MAINLY IN THE LIVER.
 CC -1- DISEASE: PROBABLY INVOLVED IN THE DEVELOPMENT OF ATHEROSCLEROSIS.
 CC -1- SIMILARITY: BELONGS TO THE BPL/CETP/LBP/PLTP FAMILY.
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 CC
 CC -----
 DR EMBL: M30185; AAA51977.1; -
 DR EMBL: M32998; AAA51978.1; -
 DR EMBL: M32992; AAA51978.1; JOINED.
 DR EMBL: M32993; AAA51978.1; JOINED.
 DR EMBL: M32994; AAA51978.1; JOINED.
 DR EMBL: M32995; AAA51978.1; JOINED.
 DR EMBL: M32996; AAA51978.1; JOINED.
 DR EMBL: M32997; AAA51978.1; JOINED.
 DR EMBL: U71187; AAD14876.1; -
 DR EMBL: AF027656; AAB86604.1; -
 DR EMBL: M63573; AAB59388.1; -
 DR PIR: A26941; A26941.
 DR MIM: 118470; -
 DR InterPro: IPR001124; LBP_BPL_CETP.
 DR Pfam: PF02886; LBP_BPL_CETP_C; 1.
 DR SMART: SM00328; BP12; 1.
 DR SMART: SM00329; BP12; 1.
 DR PROSITE: PS00400; LBP_BPL_CETP; 1.
 KW Lipid transport; Cholesterol metabolism; Glycoprotein; Signal;
 KW Atherosclerosis; Disease mutation.

FT SIGNAL 1 17
 FT CHAIN 18 493 CHOLESTERYL ESTER TRANSFER PROTEIN.
 FT CARBOHD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 358 358 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 413 413 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 459 459 D->G (IN CETP DEFICIENCY).
 FT CONFLICT 251 310 /FTID=VAR_004172.
 FT CONFLICT 422 422 MISSING (IN REF. 5).
 FT SEQUENCE 493 AA: 54770 MW: 16D47ACDC99B063C CRC64:
 SQ
 Query Match 100.0%; Score 26; DB 1; Length 493;
 Best Local Similarity 100.0%; Pred. No. 2,5e-19;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RDGFTLLQMDGFPFHLVDFLOSIS 26
 DB 468 RDGFTLLQMDGFPFHLVDFLOSIS 493
 RESULT 2
 CETP_MACFA STANDARD; PRT; 493 AA.
 ID CETP_MACFA
 AC P47896;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Cholesteryl ester transfer protein precursor (Lipid transfer protein
 DE 1).
 GN CETP.
 OS Eukarya fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheinae; Macaca.
 OX NCBI_TaxID=9541;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92031355; PubMed1931878;
 RA Pape M.E., Reiberg E.F., Marotti K.R., Melchior G.W.;
 RT "Molecular cloning, sequence, and expression of cynomolgus monkey
 RT cholesteryl ester transfer protein. Inverse correlation between
 RT hepatic cholesteryl ester transfer protein mRNA levels and plasma
 RT high density lipoprotein levels";
 RL Arterioscler. Thromb. 11:1759-1771(1991).
 CC -1- FUNCTION: CETP IS AN EXTREMELY HYDROPHOBIC PROTEIN INVOLVED IN THE
 CC TRANSFER OF INSOLUBLE CHOLESTERYL ESTERS IN THE REVERSE TRANSPORT
 CC OF CHOLESTEROL.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED MAINLY IN THE LIVER.
 CC -1- SIMILARITY: BELONGS TO THE BPL/CETP/LBP/PLTP FAMILY.
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 CC
 CC -----
 DR EMBL: M6343; AAA36840.1; -
 DR InterPro: IPR001124; LBP_BPL_CETP.
 DR Pfam: PF01273; LBP_BPL_CETP; 1.
 DR Pfam: PF02886; LBP_BPL_CETP_C; 1.
 DR SMART: SM00328; BP12; 1.
 DR SMART: SM00329; BP12; 1.
 DR PROSITE: PS00400; LBP_BPL_CETP; 1.
 KW Lipid transport; Cholesterol metabolism; Glycoprotein; Signal.
 KW SIGNAL 1 17 BY SIMILARITY.
 FT CHAIN 18 493 CHOLESTERYL ESTER TRANSFER PROTEIN.
 FT CARBOHD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 358 358 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 413 413 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 493 AA; 54743 MW; 7E82BE3C2A8FA80D CRC64;

Query Match 100.0%; Score 26; DB 1; Length 493;
 Best Local Similarity 100.0%; Pred. No. 2,5e-19;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RDGFLLQMDFGFPEHLVDFLOSL 26
 DB 468 RDGFLLQMDFGFPEHLVDFLOSL 493

RESULT 3
 CPT_MESAU STANDARD; PRT; 289 AA.
 AC P25914;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Cholesteryl ester transfer protein (Lipid transfer protein I)
 DE (Fragment).
 GN CPTP.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 CC Mesocricetus
 OK NCBI_Taxid=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91154277; PubMed=1999438;
 RA Jiang X.C., Moulin P., Quinet E., Goldberg I.J., Yacoub L.K.,
 RA Aggelon L.B., Compton D., Schnitzer-Polokoff R., Tall A.R.;
 RT "Mammalian adipose tissue and muscle are major sources of lipid
 transfer protein mRNA.";
 RL J. Biol. Chem. 266:4631-4639(1991).
 CC -1- FUNCTION: CPTP IS AN EXTREMELY HYDROPHOBIC PROTEIN INVOLVED IN THE
 TRANSFER OF INSOLUBLE CHOLESTERYL ESTERS IN THE REVERSE TRANSPORT
 OF CHOLESTEROL.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: PLASMA.
 CC -1- SIMILARITY: BELONGS TO THE BPI/CPTP/LBP/PLTP FAMILY.
 CC -----
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 CC -----
 DR EMBL: M63992; AAA37066.1; .
 DR PIR: A38700; A38700.
 DR InterPro: IPR001124; LBP_BPI_CPTP.
 DR Pfam: PF01273; LBP_BPI_CPTP; 1.
 DR Pfam: PF02886; LBP_BPI_CPTP_C; 1.
 DR SMART: SM00329; BPI2; 1.
 DR SMART: SM00329; BPI2; 1.
 DR PROSITE: PS00400; LBP_BPI_CPTP; PARTIAL.
 KW Lipid transport; Cholesterol metabolism; Glycoprotein.
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT NON_TER 1 1
 SQ SEQUENCE 289 AA; 32330 MW; CA91A06D83927747 CRC64;

Query Match 96.2%; Score 25; DB 1; Length 289;
 Best Local Similarity 100.0%; Pred. No. 1,6e-18;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 RDGFLLQMDFGFPEHLVDFLOSL 25
 DB 264 RDGFLLQMDFGFPEHLVDFLOSL 288

RESULT 4
 CPTP_RABIT STANDARD; PRT; 497 AA.
 AC P22687;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Cholesteryl ester transfer protein precursor (Lipid transfer protein
 I) (Fragment).
 GN CPTP.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 CC Oryctolagus
 OK NCBI_Taxid=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89215620; PubMed=3244015;
 RA Nagashima M., McLean J.W., Lawn R.M.;
 RT "Cloning and mRNA tissue distribution of rabbit cholesteryl ester
 transfer protein.";
 RL J. Lipid Res. 29:1643-1649(1988).
 CC -1- FUNCTION: CPTP IS AN EXTREMELY HYDROPHOBIC PROTEIN INVOLVED IN THE
 TRANSFER OF INSOLUBLE CHOLESTERYL ESTERS IN THE REVERSE TRANSPORT
 OF CHOLESTEROL.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED MAINLY IN THE LIVER.
 CC -1- SIMILARITY: BELONGS TO THE BPI/CPTP/LBP/PLTP FAMILY.
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 CC -----
 DR EMBL: M27486; AAA31199.1; .
 DR InterPro: IPR001124; LBP_BPI_CPTP.
 DR Pfam: PF01273; LBP_BPI_CPTP; 1.
 DR Pfam: PF02886; LBP_BPI_CPTP_C; 2.
 DR SMART: SM00328; BPI1; 1.
 DR SMART: SM00329; BPI2; 1.
 DR PROSITE: PS00400; LBP_BPI_CPTP; 1.
 KW Lipid transport; Cholesterol metabolism; Glycoprotein; Signal.
 FT SIGNAL 1 1
 FT CHAIN 2 497
 FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 417 417 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 497 AA; 54513 MW; E82944E1821D0332 CRC64;

Query Match 42.3%; Score 11; DB 1; Length 497;
 Best Local Similarity 100.0%; Pred. No. 0.00047;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 16 HLIVDFLOSL 26
 DB 487 HLIVDFLOSL 497

RESULT 5
 SNAI_STRPR STANDARD; PRT; 421 AA.
 ID SNAI_STRPR
 AC P54991;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)

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DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Pristinamycin IIA synthase subunit A (PIIA synthase subunit A).
GN SNA.
OS Streptomyces pristinaespiralis.
OC Bacteria: Firmicutes: Actinobacteria: Actinobacteridae;
OC Actinomycetales: Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=38300;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP92;
RC MEDLINE=95394837; PubMed=7665509;
RA Blanc V., Lagneaux D., Didier P., Lacroix P., Crouzet J.;
RT "Cloning and analysis of structural genes from Streptomyces
RT pristinaespiralis encoding enzymes involved in the conversion of
RT pristinaespiralin IIB to pristinaespiralin IIA (PIIA): PIIA synthase and
RT NADH:riboflavin 5'-phosphate oxidoreductase.";
RL J. Bacteriol. 177:5206-5214(1995).
RN [2]
RP SEQUENCE OF 1-18 AND 364-383.
RX MEDLINE=95394836; PubMed=7665508;
RA Thibaut D., Kater N., Bischoff D., Faucher D., Debussche L., Blanche F.;
RT "Purification of the two-enzyme system catalyzing the oxidation of
RT the D-proline residue of pristinaespiralin IIB during the last step of
RT pristinaespiralin IIA biosynthesis.";
RL J. Bacteriol. 177:5199-5205(1995).
CC -1- FUNCTION: CATALYZES THE OXIDATION OF THE PROLINE RESIDUE OF
CC PRISTINAMYCIN IIB (PIIB) TO PRISTINAMYCIN IIA (PIIA).
CC -1- COFACTOR: FMN.
CC -1- SUBUNIT: HETERODIMER OF TWO SUBUNITS, SNA AND SNAH.
CC -1- SIMILARITY: BELONGS TO THE NTRAA/SNAA/SOXA/OSXA FAMILY OF
CC MONOOXYGENASES.
CC -----
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CC -----
DR EMBL: U21215; AAA83563.1;
DR InterPro: IPR002103; Bac_Luciferase.
DR Pfam: PF00296; bac_Luciferase; 1.
KW Oxidoreductase; Monooxygenase; Flavoprotein; FMN.
FT INTR MET 0
SQ SEQUENCE 421 AA; 46373 MW; 341AD008A939ECFA CRC64;

Query Match 26.9%; Score 7; DB 1; Length 421;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GCPPEHL 17
Db 142 GCPPEHL 148

RESULT 6
Y240 ARATH STANDARD; PRT: 825 AA.
AC Q22224;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Protein At2g41620.
DE AT2G41620 OR T3266.14.
GN Arabidopsis thaliana (Mouse-ear cress).
OS Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustoids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronald K.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carreira A.J., Cressy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Niernan W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
RN [2]
RP IDENTIFICATION ON 2D-CELS.
RC STRAIN=CV. COLUMBIA;
RA Serrazin B., Sanchez J.-C., Hochstrasser D., Thiellement H.;
RA Heller M., Sanchez J.-C., Hochstrasser D., Thiellement H.;
RL Unpublished observations (Sep-2000).
CC -----
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CC -----
DR EMBL: AC002510; AB84345.1;
DR SEQUENCE 825 AA; 92304 MW; 1032300E814F6DAB CRC64;

Query Match 26.9%; Score 7; DB 1; Length 825;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DFLQSL 26
Db 155 DFLQSL 161

RESULT 7
VP2_BTVIA STANDARD; PRT: 961 AA.
AC P12434;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Outer capsid protein VP2.
GN S2.
OS Bluetongue virus (serotype 1 / isolate Australia).
OC Viruses: dsRNA viruses; Reoviridae; Orbivirus.
OX NCBI_TaxID=10904;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88203217; PubMed=2834696;
RA Yamaguchi S., Fukusho A., Roy P.;
RT "Complete sequence of VP2 gene of the bluetongue virus serotype 1
RT (BTV-1).";
RL Nucleic Acids Res. 16:2725-2725(1988).
RN [2]
RP REVISIONS.
RA Marshall J.;
RL Submitted (FEB-1988) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88180013; PubMed=2833046;
RA Gould A.R.;
RT "Conserved and non-conserved regions of the outer coat protein, VP2,
RT of the Australian bluetongue serotype 1 virus, revealed by sequence
RT comparison to the VP2 of North American BTV serotype 10.";
RL Virus Res. 9:145-158(1988).
CC -1- FUNCTION: THE VP2 PROTEIN IS ONE OF THE TWO PROTEINS (WITH VP5)

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CC WHICH CONSTITUTE THE VIRUS PARTICLE OUTER CAPSID. IT IS THE
CC MAJOR TARGET OF THE HOST IMMUNOGENIC RESPONSE.
CC -1- SIMILARITY: BELONGS TO THE REOVIRUSES VP2 FAMILY.
CC -----
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CC -----
CC EMBL: X06664; CAA29772.1; -
CC EMBL: M21844; AAA42844.1; -
CC PIR: S03654; P2XRAD.
CC InterPro: IPR001742; Orbl_VP2.
CC Pfam: PF00898; Orbl_VP2; 1.
CC ProDom: PD002938; Orbl_VP2; 1.
CC Coat protein. 13
CC CONFLICT 13 13 F -> V (IN REF. 3).
CC CONFLICT 72 72 L -> V (IN REF. 3).
CC CONFLICT 186 188 AVA -> LTL (IN REF. 3).
CC CONFLICT 200 200 E -> D (IN REF. 3).
CC CONFLICT 557 557 A -> D (IN REF. 3).
CC CONFLICT 750 750 D -> N (IN REF. 3).
CC SEQUENCE 961 AA; 112113 MW; 1D408D3906ACD80 CRC64;

Query Match 26.9%; Score 7; DB 1; Length 961;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GPEPHLL 18
DB 12 GPEPHLL 18

RESULT 8
VP2_BTV1S
ID VP2_BTV1S STANDARD; PRT; 961 AA.
AC P32508;
RA 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DR 15-DEC-1998 (Rel. 37, Last annotation update)
DE Outer capsid protein VP2.
GN S2.
OS Bluetongue virus (serotype 1 / Isolate South Africa).
OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.
OX NCBI_TaxID=10905;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 322-346 AND 492-503.
RA MEDLINE-90261331; PubMed-2160764;
RA Wade-Evans A.M.; Mertens P.P.C.;
RT *Expression of the outer capsid protein, VP2, from a full length cDNA
RT clone of genome segment 2 of bluetongue serotype 1 from South Africa,
RT using both Sp6 and vaccinia expression systems and a comparison of
RT the nucleic acid sequence of this segment with those of other
RT serotypes.*
RT Virus Res. 15:213-230(1990).
CC -1- FUNCTION: THE VP2 PROTEIN IS ONE OF THE TWO PROTEINS (WITH VP5)
CC MAJOR CONSTITUTE THE VIRUS PARTICLE OUTER CAPSID. IT IS THE
CC MAJOR TARGET OF THE HOST IMMUNOGENIC RESPONSE.
CC -1- SIMILARITY: BELONGS TO THE REOVIRUSES VP2 FAMILY.
CC PIR: A60014; P2XRSA.
CC InterPro: IPR001742; Orbl_VP2.
CC Pfam: PF00898; Orbl_VP2; 1.
CC ProDom: PD002938; Orbl_VP2; 1.
CC Coat protein.
CC SEQUENCE 961 AA; 111937 MW; CB8753598BFD197A CRC64;

Query Match 26.9%; Score 7; DB 1; Length 961;
Best Local Similarity 100.0%; Pred. No. 9.9;

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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GPEPHLL 18
DB 12 GPEPHLL 18

RESULT 9
VP2_BTV1V
ID VP2_BTV1V STANDARD; PRT; 961 AA.
AC 006997;
RA 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DR 15-DEC-1998 (Rel. 37, Last annotation update)
DE Outer capsid protein VP2.
GN S2.
OS Bluetongue virus (serotype 1 / Isolate South Africa-vaccine).
OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.
OX NCBI_TaxID=36422;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-91021485; PubMed-2171239;
RA Gould A.R.; Pritchard L.I.;
RT *Relationships amongst bluetongue viruses revealed by comparisons of
RT capsid and outer coat protein nucleotide sequences.*
RT Virus Res. 17:31-52(1990).
CC -1- FUNCTION: THE VP2 PROTEIN IS ONE OF THE TWO PROTEINS (WITH VP5)
CC WHICH CONSTITUTE THE VIRUS PARTICLE OUTER CAPSID. IT IS THE
CC MAJOR TARGET OF THE HOST IMMUNOGENIC RESPONSE.
CC -1- SIMILARITY: BELONGS TO THE REOVIRUSES VP2 FAMILY.
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CC -----
CC EMBL: X55800; CAA9322.1; -
CC PIR: A60017;
CC InterPro: IPR001742; Orbl_VP2.
CC Pfam: PF00898; Orbl_VP2; 1.
CC ProDom: PD002938; Orbl_VP2; 1.
CC Coat protein.
CC SEQUENCE 961 AA; 111756 MW; 361405246E7E946 CRC64;

Query Match 26.9%; Score 7; DB 1; Length 961;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GPEPHLL 18
DB 12 GPEPHLL 18

RESULT 10
YD12_ECOLI
ID YD12_ECOLI STANDARD; PRT; 96 AA.
AC P76207;
RA 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DR 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yd12.
GN YD12 OR B1724 OR Z2753 OR ECS2430.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562; 83334;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blatter F.R., Plunkett G., Ili, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / FDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G., Ili, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533(2001).
RN [13]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kihara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 8:11-22(2001).
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CC -----
CC EMBL: AE000267; AAC74794.1; -
DR EMBL: AE005395; AAG56710.1; -
DR EMBL: AP002558; BAB35853.1; -
DR Ecogene: BG13985; yd12.
KW Hypothetical protein: Complete proteome.
SQ SEQUENCE 96 AA; 10865 MW; 722C0F845B91A855 CRC64;

Query Match 23.1%; Score 6; DB 1; Length 96;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLL 6
Db 32 RDGFLL 37

RESULT 11
Y638 TREPA STANDARD: PRT; 144 AA.
AC 083645;
DT 16-OCT-2001 (rel. 40, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE Hypothetical protein TP0638.
GN TP0638.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX NCB1_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NICHOLS;
DR MEDLINE=98332770; PubMed=9665876;

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RA Fraser C.M., Norris S.J., Melnick G.M., White O., Sutton G.G.,
RA Dodson R., Gwin M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham U.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Childsberg M., Utechtack T.,
RA McDonald L., Artlich P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete."
RL Science 281:375-388(1998).
RN [1]
RP SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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CC -----
CC EMBL: AE001239; AAC65625.1; -
DR TIGR: TP0638; -
KW Hypothetical protein: Transmembrane; Complete proteome.
FT TRANSMEM 7
FT TRANSMEM 29
FT TRANSMEM 51
FT TRANSMEM 73
FT TRANSMEM 85
FT TRANSMEM 107
FT TRANSMEM 122
FT TRANSMEM 139
SQ SEQUENCE 144 AA; 15394 MW; 7D93DA0921FC7699 CRC64;

Query Match 23.1%; Score 6; DB 1; Length 144;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 LTVDFL 22
Db 71 LTVDFL 76

RESULT 12
MAUF METFL
ID MAUF METFL STANDARD: PRT; 153 AA.
AC 050418; 050419;
DT 01-NOV-1997 (rel. 35, Created)
DT 01-NOV-1997 (rel. 35, Last sequence update)
DT 01-NOV-1997 (rel. 35, Last annotation update)
DT 01-MAR-2002 (rel. 41, Last annotation update)
DE Methylamine utilization protein mauF (fragments).
GN MAUF.
OS Methylobacillus flagellatum.
OC Bacteria; Proteobacteria; beta subdivision; Methylobacillus group;
OC Methylobacillus.
OX NCB1_TaxID=405;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KT / ATCC 51484 / DSM 6875 / VKM B-1610;
RX MEDLINE=95362696; PubMed=7635847;
RA Gak E.R., Chistoserdov A.Y., Lidstrom M.E.;
RT "Cloning, sequencing, and mutation of a gene for azurin in
RT Methylobacillus flagellatum KT."
RL J. Bacteriol. 177:4575-4578(1995).
CC [1]
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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CC -----
CC EMBL: L37428; AAC41467.1; -
DR EMBL: AF188997; AAC41468.1; -

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Transmembrane.
 FT TRANSMEM 37 57 POTENTIAL.
 FT TRANSMEM 58 78 POTENTIAL.
 FT TRANSMEM 114 115
 FT TRANSMEM 127 147 POTENTIAL.
 SO SEQUENCE 153 AA; 15761 MW; 200689C3A706674 CRC64;

Query Match 23.1%; Score 6; DB 1; Length 153;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGFLL 7
 DB 131 DGFLL 136

RESULT 13
 NUB2_RHIME STANDARD; PRT; 167 AA.
 AC P56897;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE NADH dehydrogenase I chain B 2 (EC 1.6.5.3) (NADH-ubiquinone
 oxidoreductase chain B 2).
 GN NUB2 OR RA0833 OR SMA1532.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Plasmid pSym (megaplasmid 1).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=41;
 RA Putnoky P., Jady B., Chellapilla K.P., Barta F., Kiss E.;
 RT "Rhizobium meliloti carries two sets of nro genes.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21396509; Pubmed=11481432;
 RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
 RA Barloy-Hubler F., Bowser L., Cepeda D., Galibert F., Gonzy J.,
 RA Gurjal M., Hong A., Hutzar L., Hyman R.W., Kahn D., Kahn M.L.,
 RA Kaiman S., Keating D.H., Palm C., Peck M.C., Surtzcki R., Wells D.H.,
 RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
 RT "Nucleotide sequence and predicted functions of the entire
 Sinorhizobium meliloti pSym megaplasmid.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
 CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone -> NAD(+) + ubiquinol.
 CC -1- COFACTOR: MAY CONTAIN AN IRON-SULFUR 4FE-4S CLUSTER.
 CC -1- SIMILARITY: BELONGS TO THE COMPLEX I 20 kDa SUBUNIT FAMILY.
 CC -----
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 CC -----
 CC EMBL: AJ245399; CAB51630.1; -;
 DR EMBL: AE007270; CAK65491.1; -;
 DR InterPro: IPR002096; Complex1_20KD.
 DR Pfam: PF01058; oxidored_6; 1.
 KM Oxidoreductase; NAD; Ubiquinone; Iron-sulfur; 4Fe-4S; Plasmid;
 KM Complete proteome.
 FT METAL 38 38 IRON-SULFUR (4FE-4S) (POTENTIAL).
 FT METAL 39 39 IRON-SULFUR (4FE-4S) (POTENTIAL).
 FT METAL 103 103 IRON-SULFUR (4FE-4S) (POTENTIAL).
 FT METAL 132 132 IRON-SULFUR (4FE-4S) (POTENTIAL).
 FT CONFLICT 167 167 S -> L (IN REF. 1).

SQ SEQUENCE 167 AA; 18247 MW; 04D82AAED624D8CF CRC64;

Query Match 23.1%; Score 6; DB 1; Length 167;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFLLLQ 8
 DB 142 GFLLLQ 147

RESULT 14
 INA4_HUMAN STANDARD; PRT; 189 AA.
 ID INA4_HUMAN
 AC P05014; P13358;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Interferon alpha-4 precursor (interferon alpha-4B) (Interferon
 alpha-M1) (interferon alpha-7b).
 GN IFNA4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86037205; Pubmed=4057246;
 RA Henco K., Brosius J., Fujisawa J.-I., Haynes J.R.,
 RA Hochstadt J., Kovacic T., Pasek M., Schambeck A., Schmid J.,
 RA Todokoro K., Waelchli M., Nagata S., Weissmann C.;
 RT "Structural relationship of human interferon alpha genes and
 RT pseudogenes.";
 RL J. Mol. Biol. 185:227-260(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84307815; Pubmed=6089830;
 RA Linnane A.W., Bellhaz M.W., McMullen G.T., Macreadie I.G.,
 RA Murphy M., Nisbet I.T., Novitski C.E., Woodrow G.C.;
 RT "Nucleotide sequence and expression in E. coli of a human interferon-
 RT alpha gene selected from a genomic library using synthetic
 RT oligonucleotides.";
 RL Biochem. Int. 8:725-732(1984).
 CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
 CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
 CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.
 CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
 CC FAMILY.
 CC -----
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 CC -----
 CC EMBL: X02955; CAA26701.1; -;
 DR EMBL: M27318; AAA52726.1; -;
 DR PIR: E23753; IYH04B.
 DR HSSP: P01563; 2HIE.
 DR MIM: 147564; -;
 DR InterPro: IPR000471; Interferon_abd.
 DR Pfam: PF00143; Interferon_1.
 DR PRINTS: PR00266; INTERFERONAB.
 DR ProDom: PD000550; Interferon_abd; 1.
 DR SMART: SM00076; Ifabd; 1.
 DR PROSITE: PS00252; INTERFERON_A-B-D; 1.
 KM Cytokine; Antiviral; Multigene family; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 189 INTERFERON ALPHA-4.
 FT DISULFID 24 122 BY SIMILARITY.

FT DISUFLID 52 162 BY SIMILARITY.
 FT CONFLICT 74 74 T -> A (IN REF. 2).
 FT CONFLICT 137 137 V -> E (IN REF. 2).
 SO SEQUENCE 189 AA; 21808 MW; 4198F9CC8E2AE80C CRC64;

Query Match 23.1%; Score 6; DB 1; Length 189;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 DFGPE 15
 DB 58 DFGPE 63

RESULT 15
 KAD_YEREN STANDARD; PRT; 214 AA.

AC P43412; 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
 GN ADK.
 OS *Yersinia enterocolitica*.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC *Yersinia*.
 OX NCBI_TaxID=630;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=6471/76 / SEROTYPE O:3;
 RX MEDLINE=96100456; PubMed=8559076;
 RA Skurnik M., Venho R., Toivanen P., Al-Hendy A.;
 RT "A novel locus of *Yersinia enterocolitica* serotype O:3 involved in
 RT lipopolysaccharide outer core biosynthesis.";
 RL Mol. Microbiol. 17:575-594(1995).
 CC -1- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
 CC MAINTENANCE AND CELL GROWTH.
 CC -1- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
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 CC -----
 DR EMBL: Z47767; CAA87696.1; .
 DR HSP: P05082; IAKE.
 DR InterPro: IPR000850; Adenylate_kin.
 DR Pfam: PF00406; adenylatekinase.1.
 DR PRINTS: PR00094; ADENYLTKINASE.
 DR ProDom: PD000657; Adenylate_kin.1.
 DR PROSITE: PS00113; ADENYLATE_KINASE; FALSE_NEG.
 KW Transferase; Kinase; ATP-binding.
 FT NP_BIND 7
 FT SEQUENCE 214 AA; 23755 MW; 55030EA82BDDAC7 CRC64;

Query Match 23.1%; Score 6; DB 1; Length 214;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLL 6
 DB 78 RDGFLL 83

RESULT 16

KAD_YERPE STANDARD; PRT; 214 AA.
 AC O69172; 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
 GN ADK OR YPO3118.
 OS *Yersinia pestis*.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC *Yersinia*.
 OX NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Munier-Lehmann H.;
 RT "Adenylate kinase from *Yersinia pestis* and *Escherichia coli*:
 RT structural relatedness and differences linked to growth properties of
 RT these two organisms.";
 RL Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.
 RN [2]

RP SPROUCE FROM N.A.
 RC STRAIN=CO-92 / Biovar Orientalis;
 RX MEDLINE=21470413; PubMed=11586360;
 RA Parhill J., Wren B.W., Thomson N.R., Tibball R.W., Holden M.T.G.,
 RA Prentice M.B., Sebald M., James K.D., Churcher C., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Felwell T., Hamlin N., Holroyd S., Jagsels K., Kariyasev A.V.,
 RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
 RT "Genome sequence of *Yersinia pestis*, the causative agent of plague.";
 RL Nature 413:523-527(2001).
 CC -1- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
 CC MAINTENANCE AND CELL GROWTH.
 CC -1- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: AF065382; AAC17436.1; .
 DR EMBL: AJ14155; CAC92354.1; .
 DR HSP: P05082; IAKE.
 DR InterPro: IPR000850; Adenylate_kin.
 DR Pfam: PF00406; adenylatekinase.1.
 DR PRINTS: PR00094; ADENYLTKINASE.
 DR ProDom: PD000657; Adenylate_kin.1.
 DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
 KW Transferase; Kinase; ATP-binding; Complete proteome.
 FT NP_BIND 7
 FT SEQUENCE 214 AA; 23672 MW; 36D9PD13558B86CA CRC64;

Query Match 23.1%; Score 6; DB 1; Length 214;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLL 6
 DB 78 RDGFLL 83

RESULT 17
 RADB_METTH STANDARD; PRT; 234 AA.
 ID RADB_METTH
 AC O27728;

```

DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA repair and recombination protein radB.
GN RADB OR MTH1693.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC Methanothermobacter.
ON NCBI_TaxID=145262;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DELTA H.
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Delonghery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vlcare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Safer H., Patel D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT delta: functional analysis and comparative genomics.";
RL J. Bacteriol. 179.7135-7155(1997).
CC -1- FUNCTION: Involved in DNA repair and in homologous recombination.
CC May regulate the cleavage reactions of the branch-structured DNA.
CC Has a very weak ATPase activity that is not stimulated by DNA.
CC Binds DNA but does not promote DNA strand exchange (by
CC similarity).
CC -1- SIMILARITY: BELONGS TO THE EUKARYOTIC RECA-LIKE PROTEIN FAMILY.
CC RADB SUBFAMILY.
CC -----
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CC -----
DR EMBL: AE000927; AAB86165.1; -.
DR HSSP: P03017; 2REB.
DR InterPro: IPR001553; RECA.
DR PRINTS: PR00142; RECA.
DR PROSITE: PS0162; RECA_2; 1.
KW DNA damage; DNA recombination; ATP-binding; DNA-binding;
KM Complete proteome.
FT NP_BIND 37 44 ATP (POTENTIAL).
SQ SEQUENCE 234 AA; 26193 MW; ED4D957A012AAD1F CRC64;

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Query Match 23.1%; Score 6; DB 1; Length 234;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 FLLLOM 9
 Db 150 FLLLOM 155

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RESULT 18
FABI_BACSU STANDARD; PRT; 258 AA.
AC P54616; O31621;
DT 01-OCT-1996 (Rel. 34, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Enoyl-[acyl-carrier-protein] reductase [NADH] (EC 1.3.1.9) (NADH-
DE dependent enoyl-ACP reductase) (Cold-shock induced protein 15) (CS115)
DE (Vegetative protein 241) (VEG241).
GN FABI.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.

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OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DDA databases.
RN [2]
RP SEQUENCE OF 1-21.
RC STRAIN=168; JH642;
RX MEDLINE=96345629; PubMed=8755892;
RA Graumann P., Schroeder K., Schmid R., Marahel M.A.;
RT "Cold shock stress-induced proteins in Bacillus subtilis.";
RL J. Bacteriol. 178:4611-4619(1996).
RN [3]
RP SEQUENCE OF 1-15.
RC STRAIN=IS58;
RX MEDLINE=97443988; PubMed=9298659;
RA Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
RA Hecker M.;
RT "First steps from a two-dimensional protein index towards a response-
RT regulation map for Bacillus subtilis.";
RL Electrophoresis 18:1451-1463(1997).
CC -1- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + NAD(+) = trans-
CC 2,3-dehydroacyl-[acyl-carrier protein] + NADH.
CC -1- PATHWAY: SECOND REDUCTIVE STEP IN FATTY ACID BIOSYNTHESIS.
CC -1- INDUCTION: BY COLD SHOCK.
CC -1- SIMILARITY: SOME SIMILARITY TO THE SHORT-CHAIN
CC DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
CC -----
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CC -----
DR EMBL: Z99110; CAB13029.1; ALT_INIT.
DR HSSP: P29132; IDFI.
DR Subtilist; BG13152; fabI.
DR InterPro: IPR002198; ADH_short.
DR Pfam: PF00106; adh_short; 1.
DR PRINTS: PR00061; GDRHDH.
KW Oxidoreductase; NAD; Fatty acid biosynthesis; Complete proteome.
FT NP_BIND 11 37 NAD (BY SIMILARITY).
FT CONFLICT 20 20 S -> Q (IN REF. 2).
SQ SEQUENCE 258 AA; 27873 MW; 097667166B3F0470 CRC64;

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Query Match 23.1%; Score 6; DB 1; Length 258;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLL 6
 Db 112 RDGFLL 117

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RESULT 19
CYST_MESVI STANDARD; PRT; 269 AA.
AC Q9WUL9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable sulfate transport system permease protein cyst.
GN CYST.
OS Mesostigma viride.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Mesostigmatophyceae;
OC Mesostigmatales; Mesostigmataceae; Mesostigma.
OX NCBI_TaxID=41882;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN-NISS-286;
RA MEDLINE=20150907; PubMed-10688199;
RT Lemieux C., Odis C., Turmel M.;
RT "ancestral chloroplast genome in Mesostigma viride reveals an early
RT branch of green plant evolution.";
RL Nature 403:649-652(2000).
CC -1- FUNCTION: COULD BE PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT
CC SYSTEM FOR SULFATE AND THIOSULFATE. PROBABLY RESPONSIBLE FOR THE
CC TRANSLLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST; INTEGRAL MEMBRANE PROTEIN
CC (PROBABLE).
CC -1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
CC PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE CYSTM
CC SUBFAMILY.
CC -----
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CC -----
DR EMBL: AF166114; AAF43879.1; -.
DR InterPro: IPR000515; BPD.transp.
DR Pfam: PF00528; BPD.transp.1.
DR PROSITE: PS00402; BPD_TRANSF_INN_MEMBER.1.
KW Chloroplast; Sulfate transport; Transport; Transmembrane.
FT TRANSMEM 11 31 POTENTIAL.
FT TRANSMEM 60 80 POTENTIAL.
FT TRANSMEM 92 112 POTENTIAL.
FT TRANSMEM 130 150 POTENTIAL.
FT TRANSMEM 179 199 POTENTIAL.
FT TRANSMEM 208 228 POTENTIAL.
FT TRANSMEM 240 260 POTENTIAL.
SQ SEQUENCE 269 AA; 29674 MW; B20DBFPD486C59 CRC64;

Query Match 23.1%; Score 6; DB 1; Length 269;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 FLOSLS 26
Db 122 FLOSLS 127

RESULT 20
MAUF METME STANDARD; PRT; 285 AA.
AC 050230;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Methylamine utilization protein mauF.
GN MAUF.
OS Methylphilus methylotrophus (Bacterium W3A1).
OC Bacteria; Proteobacteria; beta subdivision; Methylophilus group;
OC Methylophilus.
OX NCBI_TaxID=17;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94292427; PubMed-8021188;
RA Chisosevov A.Y., McIntire W.S., Mathews F.S., Lidstrom M.E.;
RT "Organisation of the methylamine utilization (mau) genes in
RT Methylphilus methylotrophus W3A1-NS.";
RL J. Bacteriol. 176:4073-4080(1994).
CC -1- PATHWAY: METHYLAMINE UTILIZATION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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CC -----
DR EMBL: L26407; AAB46947.1; -.
KW Transmembrane.
FT TRANSMEM 39 59 POTENTIAL.
FT TRANSMEM 60 80 POTENTIAL.
FT TRANSMEM 119 139 POTENTIAL.
FT TRANSMEM 145 165 POTENTIAL.
FT TRANSMEM 188 208 POTENTIAL.
FT TRANSMEM 212 232 POTENTIAL.
FT TRANSMEM 265 285 POTENTIAL.
SQ SEQUENCE 285 AA; 30429 MW; 7A783207084879AD CRC64;

Query Match 23.1%; Score 6; DB 1; Length 285;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGFLL 7
Db 268 DGFLL 273

RESULT 21
YY74_PSEAE STANDARD; PRT; 286 AA.
AC 068826;
DT 15-DEC-1998 (Rel. 37, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein PA3474.
DE PA3474.
GN Pseudomonas aeruginosa.
OS Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 15692 / PA01;
RA Xie G., Jensen R.A.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 15692 / PA01;
RA MEDLINE=20437337; PubMed-10984043;
RA Stover C.K., Pham X.-Q.T., Ervin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reller J., Slier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -----
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CC -----
DR EMBL: AF054868; AAC08597.1; -.
DR EMBL: AE004768; AAG06862.1; -.
DR InterPro: IPR000620; DUF6.
DR Pfam: PF00892; DUF6.2.
KW Hypothetical protein; Complete proteome.
CC CONFLICT 27 27 D -> G (IN REF. 1).

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FT CONFLICT 35 35 R -> P (IN REF. 1).
FT CONFLICT 236 236 A -> V (IN REF. 1).
FT CONFLICT 255 255 N -> Y (IN REF. 1).
FT CONFLICT 261 261 P -> L (IN REF. 1).
FT CONFLICT 264 264 A -> V (IN REF. 1).
FT CONFLICT 282 282 R -> G (IN REF. 1).
SQ SEQUENCE 286 AA; 31834 MW; C84001C649BEE9CE CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFLIIO 8
DB 139 GFLIIO 144

RESULT 22
TF_RAT STANDARD; PRT; 295 AA.
ID TF_RAT
AC P42533.
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Tissue factor precursor (TF) (Coagulation factor III).
GN CFB3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
ON NCBI_TaxID=10116;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RC Rosenfield C., Guha A., Nemerson Y., Taubman M.B.;
RA Submitted (MAR-1994) to the EMBL/GenBank/DBS databases.
CC -1- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH
CC CIRCULATING FACTOR VII OR VIIA. THE (TF.VIIA) COMPLEX ACTIVATES
CC FACTORS IX OR X BY SPECIFIC LIMITED PROTEOLYSIS. TF PLAYS A ROLE IN
CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND
CC PROPAGATION OF THE COAGULATION PROTEASE CASCADE.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.
-----
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-----
CC
CC EMBL: U07619; AAA16966.1; -.
CC HSSP: P13726; ITHF.
CC InterPro: IPR000282; Cytok_receptor_2.
CC InterPro: IPR001187; Tissue_fac.
CC Pfam: PF01108; Tissue_fac.1
CC PRINTS: PR00346; TISSUEFACTOR.
CC PROSITE: PS00621; TISSUE_FACTOR; 1.
CC Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;
CC Palmitate.
CC
CC FT SIGNAL 1 28 BY SIMILARITY.
CC FT CHAIN 29 295 TISSUE FACTOR.
CC FT DOMAIN 29 252 EXTRACELLULAR (POTENTIAL).
CC FT TRAMSMEM 253 275 POTENTIAL.
CC FT DOMAIN 276 295 CYTOPLASMIC (POTENTIAL).
CC FT SITE 246 248 WKS MOTIF.
CC FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 58 58 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT DISULFID 76 84 BY SIMILARITY.
FT DISULFID 219 242 BY SIMILARITY.
FT LIPID 276 276 PALMITATE (BY SIMILARITY).
SQ SEQUENCE 295 AA; 33443 MW; EE4C15BAE362BD48 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFLIIO 8
DB 19 GFLIIO 24

RESULT 23
END4_BACHD STANDARD; PRT; 298 AA.
ID END4_BACHD
AC O9KD33.
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Probable endonuclease IV (EC 3.1.21.2) (Endodeoxyribonuclease IV).
GN NFO OR BH1386.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
ON NCBI_TaxID=8665;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C-125 / JCM 9153;
RC MEDLINE=20512582; PubMed=11058132;
RX Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RX Fuji F., Hirama C., Nakamura Y., Ogawara N., Kuhara S.,
RX Horikoshi K.;
RA "Complete genome sequence of the alkaliphilic bacterium Bacillus
RA halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -1- FUNCTION: Endonuclease IV plays a role in DNA repair. It cleaves
CC phosphodiester bonds at apurinic or apyrimidinic sites (AP sites)
CC to produce new 5' ends that are base-free deoxyribose 5-phosphate
CC residues. It preferentially attacks modified AP sites created by
CC bleomycin and neocarzinostatin (By similarity).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
CC phosphooligonucleotide end-products.
CC -1- COFACTOR: Binds 3 zinc ions (By similarity).
CC -1- SIMILARITY: BELONGS TO AP ENDONUCLEASES FAMILY 2.
-----
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-----
CC
CC EMBL: AP001511; BAB05105.1; -.
CC HSSP: P12638; IOTW.
CC InterPro: IPR001719; AP_endonuclease_2.
CC Pfam: PF01261; AP_endonuclease2; 1.
CC SMART: SM00518; AP2ec; 1.
CC PROSITE: PS00729; AP_NUCLEASE_F2_1; 1.
CC PROSITE: PS00730; AP_NUCLEASE_F2_2; 1.
CC PROSITE: PS00731; AP_NUCLEASE_F2_3; 1.
CC Hydrolase; Nuclease; Endonuclease; DNA repair; Metal-binding; Zinc;
CC Complete proteome.
CC
CC FT METAL 70 70 ZINC 1 (BY SIMILARITY).
CC FT METAL 111 111 ZINC 1 (BY SIMILARITY).
CC FT METAL 146 146 ZINC 1 AND 2 (BY SIMILARITY).
CC FT METAL 180 180 ZINC 2 (BY SIMILARITY).
CC FT METAL 183 183 ZINC 3 (BY SIMILARITY).
CC FT METAL 215 215 ZINC 2 (BY SIMILARITY).
CC FT METAL 228 228 ZINC 3 (BY SIMILARITY).

```

FT METAL 230 230 ZINC 3 (BY SIMILARITY).
 FT METAL 260 260 ZINC 2 (BY SIMILARITY).
 SQ SEQUENCE 298 AA; 32997 MW; 9A25ED81A755B4B CRC64;

Query Match 23.1%; Score 6; DB 1; Length 298;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 VDFLOS 24
 |||||
 Db 90 VDFLOS 95

RESULT 24
 PLSX_BACSU STANDARD; PRT: 333 AA.
 ID PLSX_BACSU
 AC P71018: 034561; (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Fatty acid/phospholipid synthesis protein p1sx.
 GN PLSX.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 CC Bacillus/Staphylococcus group; Bacillus.
 OK NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE OF 66-333 FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=96326321; PubMed=8759840;
 RA Morbidoni H.R., de Mendoza D., Cronan J.E. Jr.;
 RT "Bacillus subtilis acyl carrier protein is encoded in a cluster of
 RT 1 lipid biosynthesis genes.";
 RT J. Bacteriol. 178:4794-4800(1996).
 RL [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=168;
 RA Foulger D., Errington J.;
 RL Submitted (AUG-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: NOT KNOWN. PROBABLY INVOLVED IN FATTY ACID OR
 CC -1- PHOSPHOLIPID SYNTHESIS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PLSX FAMILY.
 CC -----
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 CC -----
 DR EMBL: U59433; AAC44305.1; -;
 DR EMBL: Y13937; CAAT74248.1; -;
 DR EMBL: Z59112; CAB3462.1; -;
 DR Subtilist; Bg11843; p1sx.
 DR InterPro: IPR003664; FA_synthesis.
 DR Pfam: PF02304; FA_synthesis; 1.
 KW Fatty acid biosynthesis; Phospholipid biosynthesis; Complete proteome.
 FT CONFLICT 66
 GN DEPVAVRR -> MNRSPVCEA (IN REF. 1).
 SQ SEQUENCE 333 AA; 35763 MW; 2F6A2E8A034199E CRC64;

Query Match 23.1%; Score 6; DB 1; Length 333;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGFLL 7
 |||||
 Db 133 DGFLL 138

RESULT 25

AUPL_MOUSE
 ID AUPL_MOUSE STANDARD; PRT: 410 AA.
 AC P70295;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ancient ubiquitous protein 1 precursor.
 GN AUPL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OK NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=96441699; PubMed=8812468;
 RA Jang W., Weber J.S., Bashir R., Bushby K., Meister M.H.;
 RT "AuPL, a novel gene on mouse chromosome 6 and human chromosome 2p13.";
 RL Genomics 36:366-368(1996).
 CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
 CC -1- SIMILARITY: BELONGS TO THE AUPL FAMILY.
 CC -----
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 CC -----
 DR EMBL: U41736; AAC52839.1; -;
 DR MGD; MG1:107789; AUPL.
 DR InterPro: IPR003892; CUE.
 DR Pfam: PF02845; CUE; 1.
 DR SMART; SM00546; CUE; 1.
 KW Signal.
 FT SIGNAL 1 37
 FT CHAIN 38 410
 FT SIGNAL 38 410
 SQ SEQUENCE 410 AA; 46121 MW; E7D070CEB296B5B CRC64;

Query Match 23.1%; Score 6; DB 1; Length 410;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGFLL 7
 |||||
 Db 21 DGFLL 26

RESULT 26
 AP47_CAEEL STANDARD; PRT: 422 AA.
 ID AP47_CAEEL
 AC P35602;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE Clathrin coat assembly protein AP47 (Clathrin coat associated protein
 DE AP47) (Golgi adaptor AP-1 47 kDa protein) (HA1 47 kDa subunit)
 DE (Clathrin assembly protein assembly protein complex 1 medium chain).
 GN UNC-101.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OK NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=94116859; PubMed=8288128;
 RA Lee J., Jongeward G.D., Sternberg P.W.;
 RT "unc-101, a gene required for many aspects of Caenorhabditis elegans
 RT development and behavior, encodes a clathrin-associated protein.";
 RL Genes Dev. 8:60-73(1994).

```

CC -1- FUNCTION: COMPONENT OF THE ADAPTOR COMPLEXES WHICH LINK CLATHRIN
CC TO RECEPTORS IN COATED VESICLES. CLATHRIN-ASSOCIATED PROTEIN
CC COMPLEXES ARE BELIEVED TO INTERACT WITH THE CYTOPLASMIC TAILS OF
CC MEMBRANE PROTEINS, LEADING TO THEIR SELECTION AND CONCENTRATION.
CC AP47 IS A SUBUNIT OF THE PLASMA MEMBRANE ADAPTOR.
CC -1- FUNCTION: REQUIRED FOR MANY ASPECTS OF DEVELOPMENT AND BEHAVIOR,
CC INCLUDING NEGATIVE REGULATION OF VULVAL DIFFERENTIATION.
CC -1- SUBUNIT: ASSEMBLY PROTEIN COMPLEX 1 (AP-1) IS A HETEROTETRAMER
CC COMPOSED OF TWO LARGE CHAINS (GAMMA AND BETA'), A MEDIUM CHAIN
CC (AP47) AND A SMALL CHAIN (AP19).
CC -1- CYTOPLASMIC FACE OF COATED VESICLES LOCATED AT THE GOLGI COMPLEX.
CC -1- SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES MEDIUM SUBUNITS
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: I26291; AAA72418.1;
CC DR InterPro: IPR001392; Adap_comp_sub.
CC DR Pfam: PF00928; Adap_comp_sub; 1.
CC DR PRINTS: PR00314; CLATHRINADPT.
CC DR PROSITE: PS00990; CLAT_ADAPTOR_M_1; 1.
CC DR PROSITE: PS00991; CLAT_ADAPTOR_M_2; 1.
CC KW Coated pits.
CC SEQUENCE 422 AA; 48297 MW; D57BF5D1EF496D50 CRC64;

Query Match 23.1%; Score 6; DB 1; Length 422;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MDGFP 14
DB 118 MDGFP 123

RESULT 27
ALM2_HUMAN STANDARD; PRT; 423 AA.
ID ALM2_HUMAN
AC Q9Y6G5;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Adaptor-related protein complex 1 mu 2 subunit (Clathrin coat
DE assembly protein AP47 2) (Clathrin coat associated protein AP47 2)
DE (Goldj adaptor AP-1 47 kDa protein) (HA1 47 kDa subunit 2) (Clathrin
DE assembly protein assembly protein complex 1 medium chain 2) (Ap-mu
DE chain family member mu1b).
GN APIM2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=9268457; PubMed=10338135; Okazaki Y., Aguilar R.C.,
RA Osho H., Tomemori T., Nakatsu F., Okazaki Y., Aguilar R.C.,
RA Foelsch H., Mellman I., Saito T., Shirasawa T., Bonifacio J.S.;
RT "mu1b, a novel adaptor medium chain expressed in polarized epithelial
RT cells.";
RT FEBS Lett. 449:215-220(1999).
CC -1- FUNCTION: COMPONENT OF THE ADAPTOR COMPLEXES WHICH LINK CLATHRIN
CC TO RECEPTORS IN COATED VESICLES. CLATHRIN-ASSOCIATED PROTEIN
CC COMPLEXES ARE BELIEVED TO INTERACT WITH THE CYTOPLASMIC TAILS OF
CC MEMBRANE PROTEINS, LEADING TO THEIR SELECTION AND CONCENTRATION.
CC AP47 IS A SUBUNIT OF THE PLASMA MEMBRANE ADAPTOR.

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CC -1- SUBUNIT: ASSEMBLY PROTEIN COMPLEX 1 (AP-1) IS A HETEROTETRAMER
CC COMPOSED OF TWO LARGE CHAINS (GAMMA AND BETA'), A MEDIUM CHAIN
CC (AP47) AND A SMALL CHAIN (AP19).
CC -1- CYTOPLASMIC FACE OF COATED VESICLES LOCATED AT THE GOLGI COMPLEX.
CC -1- PTM: AUTOPHOSPHORYLATED (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES MEDIUM SUBUNITS
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF020797; AAD25870.2;
CC DR InterPro: IPR001392; Adap_comp_sub.
CC DR Pfam: PF00928; Adap_comp_sub; 1.
CC DR PRINTS: PR00314; CLATHRINADPT.
CC DR PROSITE: PS00990; CLAT_ADAPTOR_M_1; 1.
CC DR PROSITE: PS00991; CLAT_ADAPTOR_M_2; 1.
CC KW Coated pits; Phosphorylation.
CC SEQUENCE 423 AA; 48108 MW; A3F6DF8659D6F7 CRC64;

Query Match 23.1%; Score 6; DB 1; Length 423;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MDGFP 14
DB 118 MDGFP 123

RESULT 28
ALM2_MOUSE STANDARD; PRT; 423 AA.
ID ALM2_MOUSE
AC Q9WVP1; Q991AA;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Adaptor-related protein complex 1 mu 2 subunit (Clathrin coat
DE assembly protein AP47 2) (Clathrin coat associated protein AP47 2)
DE (Goldj adaptor AP-1 47 kDa protein) (HA1 47 kDa subunit 2) (Clathrin
DE assembly protein assembly protein complex 1 medium chain 2) (Ap-mu
DE chain family member mu1b).
GN APIM2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=9268457; PubMed=10338135;
RA Osho H., Tomemori T., Nakatsu F., Okazaki Y., Aguilar R.C.,
RA Foelsch H., Mellman I., Saito T., Shirasawa T., Bonifacio J.S.;
RT "mu1b, a novel adaptor medium chain expressed in polarized epithelial
RT cells.";
RT FEBS Lett. 449:215-220(1999).
CC -1- FUNCTION: COMPONENT OF THE ADAPTOR COMPLEXES WHICH LINK CLATHRIN
CC TO RECEPTORS IN COATED VESICLES. CLATHRIN-ASSOCIATED PROTEIN
CC COMPLEXES ARE BELIEVED TO INTERACT WITH THE CYTOPLASMIC TAILS OF
CC MEMBRANE PROTEINS, LEADING TO THEIR SELECTION AND CONCENTRATION.
CC AP47 IS A SUBUNIT OF THE PLASMA MEMBRANE ADAPTOR.
CC -1- FUNCTION: REQUIRED FOR MANY ASPECTS OF DEVELOPMENT AND BEHAVIOR,
CC INCLUDING NEGATIVE REGULATION OF VULVAL DIFFERENTIATION.
CC -1- SUBUNIT: ASSEMBLY PROTEIN COMPLEX 1 (AP-1) IS A HETEROTETRAMER
CC COMPOSED OF TWO LARGE CHAINS (GAMMA AND BETA'), A MEDIUM CHAIN
CC (AP47) AND A SMALL CHAIN (AP19).
CC -1- CYTOPLASMIC FACE OF COATED VESICLES LOCATED AT THE GOLGI COMPLEX.
CC -1- SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES MEDIUM SUBUNITS
CC FAMILY.
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CC -----
CC EMBL: AF020797; AAD25870.2;
CC DR InterPro: IPR001392; Adap_comp_sub.
CC DR Pfam: PF00928; Adap_comp_sub; 1.
CC DR PRINTS: PR00314; CLATHRINADPT.
CC DR PROSITE: PS00990; CLAT_ADAPTOR_M_1; 1.
CC DR PROSITE: PS00991; CLAT_ADAPTOR_M_2; 1.
CC KW Coated pits; Phosphorylation.
CC SEQUENCE 423 AA; 48108 MW; A3F6DF8659D6F7 CRC64;

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RC TISSUE-Breast tumor;
RA Strausberg R.;
RU Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: COMPONENT OF THE ADAPTOR COMPLEXES WHICH LINK CLATHRIN
CC TO RECEPTORS IN COATED VESICLES. CLATHRIN-ASSOCIATED PROTEIN
CC COMPLEXES ARE BELIEVED TO INTERACT WITH THE CYTOSOLIC TAILS OF
CC MEMBRANE PROTEINS, LEADING TO THEIR SELECTION AND CONCENTRATION.
CC AP47 IS A SUBUNIT OF THE PLASMA MEMBRANE ADAPTOR.
CC -1- SUBUNIT: ASSEMBLY PROTEIN COMPLEX 1 (AP-1) IS A HETEROTETRAMER
CC COMPOSED OF TWO LARGE CHAINS (GAMMA AND BETA'), A MEDIUM CHAIN
CC (AP47) AND A SMALL CHAIN (AP19).
CC -1- SUBCELLULAR LOCATION: COMPONENT OF THE COAT SURROUNDING THE
CC CYTOSOLIC FACE OF COATED VESICLES LOCATED AT THE GOLGI COMPLEX.
CC -1- PTM: AUTOPHOSPHORYLATED (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES MEDIUM SUBUNITS
CC FAMILY.
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CC -----
DR EMBL: AF067146; AAD28085.1; -
DR EMBL: AF139416; AAF61815.1; -
DR EMBL: AF139407; AAF61815.1; JOINED.
DR EMBL: AF139408; AAF61815.1; JOINED.
DR EMBL: AF139409; AAF61815.1; JOINED.
DR EMBL: AF139410; AAF61815.1; JOINED.
DR EMBL: AF139411; AAF61815.1; JOINED.
DR EMBL: AF139412; AAF61815.1; JOINED.
DR EMBL: AF139413; AAF61815.1; JOINED.
DR EMBL: AF139414; AAF61815.1; JOINED.
DR EMBL: AF139415; AAF61815.1; JOINED.
DR EMBL: BC003704; AAH03704.1; -
DR MGD: MG1:1336974; Ap1m2.
DR InterPro: IPR001392; Adap_comp-sub.
DR Pfam: PF00928; Adap_comp-sub; 1.
DR PRINTS: PR00314; CLATHRINADPT.
DR PROSITE: PS00990; CLAT ADAPTOR_M.1; 1.
DR PROSITE: PS00991; CLAT ADAPTOR_M.2; 1.
KW Coated pits; Phosphorylation.
FT CONFLICT 112 112 D -> E (IN REF. 3).
FT SEQUENCE 423 AA; 48136 MW; FD18049309F074B5 CRC64;
SQ

```

Query Match 23.1%; Score 6; DB 1; Length 423;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 MDEGFP 14
 |||||
 DB 118 MDEGFP 123

RESULT 29
 MT17_KLU1A STANDARD; PRT; 443 AA.
 AC Q92441;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE MT17 protein [includes: O-acetylhomoserine sulfhydrylase
 (EC 4.2.99.10) (OAH sulfhydrylase); O-acetylserine sulfhydrylase
 (EC 4.2.99.8) (OAS sulfhydrylase)].
 GN MT17.
 OS Kluyveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 NCBI_TaxID=28985;

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BM27;
RA Brylwezy J., Paszowski A.;
RU Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TRANSFORMS O-ACETYLHOMOSERINE INTO HOMOCYSTEINE AND.
CC O-ACETYLSELINE INTO CYSTEINE.
CC -1- CATALYTIC ACTIVITY: O-acetyl-L-homoserine + methanethiol = L-
CC methionine + acetate.
CC -1- CATALYTIC ACTIVITY: O3-acetyl-L-serine + H(2)S = L-cysteine +
CC acetate.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- PATHWAY: FIFTH STEP IN THE SULFATE ASSIMILATION PATHWAY THAT
CC LEADS TO THE BIOSYNTHESIS OF METHIONINE AND CYSTEINE.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE TRANS-SULFURATION ENZYMES FAMILY.
CC -----
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CC -----
DR EMBL: U72486; AAB17387.1; -
DR HSSP: P00935; ICS1.
DR InterPro: IPR000277; Cys_Met_MetA_PP.
DR Pfam: PF01053; Cys_Met_MetA_PP; 1.
DR PROSITE: PS00868; CYS_MET_METAB_PP; 1.
KW Methionine biosynthesis; Cysteine biosynthesis; Lyase;
KW Pyridoxal phosphate; Multifunctional enzyme.
FT INTR MET 0 BY SIMILARITY.
FT BINDING 207 207 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT SEQUENCE 443 AA; 47975 MW; A01577BD53E1AE3A CRC64;
SQ

```

Query Match 23.1%; Score 6; DB 1; Length 443;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFLLQ 8
 |||||
 DB 280 GFLLQ 285

RESULT 30
 LEF9_NPVOP STANDARD; PRT; 489 AA.
 AC O10319;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Late expression factor 9.
 GN LEF-9.
 OS Oryzias pseudotsugata multicausid polyhedrosis virus (OPMVV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OC NCBI_TaxID=164623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97271300; Pubmed-9126251;
 RA Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
 RA Rohmann G.F.;
 RT "The sequence of the Oryzias pseudotsugata multicausid polyhedrosis virus genome."
 RT Polyhedrosis virus genome.";
 RL Virology 229:381-399(1997).
 CC -1- FUNCTION: INVOLVED IN LATE/VERY LATE GENE ACTIVATION (BY
 CC SIMILARITY).
 CC -----
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DR EMBL: U75930; AAC59064.1; -
KM Transcription regulation.
SQ SEQUENCE 489 AA; 55590 MW; 999A7699E7AB0D8 CRC64;

Query Match 23.1%; Score 6; DB 1; Length 469;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 FPEHLL 18
Db 479 FPEHLL 484

RESULT 31
ID A2AP_HUMAN STANDARD; PRT; 491 AA.
AC P08697;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Alpha-2-antiplasmin precursor (Alpha-2-plasmin inhibitor) (Alpha-2-Pi
DE (Alpha-2-AP)).
GN SERPINF2 OR PI1 OR AAP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:88139254; PubMed-2830248;
RA Tane M., Kikuno R., Kume-Iwaki A., Hashimoto-Gotoh T.;
RT "Structure of human alpha 2-plasmin inhibitor deduced from the cDNA
RT sequence.";
RL J. Biochem. 102:1033-1041(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE:88320531; PubMed-3166140;
RA Hiroseawa S., Nakamura Y., Miura O., Sumi Y., Aoki N.;
RT "Organization of the human alpha 2-plasmin inhibitor gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:6836-6840(1988).
RN [3]
RP ERRATUM.
RA Hiroseawa S., Nakamura Y., Miura O., Sumi Y., Aoki N.;
RL Proc. Natl. Acad. Sci. U.S.A. 86:1612-1613(1989).
RN [4]
RP SEQUENCE OF 4-491 FROM N.A.
RX MEDLINE:87109313; PubMed-2433286;
RA Holmes W.E., Nelles L., Lijnen H.R., Collen D.;
RT "Primary structure of human alpha 2-antiplasmin, a serine protease
RT inhibitor (serpin).";
RL J. Biol. Chem. 262:1659-1664(1987).
RN [5]
RP SEQUENCE OF 218-491 FROM N.A.
RX MEDLINE:87137400; PubMed-3818581;
RA Sumi Y., Nakamura Y., Aoki N., Sakai M., Muramatsu M.;
RT "Structure of the carboxyl-terminal half of human alpha 2-plasmin
RT inhibitor deduced from that of cDNA.";
RL J. Biochem. 100:1399-1402(1986).
RN [6]
RP SEQUENCE OF 40-491.
RX MEDLINE:87275946; PubMed-2440681;
RA Lijnen H.R., Holmes W.E., van Hoef B., Wiman B., Rodriguez H.,
RA Collen D.;
RT "Amino-acid sequence of human alpha 2-antiplasmin.";
RL Eur. J. Biochem. 166:565-574(1987).
RN [7]

RP SEQUENCE OF 40-43.
RX MEDLINE:78023887; PubMed-21075;
RA Wiman B., Collen D.;
RT "Purification and characterization of human antiplasmin, the
RT fast-acting plasmin inhibitor in plasma.";
RL Eur. J. Biochem. 78:19-26(1977).
RN [8]
RP SEQUENCE OF 28-52.
RX TRISSE-Plasma;
RC MEDLINE:93050153; PubMed-1385210;
RA Christensen S., Sottrup-Jensen L.;
RT "Bovine alpha 2-antiplasmin. N-terminal and reactive site sequence.";
RL FEBS Lett. 312:100-104(1992).
RN [9]
RP ACTIVE SITES.
RX MEDLINE:88290696; PubMed-2456616;
RA Potempa J., Shieh B.-H., Travis J.;
RT "Alpha-2-antiplasmin: a serpin with two separate but overlapping
RT reactive sites.";
RL Science 241:699-700(1988).
RN [10]
RP SEQUENCE OF 481-491, AND SULFATION.
RX MEDLINE:87137577; PubMed-243496;
RA Horton G., Fox K.F., Toren P.C., Straus A.M.;
RT "Sulfation of a tyrosine residue in the plasmin-binding domain of
RT alpha 2-antiplasmin.";
RL J. Biol. Chem. 262:3082-3085(1987).
CC -1- FUNCTION: THE MAJOR TARGETS OF THIS INHIBITOR ARE PLASMIN AND
CC TRYPsin, BUT IT ALSO INACTIVATES CHYMOTRYPSIN.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
CC CC
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DR EMBL: D00116; BAA00070.1; -
DR EMBL: D00174; BAA00124.1; -
DR EMBL: M20786; AAA51554.1; -
DR EMBL: M20782; AAA51554.1; JOINED.
DR EMBL: M20783; AAA51554.1; JOINED.
DR EMBL: M20784; AAA51554.1; JOINED.
DR EMBL: M20785; AAA51554.1; JOINED.
DR EMBL: J02654; AAA55543.1; -
DR PIR: A24708; A24708.
DR PIR: A26684; A26684.
DR PIR: A31402; A31402.
DR PIR: A32163; A32163.
DR PIR: A41504; A41504.
DR PIR: S00068; S00068.
DR HSSP: P01008; IANT.
DR SWISS-2DPAGE: P08697; HUMAN.
DR MIM: 262850; -
DR InterPro: IPR000215; Serpin.
DR Pfam: PF00079; serpin. 1.
DR SMART: SM00093; SERPIN; 1.
DR PROSITE: PS00284; SERPIN; 1.
KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma; Signal;
KW Sulfation.
FT SIGNAL 1 27
FT PROPEP 28 39
FT ACT_SITE 40 491
FT ACT_SITE 403 404
FT ACT_SITE 404 405
FT MOD_RES 484 484
FT CARBOHYD 126 126
FT CARBOHYD 295 295
FT CARBOHYD 309 309
FT CARBOHYD 316 316
FT CONFLICT 33 33
R -> W (IN REF. 1).

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FT CONFLICT 49 49 L -> G (IN REF. 6).
FT CONFLICT 105 105 N -> D (IN REF. 6).
FT CONFLICT 289 289 H -> D (IN REF. 4).
FT CONFLICT 408 408 S -> G (IN REF. 6).
FT CONFLICT 455 455 D -> N (IN REF. 6).
SQ SEQUENCE 491 AA: 54565 MW: 385A1C90E91A63CB CRC64;

Query Match 23.1%; Score 6; DB 1: Length 491;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 DFLQSL 25
DB 455 DFLQSL 460

RESULT 32
CPDF_CANFA STANDARD; PRT; 499 AA.
AC Q29473; 002859;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Cytochrome P450 2D15 (EC 1.14.14.1) (CYP1D15) (P450 DUT2).
GN CYP2D15.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=95305574; PubMed=7786018;
RA Sakamoto K., Kirita S., Baba T., Nakamura Y., Yamazoe Y., Kato R.,
RA Takahata A., Matsudaira T.,
RT "A new cytochrome P450 form belonging to the CYP2D in dog liver
RT microsomes: purification, cDNA cloning, and enzyme
RT characterization."
RL Arch. Biochem. Biophys. 319:372-382(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BEAGLE;
RX MEDLINE=98162950; PubMed=9504424;
RA Iwata T., Nakamura A., Iton S., Ohashi K., Yamamoto Y., Masuda M.,
RA Iwata H., Kazusaka A., Kametaki T., Fujita S.;
RT "Expression and characterization of dog CYP2D15 using baculovirus
RT expression system."
RL J. Biochem. 123:162-168(1998).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=98389575; PubMed=9721180;
RA Rousset F., Dulgann D.B., Lawton M.P., Obach R.S., Strick C.A.,
RA Tweedie D.J.;
RT "Expression and characterization of canine cytochrome P450 2D15."
RL Arch. Biochem. Biophys. 357:27-36(1998).
CC -1- FUNCTION: HIGH ACTIVITY FOR THE HYDROXYLATION OF BUUNITROL AND
CC IMPAMINE: LOW ACTIVITY ON DEBRISOQUINE.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) -> ROH +
CC oxidized flavoprotein + H(2)O.
CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -1- TISSUE SPECIFICITY: LIVER. ALSO DETECTED IN SEVERAL OTHER TISSUES.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -----
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CC -----
FMBL: D17397; BAA04220.1; -

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DR EMBL: AB004268; BAA20357.1; -
DR HSSP: P00179; 1DT6.
DR InterPro: IPR001128; Cyt_P450.
DR Pfam: PF00067; P450.1.
DR PRINTS: PR00385; P450.
DR PROSITE: PS00086; CYTOCHROME_P450.1.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum.
FT INIT MET 0 0
FT BINDING 445 445 HEME (BY SIMILARITY).
SQ SEQUENCE 499 AA: 56301 MW: 27E52B5B309E7F1 CRC64;

Query Match 23.1%; Score 6; DB 1: Length 499;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 LLOMDF 11
DB 48 LLOMDF 53

RESULT 33
LEP9_NPVAC STANDARD; PRT; 516 AA.
AC P41465;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Late expression factor 9.
GN LEP-9.
OS Autographa californica nuclear polyhedrosis virus (ACNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=46015;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C6;
RX MEDLINE=94303173; PubMed=8030224;
RA Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.;
RT "The complete DNA sequence of Autographa californica nuclear
RT polyhedrosis virus."
RL Virology 202:586-605(1994).
CC -1- FUNCTION: INVOLVED IN LATE/VERY LATE GENE ACTIVATION.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
FMBL: L22858; AAA6692.1; -
DR EMBL: L22858; AAA6692.1; -
KW transcription regulation.
SQ SEQUENCE 516 AA: 59305 MW: B625F9E623FC058F CRC64;

Query Match 23.1%; Score 6; DB 1: Length 516;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 PEBHL 18
DB 506 PEBHL 511

RESULT 34
HCYF_EURCA STANDARD; PRT; 628 AA.
AC Q9NFL5;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)

```

DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Hemocyanin F chain (HCF).
 GN HCF.
 OS Euryelma californica (American tarantula).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Mygalomorphae; Theraphosidae; Aphonopelma.
 RN NCBI_TaxID=293932;
 RX MEDLINE=293932;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RA Volt R., Feldmeier-Fuchs G., Schmelzer T., Decker H., Burmester T.;
 RT "Complete sequence of the 24-mer hemocyanin of the tarantula Euryelma
 californicum. Structure and intramolecular evolution of the
 subunits.";
 RL J. Biol. Chem. 275:39339-39344(2000).
 CC -1- FUNCTION: HEMOCYANIN ARE COPPER-CONTAINING OXYGEN CARRIERS
 OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
 ARTHROPODS.
 CC -1- SUBUNIT: TARANTULA HEMOCYANIN IS A 24-CHAIN POLYMER WITH SEVEN
 DIFFERENT CHAINS IDENTIFIED.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- MISCELLANEOUS: THE TWO COPPER IONS BOUND EACH HAVE 3 NITROGEN
 LIGANDS (PRESUMABLY CONTRIBUTED BY HIS RESIDUES) AND SHARE A
 BRIDGING LIGAND (POSSIBLY CONTRIBUTED BY A TYR RESIDUE) IN
 ADDITION TO BINDING OXYGEN.
 CC -1- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
 SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: AJ277491; CAB89496.1; -.
 DR HSP: P04253; ILIA.
 DR InterPro: IPR000896; Hemocyanin.
 DR PRINTS: PRO0187; HAEMOCYANIN.
 DR PROSITE: PS00209; HEMOCYANIN.1; 1.
 DR PROSITE: PS00210; HEMOCYANIN.2; 1.
 DR PROSITE: PS00498; TYROSINASE.2; 1.
 KM Transport; Oxygen transport; Copper; Glycoprotein; Hemolymph.
 FT INIT_MER 0
 FT DISULFID 533
 FT METAL 171 171
 FT METAL 175 175
 FT METAL 202 202
 FT METAL 323 323
 FT METAL 327 327
 FT METAL 363 363
 FT CARBOHYD 394 394
 FT CARBOHYD 446 446
 FT CARBOHYD 526 526
 FT CARBOHYD 614 614
 FT SEQUENCE 628 AA; 72017 MW; 539C94849CC8D4F4 CRC64;
 SO
 Query Match 23.1%; Score 6; DB 1; Length 623;
 Best Local Similarity 100.0%; Pred. No. 70;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14 PHLV 19
 DB 536 PHLV 541
 ORC3_MOUSE STANDARD; PRT; 715 AA.
 AC 09JK30;

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Origin recognition complex subunit 3 (Origin recognition complex
 subunit 3) ORC3.
 GN ORC3 OR ORC3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 RX MEDLINE=10090;
 RP SEQUENCE FROM N.A.
 RA Springer J., Nanda I., Hoehn K., Schmid M., Grunmt F.;
 RT "Identification and chromosomal localization of murine ORC3, a new
 member of the mouse origin recognition complex.";
 RL Cytogenet. Cell Genet. 87:245-251(1999).
 CC -1- FUNCTION: COMPONENT OF THE ORIGIN RECOGNITION COMPLEX (ORC) THAT
 BINDS ORIGINS OF REPLICATION. IT HAS A ROLE IN BOTH CHROMOSOMAL
 REPLICATION AND MATING TYPE TRANSCRIPTIONAL SILENCING. BINDS TO
 THE ARS CONSENSUS SEQUENCE (ACS) OF ORIGINS OF REPLICATION IN AN
 ATP-DEPENDENT MANNER.
 CC -1- SUBUNIT: ORC IS COMPOSED OF SIX SUBUNITS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE ORC3 FAMILY.
 CC -----
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 CC -----
 DR EMBL: AJ132830; CAB76399.1; -.
 DR MGD: MGI:135494; Orc3.
 DR DNA Replication; Nuclear protein; DNA-binding.
 KM SEQUENCE 715 AA; 82341 MW; 1E915A719A2E33EB CRC64;
 SO
 Query Match 23.1%; Score 6; DB 1; Length 715;
 Best Local Similarity 100.0%; Pred. No. 79;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 18 LVDF 23
 DB 80 LVDF 85
 MIS5_SCHPO STANDARD; PRT; 892 AA.
 AC P49731; G9P7R7;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE DNA replication licensing factor mis5.
 GN MIS5 OR SPBC211.04C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 RN NCBI_TaxID=4896;
 RX MEDLINE=95170112; PubMed=7865880;
 RA Takahashi K., Yamada H., Yanagida M.;
 RT "Fission yeast minichromosome loss mutants mis cause lethal
 aneuploidy and replication abnormality.";
 RL Mol. Biol. Cell 5:1145-1158(1994).
 CC [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;

RA Wood V., Rajandream M.A., Barrell B.G., Davis P., Churcher C.M.;
 RL Submitted (Feb-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Nuclear (potential).
 CC -1- SIMILARITY: BELONGS TO THE MCM FAMILY.
 CC -1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 864
 CC ONWARD AND IS SHORTER (868 AA) DUE TO A FRAMESHIFT.
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 CC -----
 CC EMBL: D31960; BAA06729.1; ALT_FRAME.
 DR EMBL: AL139314; CAB75412.1; -.
 DR InterPro: IPR001208; MCM.
 DR Pfam: PF00493; MCM.1.
 DR SMART: SM00350; MCM.1.
 DR PROSITE: PS00847; MCM_1.1.
 DR PROSITE: PS50051; MCM_2.1.
 DR Transcription regulation; DNA-binding; Nuclear protein;
 KW DNA replication; Cell cycle; ATP-binding.
 FT DOMAIN 426 633 MCM.
 FT NP_BIND 476 483 ATP (POTENTIAL).
 FT SEQUENCE 892 AA; 99549 MW; 3A00DB55B2EE08B7 CRC64;

Query Match 23.1%; Score 6; DB 1; Length 892;
 Best Local Similarity 100.0%; Pred. No. 97;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 FLOSIS 26
 |||||
 DB 405 FLOSIS 410

RESULT 37
 CHSG_ASPPU STANDARD: PRT: 911 AA.
 ID CHSG_ASPPU 009031; 009032;
 AC P54267; 009031; 009032;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Chitin synthase G (EC 2.4.1.16) (Chitin-UDP acetyl-glucosaminyl
 DE transferase G) (Class-III chitin synthase G).
 GN CHSG.
 OS Aspergillus fumigatus (Sartorya fumigata).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5085;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H237;
 RX MEDLINE=96347138; PubMed=8736545;
 RA Mellado E., Aulauvre-Brown A., Gow N.A.R., Holden D.W.;
 RT "The Aspergillus fumigatus chsc and chsg genes encode class III
 RT chitin synthases with different functions."
 RL Mol. Microbiol. 20:667-679(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SIU001;
 RA Borga P.T., Tarteouk N., Riggle P.J., Winter K.R., Koltin Y.,
 RA Bulawa C.E.;
 RU Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PLAYS A MAJOR ROLE IN CELL WALL BIOGENESIS.
 CC -1- CATALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + ((1,4)-(N-acetyl-
 CC beta-D-glucosaminyl))_(N+1) = UDP + ((1,4)-(N-acetyl-beta-D-
 CC glucosaminyl))_(N+1).
 CC -1- SUBCELLULAR LOCATION: Plasma membrane-bound.
 CC -1- SIMILARITY: BELONGS TO THE CHITIN SYNTHASE FAMILY. SUBFAMILY CLASS
 CC III.

CC -----
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 CC -----
 CC EMBL: X94244; CA63928.1; -.
 DR EMBL: U39478; AAB07679.1; -.
 DR EMBL: U39479; AAB07679.1; -.
 DR InterPro: IPR002923; Chitin_synth.
 DR Pfam: PF01644; Chitin_synth.1.
 DR ProDom: PD002998; Chitin_synth.1.
 KW Transferase; Glycosyltransferase; Transmembrane; Cell wall;
 KM Multigene family.
 FT TRANSMEM 579 599 POTENTIAL.
 FT TRANSMEM 624 644 POTENTIAL.
 FT TRANSMEM 659 679 POTENTIAL.
 FT TRANSMEM 711 731 POTENTIAL.
 FT TRANSMEM 840 860 POTENTIAL.
 FT TRANSMEM 879 899 POTENTIAL.
 FT CONFLICT 534 537 PPVQ -> LPFK (IN REF. 1).
 FT CONFLICT 537 537 R -> C (IN REF. 2; AAB07679).
 FT CONFLICT 628 629 IV -> MM (IN REF. 2; AAB07679).
 FT CONFLICT 892 892 F -> N (IN REF. 2; AAB07679).
 FT SEQUENCE 911 AA; 101669 MW; BC933F8BA0BE48D CRC64;

Query Match 23.1%; Score 6; DB 1; Length 911;
 Best Local Similarity 100.0%; Pred. No. 98;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFLLO 8
 |||||
 DB 635 GFLLO 640

RESULT 38
 PMAL_DICDI STANDARD: PRT: 1058 AA.
 ID PMAL_DICDI
 AC P34679;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable plasma membrane ATPase (EC 3.6.3.6) (Proton pump) (PAT2).
 DE PATB.
 GN Dictyostelium discoideum (Slime mold).
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX3;
 RX MEDLINE=98083743; PubMed=9421912;
 RA Coxwell M.B., Konikis J., Cameron A.M.;
 RT "The patb gene of Dictyostelium discoideum encodes a P-type H(+)-
 RT ATPase isoform essential for growth and development under acidic
 RT conditions."
 RL Microbiology 143:3877-3888(1997).
 RN [2]
 CC -1- FUNCTION: THE PLASMA MEMBRANE ATPASE IS A HYDROGEN ION PUMP. THE
 CC PROTON GRADIENT IT GENERATES DRIVES THE ACTIVE TRANSPORT OF
 CC NUTRIENTS BY H+ SYMPORT. THE RESULTING EXTERNAL ACIDIFICATION
 CC AND/OR INTERNAL ALKINIZATION MAY MEDIATE GROWTH RESPONSES.
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(IN) = ADP + PHOSPHATE +
 CC H(+)(OUT).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
 CC (E1-E2 ATPASES). SUBFAMILY I11A.
 CC -----
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DR EMBL: X98286; CA66931.1; -
 DR Dictydb; DD00061; patB.
 DR InterPro: IPR004014; Cation_ATPase.
 DR InterPro: IPR001757; E1-E2_ATPase.
 DR InterPro: IPR000695; HATPase.
 DR InterPro: IPR001454; Hydrolyase.
 DR Pfam: PF00690; Cation_ATPase_N.1.
 DR Pfam: PF00123; E1-E2_ATPase.1.
 DR Pfam: PF00702; Hydrolyase.1.
 DR PRINTS: PR00119; CATATPASE.
 DR PRINTS: PR00120; HATPASE.
 DR PROSITE: PS00154; ATPASE_E1_E2.1.
 KM Hydrolyase: Hydrogen ion transport; Transmembrane; Phosphorylation;
 KW Magnesium; ATP-binding.

FT DOMAIN 1 212 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 213 232 POTENTIAL.
 FT DOMAIN 233 237 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 238 258 POTENTIAL.
 FT DOMAIN 259 387 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 388 407 POTENTIAL.
 FT DOMAIN 408 417 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 426 447 POTENTIAL.
 FT DOMAIN 448 783 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 784 805 POTENTIAL.
 FT DOMAIN 806 810 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 811 833 POTENTIAL.
 FT DOMAIN 834 849 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 850 870 POTENTIAL.
 FT DOMAIN 871 889 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 890 910 POTENTIAL.
 FT DOMAIN 911 922 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 923 943 POTENTIAL.
 FT DOMAIN 944 967 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 968 988 POTENTIAL.
 FT DOMAIN 989 1058 CYTOPLASMIC (POTENTIAL).
 FT MOD_RES 480 480 PHOSPHORYLATION (BY SIMILARITY).
 FT METAL 728 728 MAGNESIUM (BY SIMILARITY).
 FT METAL 732 732 MAGNESIUM (BY SIMILARITY).
 FT DOMAIN 44 55 POLY-GLN.
 FT DOMAIN 113 116 POLY-SER.
 FT DOMAIN 246 249 POLY-LEU.

SO SEQUENCE 1058 AA; 117373 MW; C80E5AB9E9EB9AF2 CRC64;

Query Match 23.1%; Score 6; DB 1; Length 1058;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LVDFL 22
 |||||
 DB 403 LVDFL 408

RESULT 39
 YECS_YEAST
 ID YECS_YEAST STANDARD; PRT; 1188 AA.
 AC P39991;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Hypothetical 136.1 kDa protein in VMA3-RIP1 Intergenic region.
 GN YEL025C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-S288C / AB972;
 RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
 RA Aviles E., Bero A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
 RA Chung E., Duncun M., Guzman E., Hartzell G., Hunnicke-Smith S.,
 RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
 RA Mosedale D., Nakahara K., Nemeth A., Norgren R., Oefner P., Oh C.,
 RA Patel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
 RA Taylor P., Wei Y., Yellon M., Botstein D., Davis R.W.;
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.

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 CC or send an email to license@isb-sib.ch).

DR EMBL: U18530; AAB64502.1; -
 DR SGD: S0000751; SRI1.
 KM Hypothetical protein; Transmembrane.
 FT TRANSMEM 73 93 POTENTIAL.
 FT TRANSMEM 878 898 POTENTIAL.
 FT TRANSMEM 1089 1109 POTENTIAL.
 SO SEQUENCE 1188 AA; 136068 MW; 82C3F04D1F78AD3D CRC64;

Query Match 23.1%; Score 6; DB 1; Length 1188;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 VDFLQ 24
 |||||
 DB 523 VDFLQ 528

RESULT 40
 YMW2-CAEEL
 ID YMW2-CAEEL STANDARD; PRT; 1246 AA.
 AC P34504; P34505; P34506; P90907;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Hypothetical 130.6 kDa protein K04H4.2 in chromosome III.
 GN K04H4.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,
 RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
 RA Johnston L., Jones M., Kershaw J., Kirsten J., Lalister N.,
 RA Latreille P., Lightning J., Lloyd C., Mottimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Ralphen L., Roopa A., Saunders D., Showkhen R.,
 RA Sims M., Smaildon N., Smith A., Smith M., Sonhammer E., Staden R.,
 RA Sulston J., Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K.,
 RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
 RA Woldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans";
 RL Nature 368:32-38(1994).
 RN [2]
 RP REVISIONS.
 RA Durbin R.;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: K04H4.2A (SHOWN HERE) AND
 CC K04H4.2B; ARE PROBABLY PRODUCED BY ALTERNATIVE SPLICING.

CC STRAIN=S288C / FY1679;
 RX MEDLINE=96132033; PubMed=8553702;
 RA Maurer K.C.T., Urbanus J.H.M., Planeta R.J.;
 RT "Sequence analysis of a 30 kb DNA segment from yeast chromosome XIV
 RT carrying a ribosomal protein gene cluster, the genes encoding a
 RT plasma membrane protein and a subunit of replication factor C, and a
 RT novel putative serine/threonine protein kinase gene";
 RL Yeast 11:1303-1310(1995).
 CC -1 SIMILARITY: SOME, TO S.POMBE SPAC3D3.13C.
 CC -----
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 CC -----
 DR EMBL: U23084; AAC49101.1; -;
 DR PC5A: 271573; CAA96214.1; -;
 DR SCD: S0005241; YNL297C.
 KW Hypothetical protein.
 SQ SEQUENCE 1636 AA: 186834 MW: F0B3D8E6BD094D6 CRC64;
 Query Match 23.1%; Score 6; DB 1; Length 1636;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 20 DFL0SL 25
 Db 936 DFL0SL 941
 RESULT 43.
 PC5A_RAT STANDARD; PRT: 1877 AA.
 ID PC5A_RAT
 AC P41413; 062914;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Proteolysin convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)
 DE (Proteolysin convertase PC5) (Subtilisin/kexin-like protease PCS)
 DE (Convertase PC5) (PC5) (PC6) (Fragments).
 GN PCSK5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (SHORT ISOFORM), AND TISSUE-SPECIFICITY.
 RC TISSUE=Adrenal gland;
 RX MEDLINE=93342036; PubMed=8341687;
 RA Lawson J., Vleau D., Hamelin J., Day R., Chretien M., Seidah N.G.;
 RT "cDNA structure of the mouse and rat subtilisin/kexin-like PCS5: a
 RT candidate proteolysin convertase expressed in endocrine and
 RT nonendocrine cells";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993).
 RN [2]
 RP SEQUENCE OF 1676-1877 FROM N.A. (LONG ISOFORM).
 RC TISSUE=Adrenal gland;
 RX MEDLINE=93342036; PubMed=8341687;
 RA De Bie I., Marcinkiewicz M., Nakayama K., Lazure C., Seidah N.G.;
 RT Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SUBCELLULAR LOCATION.
 RX MEDLINE=20214819; PubMed=10749928;
 RA Xiang Y., Molloy S.S., Thomas L., Thomas G.;
 RT "The PC6B cytoplasmic domain contains two acidic clusters that direct
 RT sorting to distinct trans-Golgi network/endosomal compartments.";
 RL Mol. Biol. Cell 11:1257-1273(2000).
 RN [4]
 RP DEVELOPMENTAL EXPRESSION.
 RX MEDLINE=97166043; PubMed=9013936;

RA Zheng M., Seidah N.G., Plante J.E.;
 RT "The developmental expression in the rat CNS and peripheral tissues of
 RT proteases PC5 and PAC5A mRNAs: comparison with other proprotein
 RT processing enzymes";
 RL Dev. Biol. 181:268-283(1997).
 CC -1 FUNCTION: LIKELY TO REPRESENT A WIDESPREAD ENDOPEPTIDASE ACTIVITY
 CC WITHIN THE CONSTITUTIVE AND REGULATED SECRETORY PATHWAY. CAPABLE
 CC OF CLEAVAGE AT THE RX(K/R)R CONSENSUS MOTIF. MAY BE RESPONSIBLE
 CC FOR THE MATURATION OF GASTROINTESTINAL PEPTIDES. MAY BE INVOLVED
 CC IN THE CELLULAR PROLIFERATION OF ADRENAL CORTEX VIA THE ACTIVATION
 CC OF GROWTH FACTORS.
 CC -1 CATALYTIC ACTIVITY: RELEASE OF MAJORE PROTEINS FROM THEIR
 CC PROPEPTIDES BY CLEAVAGE OF ARG-XAA-YAA-ARG-1-ZAA BONDS, WHERE XAA
 CC CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.
 CC -1 SUBCELLULAR LOCATION: PC5A IS SECRETED THROUGH THE REGULATED
 CC SECRETORY PATHWAY. PC5B IS A TYPE I MEMBRANE PROTEIN LOCALIZED TO
 CC A PARANUCLEAR POST-GOLGI NETWORK COMPARTMENT IN COMMUNICATION WITH
 CC EARLY ENDOSOMES (BY SIMILARITY).
 CC -1 ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS: PC5B/LONG (SHOWN HERE)
 CC AND PC5A/SHORT; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1 TISSUE SPECIFICITY: EXPRESSED IN THE INTESTINE, BRAIN, ADRENAL
 CC GLAND, ANTERIOR PITUITARY, THYROID, OVARY, TESTIS AND LUNG.
 CC HIGHEST LEVELS ARE FOUND IN THE GUT, DUODENUM, JEJUNUM AND ILEUM.
 CC EXPRESSION IS HIGHER IN FEMALE THAN IN MALE REPRODUCTIVE ORGANS.
 CC -1 DEVELOPMENTAL STAGE: FIRST DETECTED AT E9 IN HIGHLY RESTRICTED
 CC REGIONS OF THE NEURAL TUBE, IN CAUDAL MYOTOMES, AND AT THE
 CC MATERNO-EMBRYONIC JUNCTION OF THE UTERUS. AT E10, RESTRICTED
 CC EXPRESSION IS DETECTED IN THE OPTIC AND OTIC VESICLES, THE ROOF OF
 CC MIDBRAIN, AND TRUNK MYOTOMES. BY MIDGESTATION (E13-E16),
 CC EXPRESSION IN THE DEVELOPING NERVOUS SYSTEM HAS EXPANDED TO
 CC MULTIPLE REGIONS INCLUDING HIPPOCAMPUS, THALAMUS, HYPOTHALAMUS,
 CC BRAIN STEM, AND SPINAL CORD. EXPRESSION IS ALSO DETECTED IN
 CC SEVERAL PERIPHERAL ORGAN SYSTEMS, INCLUDING GUT, LUNG, ADRENAL AND
 CC KIDNEY PRIMORDIA.
 CC -1 DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
 CC ASSISTING THE FOLDING OF THE ZIMOGEN WITHIN THE ENDOPLASMIC
 CC RETICULUM.
 CC -1 DOMAIN: AC 1 AND AC 2 (CLUSTERS OF ACIDIC AMINO ACIDS) CONTAIN
 CC SORTING INFORMATION. AC 1 DIRECTS TGN LOCALIZATION AND INTERACTS
 CC WITH THE TGN SORTING PROTEIN PACS-1.
 CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
 CC SUBTILASIN FAMILY.
 CC -1 SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
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 CC -----
 DR EMBL: U14933; AAA99906.1; -;
 DR PIR: U47014; AAA87888.1; -;
 DR PIR: B48225; B48225.
 DR HSSP: 099405; IMPT.
 DR MEROPS: S08.076; -;
 DR InterPro: IPR002174; Furin-like.
 DR InterPro: IPR002884; P-domain.
 DR InterPro: IPR000209; Peptidase_S8.
 DR Pfam: PF01483; P_1.
 DR Pfam: PF00082; Peptidase_S8; 1.
 DR PRINTS: PR00723; SUBTILISIN.
 DR ProDom: PD000717; P_domain; 1.
 DR SMART: SM00261; FU_6.
 DR PROSITE: PS00136; SUBTILASIN; 1.
 DR PROSITE: PS00137; SUBTILASIN; 1.
 DR PROSITE: PS00138; SUBTILASIN; 1.
 KW Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;
 KW Cleavage on pair of basic residues; Alternative splicing; Repeat;
 KW Transmembrane.
 FT SIGNAL 1 34 BY SIMILARITY.
 FT PROPEP 35 116 BY SIMILARITY.

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FT CHAIN 117 1877 PROTEIN CONVERTASE SUBSTITISIN/EXIN
FT 117 1768 TYPE 5.
FT 1769 1789 EXTRACELLULAR (POTENTIAL).
FT 1790 1877 POTENTIAL.
FT 117 452 CYTOPLASMIC (POTENTIAL).
FT 464 602 CAPALYTIC.
FT 638 1753 HOMO B.
FT 1825 1844 CYS-RICH MOTIF (CRM) REGION.
FT 1856 1877 AC 1.
FT 116 117 AC 2.
FT 521 523 CLEAVAGE (AUTO-) (BY SIMILARITY).
FT 173 173 CELL ATTACHMENT SITE (POTENTIAL).
FT 523 523 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT 214 214 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT 368 368 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT 227 227 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT 383 383 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT 667 667 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT 754 754 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT 804 804 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT 854 854 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT 1710 1710 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT 1732 1732 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT 915 915 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX ->
FT VARSPLIC 878 ATEESMAGGFCMLYKKNMLQKRYLQDLCKCTPFG
FT (IN ISOFORM PCSA).
FT VARSPLIC 916 1877 MISSING (IN ISOFORM PCSA).
FT 1877 AA; 20788 MM; 890955D060534444 CRC64;
SO SEQUENCE

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Query Match 23.1%; Score 6; DB 1; Length 1877;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 5 LILQMD 10
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Db 1718 LILQMD 1723

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RESULT 44
ATX1_PLAFA STANDARD: PRT; 1956 AA.
ID ATX1_PLAFA
AC 004956;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Plasmodium falciparum.
OS Probable cation-transporting ATPase 1 (EC 3.6.3.-).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9/96;
RX MEDLINE=9332070; PubMed=8421054;
RA Krishna S., Cowan G., Meade J.C., Wells R.A., Stringer J.R.,
RA Robson K.J.;
RT "A family of cation ATPase-like molecules from Plasmodium
RT falciparum."
RT J. Cell Biol. 120:385-398(1993).
RL -1- CATALYTIC ACTIVITY: ATP + H(2)O -> ADP + PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2
CC ATPASES). SUBFAMILY V.
CC -----
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CC -----
EMBL: X65738; CAA6646.1; -

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DR InterPro: IPR001757; E1-E2_ATPase.
DR Pfam: PF00122; E1-E2_ATPase; 1.
DR PROSITE: PS00154; ATPASE_E1_E2; 1.
KW Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding.
FT 1 35 CYTOPLASMIC (POTENTIAL).
FT 36 58 POTENTIAL.
FT 59 61 EXTRACELLULAR (POTENTIAL).
FT 62 80 POTENTIAL.
FT 81 407 CYTOPLASMIC (POTENTIAL).
FT 408 427 POTENTIAL.
FT 428 440 EXTRACELLULAR (POTENTIAL).
FT 441 462 POTENTIAL.
FT 463 1818 CYTOPLASMIC (POTENTIAL).
FT 1819 1837 POTENTIAL.
FT 1838 1845 EXTRACELLULAR (POTENTIAL).
FT 1846 1863 POTENTIAL.
FT 1864 1881 CYTOPLASMIC (POTENTIAL).
FT 1882 1905 POTENTIAL.
FT 1906 1928 EXTRACELLULAR (POTENTIAL).
FT 1929 1952 POTENTIAL.
FT 1953 1956 CYTOPLASMIC (POTENTIAL).
FT 1956 1956 PHOSPHORYLATION (BY SIMILARITY).
FT 1760 1760 MAGNESIUM (BY SIMILARITY).
FT 1764 1764 MAGNESIUM (BY SIMILARITY).
FT 246 251 POLY-ASN.
FT 252 256 POLY-LYS.
FT 937 941 POLY-ASN.
FT 1344 1347 POLY-LYS.
FT 1363 1372 POLY-ASN.
FT 1680 1684 POLY-ASN.
FT 1956 AA; 230285 MM; AE708AAE99009335 CRC64;
SO SEQUENCE

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Query Match 23.1%; Score 6; DB 1; Length 1956;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 15 EHLLVD 20
    |||||
Db 1693 EHLLVD 1700

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RESULT 45
APB_HUMAN STANDARD: PRT; 4563 AA.
ID APB_HUMAN
AC P04114; O00502; Q13787;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipoprotein
DE B-48 (Apo B-48)].
GN APOB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87016385; PubMed=3763409;
RA Knott T.C., Wallis S.C., Powell L.M., Pease R.J., Lusis A.J.,
RA Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.;
RT "Complete cDNA and derived protein sequence of human apolipoprotein
RT B-100."
RL Nucleic Acids Res. 14:7501-7503(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88003974; PubMed=3652907;
RA Ludwig E.R., Blackhart B.D., Pierotti V.R., Caiati L., Fortier C.,
RA Knott T., Scott J., Mahley R.W., Levy-Wilson B., McCarthy B.J.;
RT "DNA sequence of the human apolipoprotein B gene."
RT DNA 6:363-372(1987).
RN [3]
RP SEQUENCE FROM N.A.

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RX MEDLINE-87008488; PubMed-3759943;
 RA Chen S.-H., Yang C.-Y., Chen P.-F., Setzer D., Tanimura M., Li W.-H.,
 RA Goto A.M. Jr., Chan L.;
 RT "The complete cDNA and amino acid sequence of human apolipoprotein
 RT B-100.";
 RL J. Biol. Chem. 261:12918-12921(1986).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-87041416; PubMed-3464946;
 RA Law S.W., Grant S.M., Hignault K., Hospattankar A.V., Leckner K.J.,
 RA Lee N., Brewer H.B. Jr.;
 RT "Human liver apolipoprotein B-100 cDNA: complete nucleic acid and
 RT derived amino acid sequence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:8142-8146(1986).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-87161758; PubMed-3030729;
 RA Cladarias C., Hadzopolou-Cladarias M., Nolte R.T., Atkinson D.,
 RA Zannis V.I.;
 RT "The complete sequence and structural analysis of human
 RT apolipoprotein B-100: relationship between apob-100 and apob-48
 RT forms.";
 RL EMBO J. 5:3495-3507(1986).
 RN [6]
 RP SEQUENCE OF 709-906 FROM N.A.
 RX MEDLINE-85270450; PubMed-3860836;
 RA Deeb S.S., Muculsky A.G., Alberts J.J.;
 RT "A partial cDNA clone for human apolipoprotein B.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:4983-4986(1985).
 RN [7]
 RP SEQUENCE OF 3056-3159 FROM N.A.
 RX MEDLINE-86041888; PubMed-3903660;
 RA Mehrabian M., Schumaker V.N., Fareed G.C., West R., Johnson D.F.,
 RA Kirchgessner T.G., Lin H.-C., Wang X., Ma Y., Mendiaz E., Lusis A.J.;
 RT "Human apolipoprotein B: identification of cDNA clones and
 RT characterization of mRNA.";
 RL Nucleic Acids Res. 13:6937-6953(1985).
 RN [8]
 RP SEQUENCE OF 1937-2018 AND 3811-4334 FROM N.A.
 RX MEDLINE-86093680; PubMed-3841204;
 RA Carlsson P., Olofsson S.O., Bondjers G., Darnfors C., Wiklund O.,
 RA Bjursell G.;
 RT "Molecular cloning of human apolipoprotein B cDNA.";
 RL Nucleic Acids Res. 13:8813-8826(1985).
 RN [9]
 RP SEQUENCE OF 3109-4563 FROM N.A.
 RX MEDLINE-85300528; PubMed-2994225;
 RA Knott T.J., Rall S.C. Jr., Innerarity T.L., Jacobson S.F.,
 RA Udeka M.S., Levy-Wilson B., Powell L.M., Pease R.J., Edgely R.,
 RA Nakai H., Byers M., Priestley L.M., Robertson E., Rall I.B.,
 RA Betsholtz C., Shows T.B., Mahley R.W., Scott J.;
 RT "Human apolipoprotein B: structure of carboxyl-terminal domains,
 RT sites of gene expression, and chromosomal localization.";
 RL Science 230:37-43(1985).
 RN [10]
 RP SEQUENCE OF 1-291 FROM N.A.
 RX MEDLINE-86149335; PubMed-3513177;
 RA Procter A.A., Hardman D.A., Schilling J.W., Miller J., Appleby V.,
 RA Chen G.C., Kirsch S.W., McEnroe G., Kane J.P.;
 RT "Isolation of a cDNA clone encoding the amino-terminal region of
 RT human apolipoprotein B.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:1467-1471(1986).
 RN [11]
 RP SEQUENCE OF 1-1670 FROM N.A.
 RX MEDLINE-86287319; PubMed-3461454;
 RA Procter A.A., Hardman D.A., Sato K.Y., Schilling J.W.,
 RA Yamanaka M., Hort Y.J., Hjertild K.A., Chen G.C., Kane J.P.;
 RT "Analysis of cDNA clones encoding the entire B-26 region of human
 RT apolipoprotein B.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:5678-5682(1986).
 RN [12]
 RP PARTIAL SEQUENCE, AND IDENTIFICATION (APO-B48).
 RX MEDLINE-88018019; PubMed-3659919;

RA Chen S.-H., Habib G., Yang C.-H., Gu Z.-W., Lee B.R., Weng S.-H.,
 RA Silberman S.R., Cai S.-J., Deslypere J.P., Rosseneu M.,
 RA Goto A.M. Jr., Li W.-H., Chan L.;
 RT "Apolipoprotein B-48 is the product of a messenger RNA with an organ-
 RT specific in-frame stop codon.";
 RL Science 238:363-366(1987).
 RN [13]
 RP DOMAINS
 RX MEDLINE-87039351; PubMed-3773997;
 RA Knott T.C., Pease R.J., Powell L.M., Wallis S.C., Rall S.C. Jr.,
 RA Innerarity T.L., Blackhart B., Taylor W.R., Marcel Y., Milne R.,
 RA Johnson D., Fuller M., Lusis A.J., McCarthy B.J., Mahley R.W.,
 RA Levy-Wilson B., Scott J.;
 RT "Complete protein sequence and identification of structural domains
 RT of human apolipoprotein B.";
 RL Nature 323:734-738(1986).
 RN [14]
 RP DOMAINS
 RA Yang C.-Y., Chen S.-H., Gianturco S.H., Bradley W.A., Sparrow J.T.,
 RA Tanimura M., Li W.-H., Sparrow D.A., Deloof H., Rosseneu M.,
 RA Lee F.-S., Gu Z.-W., Goto A.M. Jr., Chan L.;
 RT "Sequence, structure, receptor-binding domains and internal repeats
 RT of human apolipoprotein B-100.";
 RL Nature 323:738-742(1986).
 RN [15]
 RP CALCIUM-BINDING DATA
 RX MEDLINE-86242245; PubMed-3087360;
 RA Dashi N., Lee D.M., Mok T.;
 RT "Apolipoprotein B is a calcium binding protein.";
 RL Biochem. Biophys. Res. Commun. 137:493-499(1986).
 RN [16]
 RP VARIANT SER-438
 RX MEDLINE-91071750; PubMed-1979313;
 RA Navajas M., Laurent A.-M., Moreel J.-F., Ragab A., Cambou J.-P.,
 RA Cuny G., Cambien F., Roizes G.;
 RT "Detection by denaturing gradient gel electrophoresis of a new
 RT polymorphism in the apolipoprotein B gene.";
 RL Hum. Genet. 86:91-93(1990).
 RN [17]
 RP VARIANT FDB GLN-3527
 RX MEDLINE-89098975; PubMed-2563166;
 RA Soria L.F., Ludwig E.H., Clarke H.R.G., Vega G.L., Grundy S.M.,
 RA McCarthy B.J.;
 RT "Association between a specific apolipoprotein B mutation and
 RT familial defective apolipoprotein B-100.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:587-591(1989).
 RN [18]
 RP VARIANT LEU-2739
 RX MEDLINE-91016974; PubMed-2216805;
 RA Huang L.-S., Gavish D., Breslow J.L.;
 RT "Sequence polymorphism in the human apob gene at position 8344.";
 RL Nucleic Acids Res. 18:5922-5922(1990).
 RN [19]
 RP VARIANT FDB CYS-3558
 RX MEDLINE-95190020; PubMed-7883971;
 RA Pullinger C.R., Hennessy L.K., Chatterton J.E., Liu W., Love J.A.,
 RA Mendel C.M., Frost P.H., Malloy M.J., Schumaker V.N., Kane J.P.;
 RT "Familial ligand-defective apolipoprotein B. Identification of a new
 RT mutation that decreases LDL receptor binding affinity.";
 RL J. Clin. Invest. 95:1225-1234(1995).
 RN [20]
 RP VARIANTS L-1437; S-1914; K-2566; T-3121; A-3945; M-4128 AND T-4481.
 RX MEDLINE-97044521; PubMed-8889592;
 RA Poirier O., Ricard S., Behague I., Sourtau C., Evans A.E.,
 RA Avelaier D., Marques-Vidal P., Luc G., Roizes G., Cambien F.;
 RT "Detection of new variants in the apolipoprotein B (Apo B) gene by
 RT PCR-SSCP.";
 RL Hum. Mutat. 8:282-285(1996).
 RN [21]
 RP VARIANTS FDB GLN-3527 AND CYS-3558
 RX MEDLINE-97403938; PubMed-9259199;
 RA Rabes J.P., Varret M., Saint-Jore B., Ellich D., Jondeau G.,
 RA Krempf M., Giraudet P., Junien C., Boileau C.;

RT Familial ligand-defective apolipoprotein B-100: simultaneous
 RT detection of the ARG3500-->GLN and ARG3531-->CYS mutations in a
 RT French population".
 RL Hum. Mutat. 10:160-163(1997).
 RL [22]
 RX VARIANTS S-1914; R-1923; L-2739; D-3319; T-3427; Q-3432 AND I-3921.
 RX MEDLINE:98141125; PubMed:9490296;
 RA Leren T.P., Bakken K.S., Hoel V., Hjermann I., Berg K.:
 RT "Screening for mutations of the apolipoprotein B gene causing
 RT hypocholesterolemia".
 RL Hum. Genet. 102:44-49(1998).
 CC -1- FUNCTION: APOLOPROTEIN B IS A MAJOR PROTEIN CONSTITUENT OF
 CC CHYLOMICRONS, VLDL AND LDL. IT FUNCTIONS AS A RECOGNITION SIGNAL
 CC FOR THE CELLULAR BINDING AND INTERNALIZATION OF LDL PARTICLES BY
 CC THE APOB/E RECEPTOR.
 CC -1- DISEASE: DEFECTS IN APOB ARE A CAUSE OF FAMILIAL LIGAND-DEFECTIVE
 CC APOLOPROTEIN B-100 (FDB). IT IS A DOMINANTLY INHERITED DISORDER
 CC OF LIPOPROTEIN METABOLISM LEADING TO HYPERCHOLESTEROLEMIA AND
 CC INCREASED PRONENESS TO CORONARY ARTERY DISEASE (CAD).
 CC THE PLASMA CHOLESTEROL LEVELS ARE DRAMATICALLY ELEVATED DUE TO
 CC IMPAIRED CLEARANCE OF LDL PARTICLES BY DEFECTIVE APOB/E RECEPTORS.
 CC -1- DISEASE: DEFECTS IN APOB ASSOCIATED WITH OTHER GENE DEFECTS
 CC (POLYGENIC) CAN BE THE CAUSE OF HYPOCHOLESTEROLEMIA.
 CC -1- MISCELLANEOUS: APO B-48 WHICH IS SYNTHESIZED ONLY BY THE
 CC INTESTINE, AND FOUND IN CHYLOMICRONS, IS A SHORTENED FORM OF APO
 Query Match 23.1%; Score 6; DB 1; Length 4563;
 Best Local Similarity 100.0%; Pred. No. 4,2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 5 LLLLOMD 10
 DB 1146 LLLLOMD 1151
 ID PRTM_PORPU STANDARD; PRT; 32 AA.
 AC P51275;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cytochrome B6-F complex subunit VII (Cytochrome b6f complex subunit
 DE PRTM).
 CN PRTM OR YCF31.
 OS Porphyra purpurea.
 OS Chloroplast.
 OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
 OX NCBL_TaxID=2787;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=AVONPORT;
 RA Reith M.E., Munholland J.:
 RT "Complete nucleotide sequence of the Porphyra purpurea chloroplast
 RT genome".
 RL Plant Mol. Biol. Rep. 13:333-335(1995).
 CC -1- FUNCTION: CYTOCHROME B6-F COMPLEX SUBUNIT.
 CC -1- SUBCELLULAR LOCATION: Thylakoid membrane-associated (By
 CC similarity).
 CC -1- SIMILARITY: BELONGS TO THE PRTM FAMILY.
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 CC -----
 DR EMBL: U38804; AAC08161.1; -
 DR Mendei; 10379; PORPU; c131.1.
 DR Electron transport; Chloroplast; Respiratory chain; Thylakoid;
 KW Transmembrane.

FT TRANSMEM 5 25 POTENTIAL.
 SQ SEQUENCE 32 AA; 3313 MW; 3F20EBB34379FDA CRC64;
 Query Match 19.2%; Score 5; DB 1; Length 32;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 3 GFLLL 7
 DB 23 GFLLL 27
 ID Y5K6_SSV1 STANDARD; PRT; 45 AA.
 AC P20198;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical 5.6 kDa protein (ORF A-45).
 OS Sulfolobus virus-like particle SSV1.
 OC Viruses; dsDNA viruses, no RNA stage; Fuselloviridae; Fusellovirus.
 OX NCBL_TaxID=10476;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE:92024080; PubMed-1926776;
 RA Palm P., Schleper C., Gramp B., Yeats S., McWilliam P., Reiter W.-D.,
 RA Zillig W.:
 RT "Complete nucleotide sequence of the virus SSV1 of the
 RT archaeobacterium Sulfolobus shibatae".
 RL Virology 185:242-250(1991).
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 CC -----
 DR EMBL: X07234; CAA30195.1; -
 DR PIR: S03227; S03227.
 DR InterPro: IPR000822; Znf-C2H2.
 DR Pfam: PF00096; zf-C2H2; 1.
 DR SMART: SM00355; Znf-C2H2; 1.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 1.
 DR PROSITE: PS00157; ZINC_FINGER_C2H2_2; 1.
 KW Hypothetical protein; Zinc-finger; Metal-binding.
 FT ZN_FING 2
 FT C2H2_TYPR 25
 SQ SEQUENCE 45 AA; 5559 MW; 38BF487E0DCA308B CRC64;
 Query Match 19.2%; Score 5; DB 1; Length 45;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 15 EHLIV 19
 DB 19 EHLIV 23
 ID ATP8_HANWT STANDARD; PRT; 48 AA.
 AC P48882;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6U).
 GN ATP8.
 GN Hansenula wingel (Yeast).
 OS Mitochondrion.

CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxID=4907;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=21;
RA Sekito T., Okamoto K., Kitano H., Yoshida K.;
RT "Yeast Hansenula wingei mitochondria genome's complete DNA sequence
RT demonstrated unique characteristics."
RL Nucleic Acids Symp. Ser. 31:233-234(1994).
CC -1- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT
CC (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
CC -1- SUBCELLULAR LOCATION: Membrane-bound.
CC -1- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.
CC -----
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CC -----
DR EMBL: D31785; BAA05655.1; -
KM Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
FT TRANSMEM 13 33 POTENTIAL.
SQ SEQUENCE 48 AA; 5879 MM; 2714F6968DB8BDC CRC64;

Query Match 19.2%; Score 5; DB 1; Length 46;
Best local similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFFLL 7
Db 16 GFFLL 20

RESULT 49
ID IAC1_BOVIN STANDARD; PRT; 63 AA.
AC P01000;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acrosin inhibitor I (BUST-I).
OS Bos taurus (Bovine).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=84133805; PubMed=6365719;
RA Meloun B., Cechova D., Jonakova V.;
RT "Homologies in the structures of bull seminal plasma acrosin
RT inhibitors and comparison with other homologous proteinase inhibitors
RT of the kazal type."
RL Hoppe-Seyler's Z. Physiol. Chem. 364:1665-1670(1983).
CC -1- FUNCTION: THIS PROTEIN IS A STRONG INHIBITOR OF ACROSIN.
CC -1- SIMILARITY: CONTAINS 1 KAZAL-LIKE DOMAIN.
DR HSSP: P01004; XTBO1.
DR HSSP: P01004; 1SGP.
DR InterPro: IPR001239; Kazal_inhb.
DR InterPro: IPR002350; kazal.
DR Pfam: PF00050; kazal.1.
DR PRINTS: PR00290; KAZALINHTR.
DR SMART: SM00280; KAZAL.1.
DR PROSITE: PS00282; KAZAL.1.
KM Serine protease inhibitor; Semen.
FT DISULFID 14 43 BY SIMILARITY.
FT DISULFID 21 40 BY SIMILARITY.
FT DISULFID 29 61 BY SIMILARITY.

FT ACT_SITE 23 24 REACTIVE BIND.
SQ SEQUENCE 63 AA; 7379 MM; A0265898ABDB2 CRC64;

Query Match 19.2%; Score 5; DB 1; Length 63;
Best local similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 DEGFP 14
Db 7 DEGFP 11

RESULT 50
ID YC55_HAEIN STANDARD; PRT; 74 AA.
AC P44141;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein H11255.
GN H11255.
OS Haemophilus influenzae.
CC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
CC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Usterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geophagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
RT influenzae Rd."
RL Science 269:496-512(1995).
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CC -----
DR EMBL: U32805; AAC22910.1; -
DT TIGR: H11255; -
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 74 AA; 8446 MM; CC22E0A66C0C98D3 CRC64;

Query Match 19.2%; Score 5; DB 1; Length 74;
Best local similarity 100.0%; Pred. No. 11e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 VDFLQ 23
Db 70 VDFLQ 74

Search completed: June 19, 2002, 11:11:22
Job time: 201 sec

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OM protein - protein search, using sw model

Run on: June 19, 2002, 11:07:41 ; Search time 25.27 Seconds
(Without alignments)
177.992 Million cell updates/sec

Title: US-09-943-334-1

Perfect score: 26

Sequence: 1 RDGFLLLQMDFGFPHLLVDFLQSL 26

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Database :

1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*
15: SP-virus:*
16: SP-bacteriap:*
17: SP-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	61.5	485	6 Q9BG59	C9bb59 tupia glis
2	7	26.9	210	11 Q9WVJ8	Q9WVJ8 mus musculus
3	7	26.9	213	11 Q9WVJ7	Q9WVJ7 mus musculus
4	7	26.9	221	11 Q9QXN7	Q9QXN7 mus musculus
5	7	26.9	227	11 Q9WU32	Q9WU32 mus musculus
6	7	26.9	227	16 Q9ZKY0	Q9ZKY0 rhizodolum m
7	7	26.9	238	11 Q9WU39	Q9WU39 mus musculus
8	7	26.9	244	11 Q9WU31	Q9WU31 mus musculus
9	7	26.9	263	10 Q9M8S3	Q9M8S3 mus musculus
10	7	26.9	280	16 Q9K8S9	Q9K8S9 bacillus ha
11	7	26.9	373	2 Q931N5	Q931N5 xanthomonas
12	7	26.9	405	10 Q91MT6	Q91MT6 arabidopsis
13	7	26.9	547	16 Q9FLJ7	Q9FLJ7 vibrio chol
14	7	26.9	846	2 Q956R3	Q956R3 escherichia
15	7	26.9	861	10 Q94CF2	Q94CF2 arabidopsis

17	7	26.9	903	5 Q9XX09	Q9XX09 caenorhabd
18	7	26.9	1300	2 Q3Z5S5	Q3Z5S5 escherichia
19	7	26.9	1300	2 Q3Z591	Q3Z591 escherichia
20	6	23.1	81	2 Q9L7I9	Q9L7I9 synechococ
21	6	23.1	88	6 Q95L08	Q95L08 atetes belz
22	6	23.1	111	9 Q9MC72	Q9MC72 bacterioph
23	6	23.1	112	11 Q9DBU1	Q9DBU1 mus muscu
24	6	23.1	115	16 Q9R317	Q9R317 pseudomon
25	6	23.1	130	16 Q67666	Q67666 aquilex aeo
26	6	23.1	150	11 Q9UM85	Q9UM85 mus muscu
27	6	23.1	155	10 Q9DB70	Q9DB70 mus muscu
28	6	23.1	163	17 Q97VI6	Q97VI6 arabidops
29	6	23.1	166	2 Q52651	Q52651 rhodobact
30	6	23.1	166	3 Q9P3B0	Q9P3B0 schizosacch
31	6	23.1	204	16 Q55840	Q55840 synechocyst
32	6	23.1	210	16 Q9A706	Q9A706 caulobacter
33	6	23.1	222	11 Q9D6M8	Q9D6M8 mus muscu
34	6	23.1	235	10 Q9ST53	Q9ST53 malus domes
35	6	23.1	241	2 Q86738	Q86738 streptomyc
36	6	23.1	260	16 Q9K909	Q9K909 bacillus su
37	6	23.1	275	16 Q99UJ1	Q99UJ1 staphylococ
38	6	23.1	279	2 Q87858	Q87858 streptomyce
39	6	23.1	279	5 Q9N535	Q9N535 caenorhabd
40	6	23.1	283	16 Q07011	Q07011 bacillus su
41	6	23.1	283	16 Q9KBA7	Q9KBA7 bacillus ha
42	6	23.1	289	10 Q9R085	Q9R085 nicotiana t
43	6	23.1	298	16 Q9KD33	Q9KD33 bacillus ha
44	6	23.1	303	16 Q85704	Q85704 staphylococ
45	6	23.1	305	4 Q9HBL5	Q9HBL5 homo sapien
46	6	23.1	311	11 Q9PB00	Q9PB00 candida alb
47	6	23.1	311	3 Q9DB26	Q9DB26 mus muscu
48	6	23.1	313	16 Q9GRY9	Q9GRY9 staphylococ
49	6	23.1	324	10 Q9F084	Q9F084 nicotiana t
50	6	23.1	324	16 Q98109	Q98109 rhizobium l
51	6	23.1	335	13 Q9DES4	Q9DES4 figu rubrip
52	6	23.1	351	4 Q13539	Q13539 homo sapien
53	6	23.1	354	4 Q96LJ5	Q96LJ5 homo sapien
54	6	23.1	354	4 Q96EM0	Q96EM0 homo sapien
55	6	23.1	354	11 Q9CXA2	Q9CXA2 mus muscu
56	6	23.1	354	11 Q9XK85	Q9XK85 mus muscu
57	6	23.1	365	10 Q9F086	Q9F086 nicotiana t
58	6	23.1	378	5 Q9VME8	Q9VME8 dirosophila
59	6	23.1	380	5 Q9VH17	Q9VH17 dirosophila
60	6	23.1	380	13 Q9DEU6	Q9DEU6 cyprinus ca
61	6	23.1	390	10 Q9F090	Q9F090 nicotiana t
62	6	23.1	393	17 Q97VGL	Q97VGL sulfolobus
63	6	23.1	394	10 Q9AVY2	Q9AVY2 guilliardea
64	6	23.1	397	16 Q26006	Q26006 helicobacte
65	6	23.1	406	16 Q9ZJ58	Q9ZJ58 helicobacte
66	6	23.1	414	5 Q9XUG7	Q9XUG7 caenorhabd
67	6	23.1	416	2 Q9RIS4	Q9RIS4 streptomyc
68	6	23.1	419	4 Q9UG83	Q9UG83 homo sapien
69	6	23.1	422	5 Q02282	Q02282 caenorhabd
70	6	23.1	425	4 Q9BS18	Q9BS18 homo sapien
71	6	23.1	425	10 Q9F091	Q9F091 nicotiana t
72	6	23.1	425	11 Q9CMP7	Q9CMP7 mus muscu
73	6	23.1	426	3 Q9HFE5	Q9HFE5 schizosacch
74	6	23.1	439	5 Q965V6	Q965V6 caenorhabd
75	6	23.1	439	5 Q965V6	Q965V6 caenorhabd

ALIGNMENTS

RESULT 1
Q9BG59
ID Q9BG59; PRELIMINARY; PRT: 485 AA.
AC 01-JUN-2001 (TRENBLREL. 17, Created)
DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE CHOLESTERYL ESTER TRANSFER PROTEIN (FRAGMENT).
OS Tupia glis (Tree shrew).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Scandentia; Tupalidae; Tupaiia.
OX NCBI_TaxID=9395;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Zeng W.W., Chen B.S., Zhang J.;
RT "Cloning and sequencing of tree shrew cholesterol ester transfer
protein (CETP) cDNA."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF334033; AAK08086.1; -
DR InterPro: IPR001124; LBP_BPL_CETP.
DR Pfam; PF01273; LBP_BPL_CETP; 1.
DR Pfam; PF02886; LBP_BPL_CETP_C; 1.
DR SMART; SM00328; BPL; 1.
DR SMART; SM00329; BPL2; 1.
DR PROSITE; PS00400; LBP_BPL_CETP; 1.
FT NON_TER 1
SQ SEQUENCE 485 AA; 53993 MW; 2605E76D2635C367 CRC64;

Query Match 61.5%; Score 16; DB 6; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DFFLLQMDGFPEHL 17
DB 461 DFFLLQMDGFPEHL 476

RESULT 2
O9WVJ8 PRELIMINARY; PRT; 210 AA.
ID O9WVJ8;
AC O9WVJ8;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE NATURAL KILLER CELL PROTEIN GROUP 2-A2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=9929364; PubMed=10369936;
RA Silver E.T., Lau J.C., Kane K.P.;
RT "Molecular cloning of mouse NKG2A and C.";
RL Immunogenetics 49:727-730(1999).
DR EMBL; AF106009; AAD40222.1; -
DR InterPro: IPR001304; lectin_c.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 210 AA; 24210 MW; 0F7F9C3903F34E97 CRC64;

Query Match 26.9%; Score 7; DB 11; Length 210;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 DFLQSL 26
DB 139 DFLQSL 145

RESULT 3
O9WVJ7 PRELIMINARY; PRT; 213 AA.
ID O9WVJ7;
AC O9WVJ7;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE NATURAL KILLER CELL PROTEIN GROUP 2-C2.
GN KIRC2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=9929364; PubMed=10369936;
RA Silver E.T., Lau J.C., Kane K.P.;
RT "Molecular cloning of mouse NKG2A and C.";
RL Immunogenetics 49:727-730(1999).
DR EMBL; AF106011; AAD40224.2; -
DR MGD; MGI:1336163; KIRC2.
DR InterPro: IPR001304; lectin_c.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 213 AA; 23951 MW; 6633CB9DFC46C4DD CRC64;

Query Match 26.9%; Score 7; DB 11; Length 213;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 DFLQSL 26
DB 142 DFLQSL 148

RESULT 4
O9QXN7 PRELIMINARY; PRT; 221 AA.
ID O9QXN7;
AC O9QXN7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE NATURAL KILLER CELL GROUP 2E CELL RECEPTOR NKG2E.
GN KIRC3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=20069888; PubMed=10601355;
RA Vance R.E., Jamieson A.M., Raulat D.H.;
RT "Recognition of the class II molecule Qa-1b by putative activating
receptors CD94/NKG2c and CD94/NKG2e on mouse natural killer cells.";
RL J. Exp. Med. 190:1801-1812(1999).
DR EMBL; AF195779; AAF24982.1; -
DR MGD; MGI:1929720; KIRC3.
DR InterPro: IPR001304; lectin_c.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
RN Receptor.
SQ SEQUENCE 221 AA; 24925 MW; FA521B9017BD0473 CRC64;

Query Match 26.9%; Score 7; DB 11; Length 221;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 DFLQSL 26
DB 150 DFLQSL 156

RESULT 5
O9WU32

ID Q9W032 PRELIMINARY; PRT; 227 AA.
 AC Q9W032;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE NATURAL KILLER CELL RECEPTOR NKG2B.
 GN KIRCL OR NKG2B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=99190498; PubMed=10092077;
 RA Lohwasser S., Hande P., Mager D.L., Takel F.;
 RT Cloning of murine NKG2A, B and C: second family of C-type lectin
 RT receptors on murine NK cells.*;
 RL Eur. J. Immunol. 29:755-761(1999).
 DR EMBL; AF109784; AAD24970.1; -;
 DR MGD; MGI:1336161; Klrcl.
 DR InterPro: IPR001304; lectin_c.
 DR Pfam: PF00059; lectin_c.1.
 DR SMART: SM00034; CLECT.1.
 DR PROSITE: PS50041; C-TYPE_LLECTIN_2; 1.
 KW Receptor.
 SQ SEQUENCE 227 AA; 25746 MW; 1651968539C28C86 CRC64;

Query Match 26.9%; Score 7; DB 11; Length 227;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 DFLQSLs 26
 Db 156 DFLQSLs 162
 |||||
 RESULT 6
 Q92KYO PRELIMINARY; PRT; 227 AA.
 ID Q92KYO;
 AC Q92KYO;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PUTATIVE CARBONIC ANHYDRASE PROTEIN (EC 4.2.1.1).
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21368234; PubMed=11474104;
 RA Galibert F., Finan T.M., Long S.R., Puehler A., Abola F., Ampe F.,
 RA Barloy-Hubier F., Barnett M.J., Becker A., Boissard P., Botne G.,
 RA Boutry M., Bowser L., Burnmaster J., Cadieu E., Capela D., Chail P.,
 RA Cowie A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F.,
 RA Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M.,
 RA Hernandez-Jucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D.,
 RA Kahn M.L., Kaiman S., Keating D.H., Kiss E., Komp C., Lelaure V.,
 RA Masny D., Palm C., Peck M.C., Pohl T.M., Portetelle D., Purnelle B.,
 RA Rameberger U., Surzycki R., Thebaud P., Vandenbol M.,
 RA Vorholter F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.;
 RT The composite genome of the legume symbiont Sinorhizobium meliloti.*;
 RL Science 293:668-672(2001).
 DR EMBL; AL591793; CAC47897.1; -;
 KW Lyase; Complete proteome.
 SO SEQUENCE 227 AA; 25244 MW; D34001C07F69D76F CRC64;

Query Match 26.9%; Score 7; DB 16; Length 227;
 Best Local Similarity 100.0%; Pred. No. 13;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 12 GPEHLL 18
 Db 17 GPEHLL 23

RESULT 7
 Q9WTJ9 PRELIMINARY; PRT; 238 AA.
 ID Q9WTJ9;
 AC Q9WTJ9;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE NATURAL KILLER CELL PROTEIN GROUP 2-C1.
 GN KLRK2 OR NKG2C.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=99299364; PubMed=10369936;
 RA Silver E.T., Lau J.C.Y., Kane K.P.;
 RT Molecular cloning of mouse NKG2A and C.*;
 RL Immunogenetics 49:727-730(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=99190498; PubMed=10092077;
 RA Lohwasser S., Hande P., Mager D.L., Takel F.;
 RT Cloning of murine NKG2A, B and C: second family of C-type lectin
 RT receptors on murine NK cells.*;
 RL Eur. J. Immunol. 29:755-761(1999).
 DR EMBL; AF106010; AAD40223.1; -;
 DR MGD; MGI:1336162; Klrcl.
 DR InterPro: IPR001304; lectin_c.
 DR Pfam: PF00059; lectin_c.1.
 DR SMART: SM00034; CLECT.1.
 DR PROSITE: PS50041; C-TYPE_LLECTIN_2; 1.
 KW Receptor.
 SQ SEQUENCE 238 AA; 26811 MW; 8C3EDAA22D650451 CRC64;

Query Match 26.9%; Score 7; DB 11; Length 238;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 DFLQSLs 26
 Db 167 DFLQSLs 173
 |||||
 RESULT 8
 Q9Z202 PRELIMINARY; PRT; 244 AA.
 ID Q9Z202;
 AC Q9Z202;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE NATURAL KILLER CELL RECEPTOR NKG2A.
 GN KIRCL OR NKG2A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=99034608; PubMed=9815261;
 RA Vance R.E., Kraft J.R., Altman J.D., Jensen P.E., Raulat D.H.;

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RT "Mouse CD94/NGG2A is a natural killer cell receptor for the
RT nonclassical major histocompatibility complex (MHC) class I molecule
RT Qa-1(b).";
RL J. Exp. Med. 188:1841-1848(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6;
RX MEDLINE-99299364; PubMed-10369936;
RA Silver E.T., Lau J.C.Y., Kane K.P.;
RT "Molecular cloning of mouse NKG2A and C.";
RL Immunogenetics 49:727-730(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6;
RX MEDLINE-99190498; PubMed-10092077;
RA Lohwasser S., Hande P., Mager D.L., Takel F.;
RT "Cloning of murine NKG2A, B and C: second family of C-type lectin
RT receptors on murine NK cells.";
RL Eur. J. Immunol. 29:755-761(1999).
DR EMBL: AF095447; AAD03419.1; -;
DR EMBL: AF106008; AAD40221.1; -;
DR EMBL: AF109782; AAD4968.1; -;
DR MGD: MGI:1336161; K1rc1.
DR InterPro: IPR001304; lectin_c.
DR Pfam: PF00059; lectin_c.1.
DR SMART: PS50034; CLECT.1.
DR PROSITE: PS50041; C_Type_Lectin_2; 1.
KW Receptor.
SQ SEQUENCE 244 AA; 27675 MW; 187E7A8439FBF68A CRC64;

Query Match 26.9%; Score 7; DB 11; Length 244;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 DFLOSLS 26
DB 173 DFLOSLS 179

RESULT 9
O9W031 PRELIMINARY; PRT; 244 AA.
AC O9W031;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE NATURAL KILLER CELL RECEPTOR NKG2A.
GN K1RC1 OR NKG2A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RX MEDLINE-99190498; PubMed-10092077;
RA Lohwasser S., Hande P., Mager D.L., Takel F.;
RT "Cloning of murine NKG2A, B and C: second family of C-type lectin
RT receptors on murine NK cells.";
RL Eur. J. Immunol. 29:755-761(1999).
DR EMBL: AF109783; AAD24969.1; -;
DR MGD: MGI:1336161; K1rc1.
DR InterPro: IPR001304; lectin_c.
DR Pfam: PF00059; lectin_c.1.
DR SMART: SM00034; CLECT.1.
DR PROSITE: PS50041; C_Type_Lectin_2; 1.
KW Receptor.
SQ SEQUENCE 244 AA; 27605 MW; 072003BD7F5AAD9E CRC64;

Query Match 26.9%; Score 7; DB 11; Length 244;
Best Local Similarity 100.0%; Pred. No. 14;

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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 DFLOSLS 26
DB 173 DFLOSLS 179

RESULT 10
O9W9S3 PRELIMINARY; PRT; 263 AA.
AC O9W9S3;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE F14L17.18 PROTEIN (HYPOTHETICAL 29.1 KDA PROTEIN).
GN F14L17.18.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RA Liu S., Sakano H., Yu G., Lee J., Lenz C., Pham P., Toriumi M.,
RA Chin C., Chlou J., Choi E., Chung M., Gonzalez A., Hwang B., Liu A.,
RA Vaysberg M., Altafi H., Brooks S., Buehler E., Chao Q., Conn L.,
RA Conway A., Hansen M., Johnson-Hopson C., Khan S., Kim C., Lam B.,
RA Miranda M., Nguyen M., Palm C., Shinn P., Southwick A., Davis R.,
RA Ecker J., Federspiel N., Theologis A.;
RT "The sequence of BAC F14L17 from Arabidopsis thaliana chromosome 1.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RA Theologis A.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RA Theologis A.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RA Theologis;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Etgu P., Lee J.M.,
RA Toriumi M., Yu G., Brooks S., Chao Q., Chen H., Karlin-Neumann G.,
RA Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shinn P.,
RA Southwick A., Davis R.W., Ecker J.R., Theologis A.;
RT "Full length cDNA of gene F14L17.18 (GI:7262683).";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
RA Lee J.M., Ondera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,
RA Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Kim C., Koeseima E., Lam B., Lin J., Meyers M.C., Miranda M.,
RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
RA Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,
RA Ecker J.R., Theologis A.;
RT "Full length cDNA of gene F14L17.18 (GI:7262683).";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Tang C., Toriumi M., Yu G.,
RA Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J.,
RA Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koeseima E.,

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RA Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M.,
 RA Palm C.J., Sakurai T., Saeu M., Seki M., Shinn P., Southwick A.,
 RA Shinohara K., Davis R.W., Ecker J.R., Theologis A.;
 RT *Full Length cDNA of gene F14L17.18 (GI:7262683).";
 RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC012188; AAF3941.1; -;
 DR EMBL: AF332452; AAC48815.1; -;
 DR EMBL: AF059097; AAL15203.1; -;
 DR EMBL: AF370156; AAK43971.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 263 AA; 29058 MW; E90F85763198C614 CRC64;

Query Match 26.9%; Score 7; DB 10; Length 263;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGFLLQ 8
 DB 116 DGFLLQ 122

RESULT 11
 O9K8S9 PRELIMINARY; PRT; 280 AA.
 AC O9K8S9;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE MALTOSE/MALTODEXTRIN TRANSPORT SYSTEM (PERMEASE).
 GN BH2924.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C-125 / JCM 9153;
 RX MEDLINE:20512562; PubMed:11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirata C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 RT *Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis.";
 RL Nucleic Acids Res. 28:4317-4331(2000)
 CC -1- FUNCTION: PROBABLY PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT
 CC SYSTEM. PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION OF THE
 CC SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
 CC PROTEIN-DEPENDENT TRANSPORT SYSTEMS.
 DR EMBL: AP001517; BAB06643.1; -;
 DR InterPro: IPR000515; BPD_transp.
 DR Pfam: PF00528; BPD_transp. 1.
 DR PROSITE: PS00402; BPD_TRANSF. INN_MEMBR. 1.
 KW Complete proteome; Transmembrane; Transport.
 SQ SEQUENCE 280 AA; 31670 MW; E7CBF596591B95C4 CRC64;

Query Match 26.9%; Score 7; DB 16; Length 280;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFLLLQ 9
 DB 112 GFLLLQ 118

RESULT 12
 O93LNS PRELIMINARY; PRT; 373 AA.
 AC O93LNS;
 DE 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE OUTER PROTEIN J.
 OS Xanthomonas campestris (pv. vesicatoria).
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 OC Xanthomonas.
 OX NCBI_TaxID=341;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Noel L.D., Thieme F., Nennstiel D., Bonas U.;
 RT *cDNA-AFLP analysis unravels a genome-wide hrp-regulon in the plant
 RT pathogen Xanthomonas campestris pv. vesicatoria.";
 RL Mol. Microbiol. 0:0-0(2001).
 DR EMBL: AY036108; AAK72486.1; -;
 SQ SEQUENCE 373 AA; 40600 MW; 6AFEA76783ACE642 CRC64;

Query Match 26.9%; Score 7; DB 2; Length 373;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 DFLQSL 26
 DB 146 DFLQSL 152

RESULT 13
 O9LMT6 PRELIMINARY; PRT; 405 AA.
 AC O9LMT6;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE F2H15.16.
 GN F2H15.16.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Euphorbia II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA Sakano H., Liu S.X., Egu P., Lee J.M., Lenz C., Pham P., Toriumi M.,
 RA Yu G., Chan A., Chung M., Goldsmith A., Liu A., Smith A., Vaysberg M.,
 RA Altieri H., Brooks S., Buehler E., Chao Q., Conn L., Conway A.B.,
 RA Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M.,
 RA Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R.,
 RA Federspiel N.A., Theologis A.;
 RT The sequence of BAC F2H15 from Arabidopsis thaliana chromosome 1.";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC034106; AAF97273.1; -;
 SQ SEQUENCE 405 AA; 45080 MW; B681476986480D5D CRC64;

Query Match 26.9%; Score 7; DB 10; Length 405;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 VDFLOSL 25
 DB 37 VDFLOSL 43

RESULT 14
 O9KLJ7 PRELIMINARY; PRT; 547 AA.
 AC O9KLJ7;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ANAEROBIC GLYCEROL-3-PHOSPHATE DEHYDROGENASE, SUBUNIT A.
 GN VCA0747.

OS *Vibrio cholerae*.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; *Vibrio*.
 OX NCBI_TaxID=66;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EL TOR N16961 / SEROTYPE O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
 Dodson R.D., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen *Vibrio*
 cholerae.";
 RL Nature 406:477-483(2000).
 DR EMBL: AE004403; AAF96645.1; -.
 DR TIGR: VCA0747; -.
 DR InterPro: IPR000447; FAD_GLY3P_dh.
 DR InterPro: IPR001345; PG_mutase.
 DR PRINTS: PR01001; FADG3PDH.
 DR PROSITE: PS00978; FAD_G3PDH_2; 1.
 DR PROSITE: PS00175; PG_MUTASE; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 547 AA; 59915 MW; AC5942DED04165A8 CRC64;

Query Match 26.9%; Score 7; DB 16; Length 547;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 LTVDFL 22
 |||||
 DB 495 LTVDFL 501

RESULT 15
 ID 0956R3 PRELIMINARY; PRT; 846 AA.
 AC 0956R3;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE ESPP PROTEIN (FRAGMENT).
 GN ESPP.
 OS *Escherichia coli*.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99303308; PubMed=10376815;
 RA Brunder W., Schmidt H., Frosch M., Karch H.;
 RT "The large plasmids of Shiga-toxin-producing *Escherichia coli* (STEC)
 are highly variable genetic elements.";
 RL Microbiology 145:1005-1014(1999).
 DR EMBL: AJ010390; CAB42538.1; -.
 DR InterPro: IPR000710; IGA_S6.
 DR Pfam: PF02395; IGA1; 1.
 KW Plasmid.
 RT none;
 FT NON_TER
 SQ SEQUENCE 846 AA; 91894 MW; 124C9E23421CDEB CRC64;

Query Match 26.9%; Score 7; DB 2; Length 846;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 17 LTVDFL 23
 |||||
 DB 479 LTVDFL 485

RESULT 16
 ID 094CF2 PRELIMINARY; PRT; 861 AA.
 AC 094CF2;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE HYDROTICAL 96.6 KDA PROTEIN.
 OS *Arabidopsis thaliana* (mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Goldsmith A.D., Lee J.M., Quach H.L., Tang C., Toriumi M., Yu G.,
 RA Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J.,
 RA Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koeseema E.,
 RA Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M.,
 RA Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A.,
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "Full length cDNA of gene T326.14/At2g41520 (G1261858).";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY034907; AAK59414.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 861 AA; 96615 MW; 9F53F0BFF013D673 CRC64;

Query Match 26.9%; Score 7; DB 10; Length 861;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 DFLOSL 26
 |||||
 DB 146 DFLOSL 152

RESULT 17
 ID 09XX09 PRELIMINARY; PRT; 903 AA.
 AC 09XX09;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE Y39A1A.15C PROTEIN.
 GN Y39A1A.15C.
 OS *Caenorhabditis elegans*.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Pelodermidae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wall M.;
 RT Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode *C. elegans*: A platform for
 investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL: AL031633; CAA21032.1; -.
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR001849; PH.
 DR InterPro: IPR001806; Ras_trnsfrmng.
 DR InterPro: IPR003575; Small_GTPase.
 DR InterPro: IPR001164; Znf_GCS.
 DR Pfam: PF00023; ank; 2.
 DR Pfam: PF01412; ArfGAP; 1.
 DR Pfam: PF00169; PH; 1.


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FT  NON-TER      1      1
SQ  SEQUENCE      81 AA; 8455 MM; 606190ATG5B0CB76 CRC64;

Query Match
Best Local Similarity 100.0%; Score 6; DB 2; Length 81;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  2 DGFLL 7
    |||||
Db  9 DGFLL 14

RESULT 21
O95L08 PRELIMINARY; PRT; 88 AA.
AC  O95L08;
DT  01-DEC-2001 (TREMBLrel. 19, Created)
DT  01-DEC-2001 (TREMBLrel. 19, last sequence update)
DE  APOLOPORTEIN B (FRAGMENT).
OS  Ateles belzebuth chamek (Chamek spider monkey).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX  Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateles;
    NCBI_TaxID=116643;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Suenes H.N., Lima C.R., Lemos B., Bonvicino C.R., Moreira M.M.,
RA  Canavez F.C.;
RT  *Gene assignment in Ateles paniscus chamek (Platyrrhini, Primates).
RT  Allocation of 18 markers of human syntenic groups 1, 2, 7, 14, 15, 17,
RT  and 22.*;
RL  Chromosome Res. 9:631-639(2001).
DR  EMBL; AY040549; AAK82940.1; -.
KW  Lipoprotein.
FT  NON-TER      1      1
FT  NON-TER      88     88
SQ  SEQUENCE      88 AA; 9981 MM; 95E7947A3DB73142 CRC64;

Query Match
Best Local Similarity 100.0%; Score 6; DB 6; Length 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  5 LLLQMD 10
    |||||
Db  15 LLLQMD 20

RESULT 22
O9MC72 PRELIMINARY; PRT; 111 AA.
AC  O9MC72;
DT  01-OCT-2000 (TREMBLrel. 15, Created)
DT  01-OCT-2000 (TREMBLrel. 15, last sequence update)
DE  01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE  ORF50.
GN  ORF50.
OS  Bacteriophage D3.
OC  Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OX  Lambda phage group.
OX  NCBI_TaxID=31535;
    [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=20042341; PubMed=10572124;
RA  Glajakjan Z.A., Kropinski A.M.;
RT  Cloning and analysis of the capsid morphogenesis genes of Pseudomonas
RT  aeruginosa bacteriophage D3: another example of protein chain mal1?;
RL  J. Bacteriol. 181:7221-7227(1999).
RN  [2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=20485557; PubMed=11029426;
RA  Kropinski A.M.;

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RT  "Sequence of the Genome of the Temperate, Serotype-Converting,
RT  Pseudomonas aeruginosa Bacteriophage D3.";
RL  J. Bacteriol. 182:6066-6074(2000).
DR  EMBL; AF165214; AAF80809.1; -.
SQ  SEQUENCE      111 AA; 12720 MM; 426E2DD0BAAD7413 CRC64;

Query Match
Best Local Similarity 100.0%; Score 6; DB 9; Length 111;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  2 DGFLL 7
    |||||
Db  37 DGFLL 42

RESULT 23
O9D8U1 PRELIMINARY; PRT; 112 AA.
AC  O9D8U1;
DT  01-JUN-2001 (TREMBLrel. 17, Created)
DT  01-JUN-2001 (TREMBLrel. 17, last sequence update)
DE  01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE  1810033P05RIK PROTEIN.
GN  1810033P05RIK.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
    NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX  MEDLINE=21085660; PubMed=11217851;
RA  Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA  Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA  Arakawa K., Izawa M., Nishi K., Kiyosawa H., Konno S., Yamataka I.,
RA  Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA  Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA  Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA  Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA  Schirral L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA  Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bash G.,
RA  Blake J., Boiffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA  Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA  Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA  Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA  Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA  Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA  Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,
RA  Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA  Hayashizaki Y.;
RT  "Functional annotation of a full-length mouse cDNA collection.";
RL  Nature 409:685-690(2001).
DR  EMBL; AK007686; BAB25190.1; -.
DR  MGD; MGI:1916434; 1810033P05RIK.
SQ  SEQUENCE      112 AA; 12043 MM; D97AAEA236659EFF CRC64;

Query Match
Best Local Similarity 100.0%; Score 6; DB 11; Length 112;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  3 GFLLQ 8
    |||||
Db  39 GFLLQ 44

RESULT 24
O9R317 PRELIMINARY; PRT; 115 AA.
AC  O9R317;
DT  01-MAY-2000 (TREMBLrel. 13, Created)
DT  01-MAY-2000 (TREMBLrel. 13, last sequence update)

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DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 12.9 KDA PROTEIN (HYPOTHETICAL PROTEIN PA0634).
 GN PA0634.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision: Pseudomonadaceae;
 OC Pseudomonas.
 NC NCB1_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01, AND PM14;
 RA Nakayama K., Takashima K., Ishihara H., Shinomiya T., Kageyama M.,
 Kanaya S., Ohnishi M., Murata T., Terawaki Y., Mori H., Hayashi T.,
 Genetic relationship between bacteriophages and bacteriophages";
 RT Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RA MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
 Hickey M.J., Brinkman F.S.L., Huffnagle W.O., Kowalik D.J., Lagrou M.,
 Garber R.L., Goltzy L., Tolentino E., Westbrook-Madman S., Yuan Y.,
 Brody L.L., Coulter S.N., Folger K.R., Kas A., Laidig K., Lim R.M.,
 Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 Reiter J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.,
 Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen.";
 RL Nature 406:959-964(2000).
 DR EMBL; AB030825; BAA83173.1; -;
 DR EMBL; AB030825; BAA83141.1; -;
 DR EMBL; AE004499; AAC04023.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 115 AA; 12870 MW; B869B89D3D19E49 CRC64;

Query Match 23.1%; Score 6; DB 16; Length 115;
 Best Local Similarity 100.0%; Pred. No. 70;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFLIQL 8
 DB 96 GFLIQL 101
 RESULT 25
 ID 067666 PRELIMINARY; PRT; 130 AA.
 AC 067666;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE HYPOTHETICAL 15.6 KDA PROTEIN.
 GN AO_1797.
 OS Aquifex aeolicus.
 OC Bacteria; Aquificales; Aquificaceae; Aquifex.
 NC NCB1_TaxID=63363;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VF5;
 RA MEDLINE=98196666; PubMed=9537320;
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 Graham D.E., Overbeek R., Sneed M.A., Keller M., Nijay M., Huber R.,
 Feilman R.A., Short J.M., Olson G.J., Swanson R.V.,
 "The complete genome of the hyperthermophilic bacterium Aquifex
 RT aeolicus.";
 RT Nature 392:353-358(1998).
 RL Nature 392:353-358(1998).
 DR EMBL; AE000756; AAC07630.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 130 AA; 15626 MW; 45CF04E5F6D90DDF CRC64;

Query Match 23.1%; Score 6; DB 16; Length 130;
 Best Local Similarity 100.0%; Pred. No. 78;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 LLYDFL 22
 DB 80 LLYDFL 85
 RESULT 26
 ID 09JMB5 PRELIMINARY; PRT; 150 AA.
 AC 09JMB5;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE DD64 PROTEIN.
 GN EROS1 OR DD64.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ikegawa S., Nakamura Y.;
 RT DD64, a novel mouse gene implicated in the early stage of ectopic
 RT ossification.";
 RL Submitted (Jan-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB036742; BAA95410.1; -;
 DR MGD; MGI:2149837; Eros1.
 SQ SEQUENCE 150 AA; 17248 MW; 233309C51DB484C7 CRC64;

Query Match 23.1%; Score 6; DB 11; Length 150;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFLIQL 8
 DB 120 GFLIQL 125
 RESULT 27
 ID 09DB70 PRELIMINARY; PRT; 155 AA.
 AC 09DB70;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE 1500005J14RIK PROTEIN (RIKEN CDNA 1500005J14 GENE).
 GN 1500005J14RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=CEREBELLUM;
 RA MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 Aitawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
 Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 Schiraldi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 Sakai K., Okido T., Furuno M., Kono H., Baldarelli R., Barsh G.,
 Blake J., Boileau D., Bojunga N., Carninci P., de Bonaldo M.F.,
 Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 Guenichon S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
 Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,
 Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,

RA Hayashizaki Y.;
 RT *Functional annotation of a full-length mouse cDNA collection.*;
 RL Nature 409:685-690(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK005163; BAB23854.1; -;
 DR EMBL; BC012515; AAH12515.1; -;
 DR MGI; MGI:1919268; 1500005J14RIK.
 SQ SEQUENCE 155 AA; 17158 MW; 8AAA46566714ED80 CRC64;

Query Match 23.1%; Score 6; DB 11; Length 155;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFLIQQ 8
 DB 82 GFLIQQ 87

RESULT 28
 Q9SKX1 PRELIMINARY; PRT; 156 AA.
 AC Q9SKX1;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE AT2G43060 PROTEIN.
 GN AT2G43060.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
 RA Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
 RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
 RA Coppenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
 RA Salzberg S.L., Fraser C.M., Venter J.C.;
 RT *Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana*;
 RL Nature 402:761-768(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Lin X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC006224; AAD22125.1; -;
 SQ SEQUENCE 156 AA; 17823 MW; 7D8C75BE4047A48A CRC64;

Query Match 23.1%; Score 6; DB 10; Length 156;
 Best Local Similarity 100.0%; Pred. No. 93;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 FLOSLS 26
 DB 22 FLOSLS 27

RESULT 29
 Q97VI6 PRELIMINARY; PRT; 163 AA.
 AC Q97VI6;
 DT 01-OCT-2001 (TREMBLrel. 18, Created)

DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
 DE CARBON MONOXIDE DEHYDROGENASE, SMALL CHAIN, AMINO-END FRAGMENT
 DE (CUTC-2) (EC 1.2.99.2).
 GN CUTC-2.
 OS Sulfolobus solfataricus.
 OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
 OX NCBI_TaxID=2287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35092 / DSM 1617 / P2;
 RX MEDLINE=2133296; PubMed=11427726;
 RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
 RA Awatez M.J., Chan-Weiler C.C.-Y., Clausen I.G., Curtis B.A.,
 RA De Moers A., Erasuo G., Fletcher C., Gordon P.M.R.,
 RA Helkamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
 RA Thi-Ngoc H.P., Redder P., Schenk M.E., Thériault C., Tolstrup N.,
 RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
 RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
 RT *The complete genome of the crenarchaeon Sulfolobus solfataricus P2.*;
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
 DR EMBL; AE006859; AAK42758.1; -;
 DR InterPro; IPR002888; 2Fe-2S_BD.
 DR InterPro; IPR001041; Ferredoxin.
 DR Pfam; PF00111; fer2; 1.
 DR Pfam; PF01799; fer2-2; 1.
 DR Prodom; PD186071; 2Fe-2S_BD; 1.
 KW Oxidoreductase; Complete proteome.
 SQ SEQUENCE 163 AA; 17933 MW; FDCD218ECFDF5F6 CRC64;

Query Match 23.1%; Score 6; DB 17; Length 163;
 Best Local Similarity 100.0%; Pred. No. 97;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LLYDFL 22
 DB 30 LLYDFL 35

RESULT 30
 Q52661 PRELIMINARY; PRT; 166 AA.
 AC Q52661;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PRIMARY SIGMA FACTOR RPOD (RPOD) AND UNKNOWN ORF 1 GENES, AND UNKNOWN
 DE ORF 2.
 OS Rhodospirillum rubrum (Rhodospirillum rubrum).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhodospirillum group;
 OC Rhodospirillum.
 OX NCBI_TaxID=1061;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SB1003;
 RA Zheng S., Scappino L., Haselkorn R.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U28162; AAA70412.1; -;
 SQ SEQUENCE 166 AA; 18009 MW; 95AF53474634B9DB CRC64;

Query Match 23.1%; Score 6; DB 2; Length 166;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DFLQSL 25
 DB 154 DFLQSL 159

RESULT 31
 Q9P380

ID Q9P3B0 PRELIMINARY; PRT; 166 AA.
 AC Q9P3B0;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE VERY HYPOTHETICAL PROTEIN.
 GN SPAC1565.03.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxId=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972H-;
 RA Seeger K., Harris D., Wood V., Rajandream M.A., Barrell B.G.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL390274; CAB9270.1; -;
 DR InterPro: IPR001230; Prenyltn.
 DR PROSITE: PS00294; PRENYLTATION; UNKNOWN_1.
 KW Hypothetical protein.
 KM SEQUENCE 166 AA; 18985 MW; D52D50C4DCB02297 CRC64;

Query Match 23.1%; Score 6; DB 3; Length 166;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 FLOSLS 26
 Db 135 FLOSLS 140

RESULT 32
 ID Q55840 PRELIMINARY; PRT; 204 AA.
 AC Q55840;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE HYPOTHETICAL 23.4 KDA PROTEIN.
 GN SLR0517.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxId=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96127529; PubMed=8590279;
 RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
 RA Sugita M., Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
 region from map positions 648 to 928 of the genome.";
 RL DNA Res. 2:153-166(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hikosawa M., Sugita M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 RA Shampo S., Takeuchi C., Wada T., Watanabe A., Yamada M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 Synechocystis sp. strain PCC6803. II. Sequence determination of the
 entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 DR EMBL; D64004; BAA10596.1; -;
 DR InterPro: IPR000182; Acetyltransf_GCN5.
 DR Pfam: PF00583; Acetyltransf_1.
 KW Hypothetical protein; Complete proteome.
 KM SEQUENCE 204 AA; 23376 MW; 4A60C87CCDDA6B4 CRC64;

Query Match 23.1%; Score 6; DB 16; Length 204;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LVDFL 22
 Db 23 LVDFL 28

RESULT 33
 ID Q9A706 PRELIMINARY; PRT; 210 AA.
 AC Q9A706;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE TRANSCRIPTIONAL REGULATOR, TETR FAMILY.
 GN CC1664.
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
 OC Caulobacter
 OX NCBI_TaxId=69394;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 19089 / CB15;
 RX MEDLINE=2173698; PubMed=11259647;
 RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Potočka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
 RA Deboy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
 RA Usterback T., Tran K., Wolf A., Yamathavan J., Ermolaeva M., White O.,
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
 RT "Complete genome sequence of Caulobacter crescentus.";
 RL Proc Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
 CC -1- SIMILARITY: BELONGS TO THE TETR/ACR FAMILY OF TRANSCRIPTIONAL
 REGULATORS.
 CC EMBL; AE005841; AAK23642.1; -;
 DR TIGR; CC1664; -;
 DR InterPro: IPR001647; HTH_Tetr.
 DR Pfam: PF00440; tetr_1.
 DR PRINTS: PR00455; HHTETR.
 KW Complete proteome; DNA-binding; Transcription regulation.
 KM SEQUENCE 210 AA; 22742 MW; B181DCD406C2CF41 CRC64;

Query Match 23.1%; Score 6; DB 16; Length 210;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 VDFLOS 24
 Db 182 VDFLOS 187

RESULT 34
 ID Q9D6M8 PRELIMINARY; PRT; 222 AA.
 AC Q9D6M8;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE 2310075G12RIK PROTEIN.
 GN 2310075G12RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=TONGUE;
 RX MEDLINE=21085660; PubMed=11217851;
 KW Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Atrakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojodori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fletschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirral L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Wittaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontutski S.,
 RA Hayashizaki Y.,
 RT *Functional annotation of a full-length mouse cDNA collection.*;
 RL Nature 409:685-690(2001).
 DR EMBL: AK010175; BAB26748.1; -;
 DR MGP: MGI:1916924; 2310075612R1K.
 DR InterPro: IPR003890; ETRF4G-cent.
 DR SMART: SM00543; MIF4G; 1.
 SQ SEQUENCE 222 AA; 25493 MW; 2A0D56790F33701E CRC64;

Query Match 23.1%; Score 6; DB 11; Length 222;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLL 6
 111111
 DB 178 RDGFLL 183

RESULT 35
 Q9ST53 PRELIMINARY; PRT; 235 AA.
 AC Q9ST53;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MADS-BOX PROTEIN 4.
 OS Malus domestica (Apple) (Malus sylvestris).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids I; Rosales; Rosaceae; Maloideae; Malus.
 OC NCBI_TaxID=3750;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. FUJI; TISSUE=FLOWER BUDS;
 RX MEDLINE-20246725; PubMed=10787044;
 RA Sung S.K., Yu G.H., Nam J., Jeong D.H., An G.;
 RT "Developmentally regulated expression of two MADS-box genes, MdMADS3
 and MdMADS4, in the morphogenesis of flower buds and fruits in
 apple.";
 RT apple.";
 RL Planta 210:519-528(2000).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
 DR EMBL: U78950; AAD51423.1; -;
 DR HSSP: P11831; 1SRS.
 DR TRANSFAC: T04732; -;
 DR InterPro: IPR002487; K-box.
 DR InterPro: IPR002100; MADS-box.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRF-TP; 1.
 DR PRINTS: PR00404; MADSBOXAIN.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS00350; MADS_BOX_1; 1.
 DR PROSITE: PS00350; MADS_BOX_2; 1.
 DR DNA-binding; Nuclear protein; Transcription regulation.
 KW SEQUENCE 235 AA; 26690 MW; 6613CA8601CA8F1B CRC64;

Query Match 23.1%; Score 6; DB 10; Length 235;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 GFPEHL 17
 111111
 DB 193 GFPEHL 198

RESULT 36
 Q86738 PRELIMINARY; PRT; 241 AA.
 AC Q86738;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 26.3 KDA PROTEIN.
 DE SC6A9.06.
 GN SC6A9.06.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OC NCBI_TaxID=1902;
 OX [1]
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Murphy L., Harris D.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Parkhill J., Barrell B.G., Rajandream M.A.;
 RA Parkhill J., Barrell B.G., Rajandream M.A.;
 RA Redenbach M., Kleser H.M., Denapate D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 DR EMBL: AL031035; CA19891.1; -;
 DR InterPro: IPR004129; GDPD.
 DR InterPro: IPR000909; PL_PLC_X.
 DR Pfam: PF03009; GDPD; 1.
 DR PROSITE: PS50007; PIPLC_X_DOMAIN; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 241 AA; 26349 MW; D238AC642110406A CRC64;

Query Match 23.1%; Score 6; DB 2; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLL 6
 111111
 DB 193 RDGFLL 198

RESULT 37
 Q9K909 PRELIMINARY; PRT; 260 AA.
 AC Q9K909;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ENOYL-[ACYL-CARRIER PROTEIN] REDUCTASE.
 GN BH2843.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=86665;

RA [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C-125 / JCM 9153;
RX MEDLINE-20512582; PubMed-11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fujii F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL: AP001516; BAB06562.1; -;
DR HSSP: P29132; 1DFT.
KM Complete proteome.
SQ SEQUENCE 260 AA; 28101 MW; 155D849AAF40C03F CRC64;

Query Match 23.1%; Score 6; DB 16; Length 260;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLL 6
|||||
DB 113 RDGFLL 118

RESULT 38
O99UJ1 PRELIMINARY; PRT; 275 AA.
AC O99UJ1;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHETICAL PROTEIN SA1124 (HYPOTHETICAL PROTEIN SAV1281).
GN SA1124 OR SAV1281.
OS Staphylococcus aureus (strain N315), and
OC Staphylococcus aureus (strain M50).
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=158879; 158878;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S. aureus (strain N315), and S. aureus (strain M50);
RX MEDLINE-21311952; PubMed-11618146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanemori M., Matsuura H., Murayama A., Murakami H., Hoshoyama A.,
RA Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL: AP003133; BAB4376.1; -;
DR EMBL: AP003361; BAB57443.1; -;
DR InterPro: IPR002912; ACT.
DR Pfam: PF01842; ACT. 1.
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 275 AA; 31478 MW; AD7A1FCE4DB69CAE CRC64;

Query Match 23.1%; Score 6; DB 16; Length 275;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 LLYDFL 22
|||||
DB 114 LLYDFL 119

RESULT 39
O87858 PRELIMINARY; PRT; 279 AA.
ID O87858

AC O87858;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PUTATIVE TRANSMEMBRANE SUGAR TRANSPORT PROTEIN.
GN SC8A6.24.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Seeger K.J., Harris D.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Parkhill J., Barrell B.G., Rastandream M.A.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RX MEDLINE-97000351; PubMed-8843436;
RA Redenbach M., Kieser H.M., Denapalte D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
CC -!- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM.
CC PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION OF THE SUBSTRATE ACROSS
CC THE MEMBRANE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
CC PROTEIN-DEPENDENT TRANSPORT SYSTEMS.
DR EMBL: AL031013; CA19796.1; -;
DR InterPro: IPR000515; BPD_transp.
DR InterPro: IPR000531; TONB_boxC.
DR Pfam: PF00528; BPD_transp. 1.
DR PROSITE: PS00402; BPD_TRANSF_INN_MEMBR. 1.
DR PROSITE: PS00430; TONB_DEPENDENT_REC.1; UNKNOWN.1.
KM Sugar transport; Transmembrane; Transport.
SQ SEQUENCE 279 AA; 30335 MW; 8860633858F3BFA CRC64;

Query Match 23.1%; Score 6; DB 2; Length 279;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFLLIQ 8
|||||
DB 261 GFLLIQ 266

RESULT 40
O9N535 PRELIMINARY; PRT; 279 AA.
AC O9N535;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 31.8 KDA PROTEIN.
GN Y32H12A.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE-99069613; PubMed-9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for

RT Investigating biology. The C. elegans Sequencing Consortium.*;
 RL Science 282:2012-2018(1998).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2:
 RA Holmes A., Elliot G., Cloud J.;
 RT "The sequence of C. elegans cosmid Y3H12A.*";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2:
 RA Waterston R.;
 RT "Direct Submission.*";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC006733; AAF60484.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 279 AA: 31829 MW: 47286DB425912264 CRC64;

Query Match 23.1%; Score 6; DB 5; Length 279;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 LLLQMD 10
 |||||
 Db 236 LLLQMD 241

RESULT 41
 007011 PRELIMINARY; PRT; 283 AA.
 AC 007011;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE HYPOTHETICAL 31.3 KDA PROTEIN.
 GN YFM.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Denizot F.C.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RX MEDLINE-98044033; PubMed-9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azavedo V., Bertoletti M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borstis R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Enlart K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaeser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klier-Blanchard M., Klein C.,
 RA Kobayashi Y., Koelter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,
 RA Paro V., Pohl T.M., Portelle D., Porwollik S., Prescott A.M.,
 RA Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
 RA Sato T., Scanlan E., Schleich S., Schoeter R., Scoffone F.,
 RA Sekiyuchi J., Sekowska A., Serot S.J., Serrif P., Shin B.S., Solido B.,
 RA Sorokin A., Taccini E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,

RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the gram-positive bacterium Bacillus
 subtilis.*";
 RL Nature 390:249-256(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;

RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PROBABLY PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT
 CC SYSTEM. PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION OF THE
 CC SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
 CC PROTEIN-DEPENDENT TRANSPORT SYSTEMS.
 DR EMBL: 294043; CAB08007.1; -.
 DR EMBL: 299121; CAB15419.1; -.
 DR InterPro: IPR000515; BPD_transp.
 DR Pfam: PF00528; BPD_transp. 1.
 DR PROSITE: PS00402; BPD_TRANS_P_INN_MEMBER; 1.
 KW Complete proteome; Hypothetical protein; Transmembrane; Transport.
 SQ SEQUENCE 283 AA: 31305 MW: 168D39BCB72ICE2E CRC64;

Query Match 23.1%; Score 6; DB 16; Length 283;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 FLLQMD 9
 |||||
 Db 116 FLLQMD 121

RESULT 42
 09KBA7 PRELIMINARY; PRT; 283 AA.
 AC 09KBA7;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE MALTOSE/MALTODEXTRIN TRANSPORT SYSTEM (PERMEASE).
 GN BH2021.
 GN Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C-125 / JCM 9153;
 RX MEDLINE-20512582; PubMed-11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kohara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis.*";
 RL Nucleic Acids Res. 28:4317-4331(2000).
 CC -1- FUNCTION: PROBABLY PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT
 CC SYSTEM. PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION OF THE
 CC SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
 CC PROTEIN-DEPENDENT TRANSPORT SYSTEMS.
 DR EMBL: AP001514; BAB05740.1; -.
 DR InterPro: IPR000515; BPD_transp.
 DR Pfam: PF00528; BPD_transp. 1.
 DR PROSITE: PS00402; BPD_TRANS_P_INN_MEMBER; 1.
 KW Complete proteome; Transmembrane; Transport.
 SQ SEQUENCE 283 AA: 31353 MW: 2072AF8FC7C00FF8 CRC64;

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Query Match      23.1%; Score 6; DB 16; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 FLLIOM 9
      |||||
Db      116 FLLIOM 121

RESULT 43
09F085 PRELIMINARY; PRT: 289 AA.
AC 09F085;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE PUTATIVE CHLOROPLAST RNA HELICASE VDL' ISOFORM 5 (FRAGMENT).
GN VDL'.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
XP [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CY. SRI;
RX MEDLINE=20541613; PubMed=11090214;
RA Wang Y., Dudy G., Purnelle B., Boutry M.;
RT "Proboeco VDL Gene Encodes a Plastid DEAD Box RNA Helicase and Is
RT Involved in Chloroplast Differentiation and Plant Morphogenesis.";
RL Plant Cell 12:2129-2142(2000).
DR EMBL: AF261032; AAG38497.1; -.
DR InterPro: IPR001410; DEAD.
DR Pfam: PF00270; DEAD; 1.
DR SMART: SM00487; DEXDC; 1.
KM ATP-binding; Helicase.
PT NON_TER
SQ SEQUENCE 289 AA; 31822 MW; FE5AA248C78F4F2 CRC64;

Query Match      23.1%; Score 6; DB 10; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      17 LLVDFL 22
      |||||
Db      271 LLVDFL 276

RESULT 44
09KD33 PRELIMINARY; PRT: 298 AA.
AC 09KD33;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE ENDONUCLEASE IV.
GN BHL366.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=86665;
XP [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fujii F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL: AP001511; BAB05105.1; -.

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DR HSSP: P12638; 1Q7W.
DR InterPro: IPR001719; AP_endonuclease_2.
DR Pfam: PF01261; AP_endonuclease2; 1.
DR SMART: SM00518; AP2EC; 1.
DR PROSITE: PS00729; AP_NUCLEASE_F2_1; 1.
DR PROSITE: PS00730; AP_NUCLEASE_F2_2; UNKNOWN_1.
DR PROSITE: PS00731; AP_NUCLEASE_F2_3; 1.
KW Complete proteome.
SQ SEQUENCE 298 AA; 32997 MW; 9A25ED81A755B4B CRC64;

Query Match      23.1%; Score 6; DB 16; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      19 VDFLOS 24
      |||||
Db      90 VDFLOS 95

RESULT 45
085704 PRELIMINARY; PRT: 303 AA.
AC 085704;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE PUTATIVE HEME A SYNTHASE (SM0964 PROTEIN) (HYPOTHETICAL PROTEIN
DE SAV1115).
GN CTPA OR SA0964 OR SAV1115.
OS Staphylococcus aureus,
OS Staphylococcus aureus (strain N315), and
OS Staphylococcus aureus (strain Mu50).
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280; 158679; 158678;
XP [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus; STRAIN=8325-4;
RA Clements M.O., Watson S.P., Foster S.J.;
RT "Starvation-survival and recovery of Staphylococcus aureus require
RT CtaA, a putative heme A synthase.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus (strain N315), and S.aureus (strain Mu50);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kato C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiratake K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL: AF072726; AAD09875.1; -.
DR EMBL: AP003132; BAB42212.1; -.
DR EMBL: AP003361; BAB57277.1; -.
DR InterPro: IPR003780; COX15_CtaA.
DR Pfam: PF02628; COX15_CtaA; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 303 AA; 34059 MW; 21D3BEC1812C260 CRC64;

Query Match      23.1%; Score 6; DB 16; Length 303;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GFLLIQ 8
      |||||
Db      100 GFLLIQ 105

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RESULT 46
ID Q9HBL5 PRELIMINARY; PRT; 305 AA.
AC Q9HBL5;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE AD023.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ADRENAL GLAND;
RA Xiao H., Song H., Gao G., Ren S., Chen Z., Han Z.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF225422; AAG09724.1; -.
SQ SEQUENCE 305 AA; 34261 MW; 452D9F85F9FE70F CRC64;

Query Match 23.1%; Score 6; DB 4; Length 305;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DGFLL 6
Db 178 DGFLL 183

RESULT 47
ID Q9P800 PRELIMINARY; PRT; 311 AA.
AC Q9P800;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE NTG1 (FRAGMENT).
GN NTG1.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RA Dicken S., Koetter P., Entian K.;
RT "Characterization of CAT8 of Candida albicans.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF222908; AAF35322.1; -.
DR HSSP; P20625; 2ABK.
DR InterPro; IPR004036; Endonuclease_IIL_HNH.
DR InterPro; IPR003265; Endo_3c.
DR Pfam; PF00730; HhH-GDP; 1.
DR SMART; SM00478; ENDO3c; 1.
DR PROSITE; PS01155; ENDONUCLEASE_IIL_2; UNKNOWN_1.
FT NON_TER 311
SQ SEQUENCE 311 AA; 35180 MW; 5908B89859C0B71 CRC64;

Query Match 23.1%; Score 6; DB 3; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFLIQ 8
Db 199 GFLIQ 204

RESULT 48
ID Q9DB26 PRELIMINARY; PRT; 311 AA.

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AC Q9DB26;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE ADULT MALE CEREBELLUM CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE CLONE:1500019N11, FULL INSERT SEQUENCE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=CEREBELLUM;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Mashio T.,
RA Sakai K., Oikido T., Furuno M., Aono H., Baldarelli R., Barish G.,
RA Blake J., Boilelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald C., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Winking L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK005293; BAB23937.1; -.
SQ SEQUENCE 311 AA; 34614 MW; D89EBF6E84D2C5 CRC64;

Query Match 23.1%; Score 6; DB 11; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGFLL 7
Db 35 DGFLL 40

RESULT 49
ID Q99RY9 PRELIMINARY; PRT; 313 AA.
AC Q99RY9;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE SA2078 PROTEIN (HYPOTHETICAL PROTEIN SA2283).
GN SA2078 OR SAV2283.
OS Staphylococcus aureus (strain N315), and
OS Staphylococcus aureus (strain Mu50).
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=158879, 158878;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S. aureus (strain N315), and S. aureus (strain Mu50);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hirataki K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus

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RT aureus.";
 RL Lancet 357:1225-1240(2001).
 DR EMBL; AP003136; BAB43375.1; -;
 DR EMBL; AP003364; BAB58445.1; -;
 DR InterPro: IPR001910; IUNH.
 DR Pfam: PF01156; IU_nuc_hydro; 1.
 DR PRODOM: PD007736; IUNH; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 313 AA; 35362 MW; E335FAF497CB755A CRC64;

Query Match 23.1%; Score 6; DB 16; Length 313;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 FILLUM 9
 |||||
 DB 20 FILLUM 25

RESULT 50
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 ID O9FQ84 PRELIMINARY; PRT; 324 AA.
 AC O9FQ84;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE PUTATIVE CHLOROPLAST RNA HELICASE VDL' ISOFORM 4 (FRAGMENT).
 GN VDL'.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; eunsterids I; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. SR1;
 RX MEDLINE=20541613; PubMed=11090214;
 RA Wang Y., Duby G., Purnelle B., Boutry M.;
 RT "Tobacco VDL Gene Encodes a Plastid DEAD Box RNA Helicase and Is
 RT Involved in Chloroplast Differentiation and Plant Morphogenesis.";
 RL Plant Cell 12:2129-2142(2000).
 DR EMBL; AF261032; MAG38496.1; -;
 DR InterPro: IPR001410; DEAD.
 DR Pfam: PF00270; DEAD; 1.
 DR SMART: SM00487; DEXDC; 1.
 KW ATP-binding; Helicase.
 FT NON_TER 324
 SQ SEQUENCE 324 AA; 36250 MW; C3118BCBDC8A53BC CRC64;

Query Match 23.1%; Score 6; DB 10; Length 324;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 LVDVFL 22
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 DB 306 LVDVFL 311

Search completed: June 19, 2002, 11:11:05
 Job time: 204 sec

10

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 19, 2002, 11:05:35 ; Search time 29.84 Seconds
(without alignments)

96.780 Million cell updates/sec

Title: US-09-943-334-1

Perfect score: 26
Sequence: 1 RDCFLLLQMDFGFPHLLVDFLOSLS 26

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 11073796 residues

Word size : 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Database :

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22: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	26	17 AAM06128	Human cholesterol
2	26	100.0	26	21 AAY13801	Rabbit CERP Immuno
3	26	100.0	26	21 AAY91228	Human cholesterol
4	26	100.0	46	21 AAY91232	Modified MYF Th ep
5	26	100.0	46	21 AAY91233	Human cholesterol
6	26	100.0	476	17 AAM06127	Human mature chole
7	26	100.0	476	18 AAM46446	Human cholesterol
8	26	100.0	476	20 AAY02466	Human cholesterol
9	26	100.0	491	15 AAR60342	Partial human Lipi
10	26	100.0	493	20 AAY49556	Human cholesterol
11	26	100.0	493	20 AAY49568	Human cholesterol

12	26	100.0	493	22 AAG56636	Human cholesterol
13	22	84.6	22	20 AAY13815	Rabbit CERP Immuno
14	22	84.6	22	20 AAY13821	Human CERP Immuno
15	22	84.6	496	20 AAY02469	Humanised rabbit c
16	26	61.5	16	21 AAY91229	Human cholesterol
17	16	61.5	31	17 AAM06129	Anti-cholesterol
18	16	61.5	31	20 AAY02470	Fusion of a tetanu
19	16	61.5	35	21 AAY91236	Modified HBVarfac
20	16	61.5	36	21 AAY91234	Modified MYF Th ep
21	16	61.5	36	21 AAY91235	Modified MYF Th ep
22	16	61.5	36	21 AAY91237	Modified MYF Th ep
23	16	61.5	50	17 AAM06131	Anti-cholesterol
24	16	61.5	50	18 AAM06129	Human/rabbit CERP
25	11	42.3	16	21 AAY91230	Human cholesterol
26	11	42.3	22	20 AAY13803	Rabbit CERP Immuno
27	11	42.3	26	21 AAY13802	Rabbit CERP Immuno
28	11	42.3	26	21 AAY91231	Human cholesterol
29	11	42.3	36	21 AAY91238	Modified MYF Th ep
30	11	42.3	36	21 AAY91239	Modified MYF Th ep
31	11	42.3	46	21 AAY91240	Modified MYF Th ep
32	11	42.3	46	21 AAY91241	Modified MYF Th ep
33	11	42.3	50	17 AAM06132	Anti-cholesterol
34	11	42.3	50	18 AAM46447	CERP B cell epitop
35	11	42.3	477	20 AAY02468	Modified rabbit ch
36	11	42.3	496	17 AAM06133	Rabbit cholesterol
37	11	42.3	496	18 AAM46445	Mature rabbit chol
38	11	42.3	496	20 AAY02467	Rabbit cholesterol
39	7	26.9	51	22 AAM31066	Peptide #5103 enco
40	7	26.9	51	22 AAM17886	Novel human respit
41	7	26.9	186	22 AAG07716	Novel human diagno
42	7	26.9	401	22 AAG17572	Novel human diagno
43	7	26.9	417	22 AAG07733	Novel human diagno
44	7	26.9	422	15 AAR54202	snaa gene product
45	7	26.9	466	22 AAG16251	Novel human diagno
46	7	26.9	478	22 AAG15687	Novel human diagno
47	7	26.9	1501	22 AAG83878	S. epidermidis ope
48	6	23.1	14	20 AAY27814	Human secreted pro
49	6	23.1	31	21 AAB51836	Human secreted pro
50	6	23.1	42	21 AAB38991	Human secreted pro
51	6	23.1	56	22 ABB03312	Human musculoskele
52	6	23.1	55	22 ABB44219	Peptide #11725 enc
53	6	23.1	65	22 ABB27096	Protein #9095 enco
54	6	23.1	65	22 AAM65251	Human brain expres
55	6	23.1	65	22 AAM77956	Human bone marrow
56	6	23.1	65	22 AAM21850	Peptide #8284 enco
57	6	23.1	65	22 AAM38174	Peptide #12211 enc
58	6	23.1	69	22 AAG73544	Human colon cancer
59	6	23.1	70	22 AAY19484	Amino acid sequenc
60	6	23.1	75	22 ABB44253	Peptide #11759 enc
61	6	23.1	75	22 ABB27126	Protein #9125 enco
62	6	23.1	75	22 AAM65292	Human brain expres
63	6	23.1	75	22 AAM77990	Human bone marrow
64	6	23.1	75	22 AAM21883	Peptide #8317 enco
65	6	23.1	75	22 AAM38210	Peptide #12247 enc
66	6	23.1	77	20 AAY00283	Human secreted pro
67	6	23.1	86	22 AAY20330	Human novel endocr
68	6	23.1	99	22 AAO13234	Human polypeptide
69	6	23.1	112	22 AAU29655	Novel human secret
70	6	23.1	116	22 ABB27938	Novel human diagno
71	6	23.1	121	21 AAG01114	Human secreted pro
72	6	23.1	155	21 AAY53001	Human secreted pro
73	6	23.1	155	22 AAM39518	Human polypeptide
74	6	23.1	166	6 AAY50023	Sequence of new mo
75	6	23.1	166	16 AAR67762	Interferon-alpha-7

ALIGNMENTS

RESULT 1
AAM06128 standard: peptide: 26 AA.
XX

AC	AAW06128,	
XX		
DT	07-FEB-1997	(first entry)
XX		
DE	Human cholesterol ester transfer protein C-terminal B-cell epitope.	
XX		
KW	Cholesterol ester transfer protein; CERP; antigen; vaccine;	
KM	cardiovascular disease; atherosclerosis; B-cell epitope.	
OS	Homo sapiens.	
XX		
PN	W09634888-A1.	
XX		
PD	07-NOV-1996.	
XX		
PF	01-MAY-1996;	96WO-US06147.
XX		
PR	01-MAY-1995;	95US-0432483.
XX		
PA	(TCEL-) T CELL SCI INC.	
XX		
PI	Rittershaus CW, Thomas LJ;	
XX		
DR	WPI; 1996-506103/50.	
XX		
PT	Cholesterol ester transfer protein B cell epitope linked to T cell	
PT	epitope - used to generate vaccine to regulate CERP activity for	
PT	decreasing the risk of developing a cardiovascular disease e.g.	
PT	atherosclerosis	
XX		
PS	Claim 5, Page 41; 72pp; English.	
XX		
CC	A B-cell epitope (AAW06128) comprising the C-terminal 26 amino acids	
CC	of human liver mature cholesterol ester transfer protein (CERP)	
CC	(see also AAW06127) is involved in a neutral lipid binding or a	
CC	transfer activity of CERP. It can be linked to a universal or	
CC	broad range immunogenic T-cell epitope, such as that found at amino	
CC	acids 830-843 of tetanus toxoid epitope, to produce a synthetic	
CC	vaccine (see also AAW06129) that elicits an immune response against	
CC	endogenous CERP activity, thereby treating or preventing	
CC	cardiovascular disease, such as atherosclerosis. It may also be	
CC	incorporated into a multivalent vaccine (see also AAW06131)	
CC	including another CERP B-cell epitope.	
XX		
SQ	Sequence	26 AA;
	Query Match	100.0%; Score 26; DB 17; Length 26;
	Best Local Similarity	100.0%; Pred. No. 3,1e-17;
	Matches	26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 RDGELLQMDGFPFHHLVDFLOSLS	26
DB	1 rdgfillqmdfgfepnhlvdfllqsls	26
RESULT	2	
AAI13801		
ID	AAV13801 standard; peptide; 26 AA.	
XX		
AC	AAV13801;	
XX		
DT	08-JUL-1999	(first entry)
XX		
DE	Rabbit CERP immunogenic fragment.	
XX		
KW	CERP; cholesterol ester transfer protein; recombinant DNA vaccine; HDL;	
KM	antibody production; cholesterol ester transfer; therapy;	
KM	high density lipoprotein; HDL cholesterol concentration;	
KM	pro-atherogenic dyslipoproteinaemia.	
XX		
OS	Oryctolagus sp.	
XX		

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PN      WO9915655-A1.
XX
PD      01-APR-1999.
XX
XX      17-SEP-1998;    98WO-US19366.
PF
XX      19-SEP-1997;    97US-0934367.
PR
XX      (MONS ) MONSANTO CO.
PA
XX      Glenn K, Needleman P;
PI
XX      WPI, 1999-276984/23.
DR
XX
PT      New recombinant DNA vaccines
PS
XX      Claim 15; Page 85; 99pp; English.
XX
CC      This sequence represents an immunogenic fragment of the rabbit
CC      cholesterol ester transferase protein (CETP).
CC      The invention relates to recombinant DNA vaccines that contain DNA
CC      encoding CETP, which can be used for producing antibodies to lessen the
CC      transfer of cholesteryl esters from high density lipoprotein (HDL). The
CC      method can provide an autologous immunological process for lessening the
CC      transfer of cholesteryl esters from HDL particles and for increasing the
CC      HDL cholesterol concentration of a mammal whose blood also contains
CC      CETP. The method may be useful in treating human pro-atherogenic
CC      dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
CC      method can have an effect that lasts for months as compared to the
CC      short-term effects of the small molecule drugs now available.
XX
SQ      Sequence        26 AA;

Query Match              100.0%; Score 26; DB 20; Length 26;
Best Local Similarity   100.0%; Pred. No. 3,1e-17;
Matches     26; Conservative    0; Mismatches    0; Indels    0; Gaps    0.

QY      1 RDGFLLLQMDFGFPEHLVDFLOSLS 26
       |||||
Db      1 rdgfillqmdfgfpehlvdfiqsls 26

RESULT      3
AA9Y1228
ID      AAY91228 standard; peptide; 26 AA.
XX
XX      AAY91228;
AC
XX
DT      22-MAY-2000 (first entry)
DE
XX      Human cholesteryl transport protein (CETP) peptide, SEQ ID NO:106.
XX
XX      Promiscuous T-cell epitope; measles virus F protein; MYF;
KW      hepatitis B virus surface antigen; HBV; immunogenetic; B-cell epitope;
KW      leucine-rich hormone releasing hormone; LHRH; contraceptive; anticancer;
KW      somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; PMDV;
KW      foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KW      Plasmodium falciparum; circumsporozoite; antimalarial; CETP;
KW      cholesteryl ester transport protein; anti-arteriosclerotic.
XX
OS      Homo sapiens.
XX
PN      WO9966957-A2.
XX
PD      29-DEC-1999.
XX
PF      21-JUN-1999;    99WO-US13975.
PR
XX      20-JUN-1998;    98US-0100412.
PA
XX      (UNBI-) UNITED BIOMEDICAL INC.
XX

```


PI Wang CY:

XX AAY91232

DR WPI: 2000-160564/14.

PT New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus

PS Claim 10; Page 49; 129pp; English.

XX The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesterol ester transport
 CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of luteinising hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunosuppression; for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
 CC from the measles virus F (VWF) protein and sequences AAY91122-Y91142,
 CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
 CC VWF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
 CC peptides comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AAY91208 is a
 CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVA Th
 CC epitopes/CD4 CDR2 antigenic peptides which may be used to prevent HIV
 CC infection of T cells. AAY90212 is a modified version of a human IGE
 CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitopes/IGE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
 CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVA Th
 CC epitope, and may be used in a malaria vaccine. AAY91228-Y91231 represent
 CC CETP-derived peptides and AAY91232-Y91241 are immunogens comprising a
 CC CETP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91248 and AAY91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91249-Y91251 and
 CC AAY91256-Y91273 are antigenic peptides comprising MVA Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91198 and AAY91199 are respectively an immunostimulatory invasive
 CC protein epitope from Yersinia species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the invention.
 CC Note: Sequence AAY91227 is also designated SEQ ID NO:106 in the
 CC specification.

XX Sequence 26 AA;

Query Match 100.0%; Score 26; DB 21; Length 26;

Best Local Similarity 100.0%; Pred. No. 3,1e-17;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFTLLQNDGFRPEHLVDFQSLG 26

DQ 1 rdgftllqndgfrpehlvdfqslg 26

RESULT 4
 AAY91232
 ID AAY91232 standard; peptide: 46 AA.

AC AAY91232;

DT 22-MAY-2000 (first entry)

DE Modified MVA Th epitope/CETP peptide, SEQ ID NO:110.

XX Promiscuous T-cell epitope; measles virus F protein; MVA;
 KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
 KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
 KW foot and mouth disease virus; immunoglobulin E; IGE; anti-allergic;
 KW Plasmodium falciparum; circumsporozoite; antimalarial; CETP;
 KW cholesterol ester transport protein; anti-arteriosclerotic.

OS Chimeric - Measles virus.
 OS Chimeric - Homo sapiens.

PN MO966957-A2.

PD 29-DEC-1999.

PF 21-JUN-1999; 99MO-US13975.

PR 20-JUN-1998; 98US-0100412.

PX (UNBI-) UNITED BIOMEDICAL INC.

PY Wang CY:

WPI: 2000-160564/14.

PT New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus

PS Claim 11; Page 104; 129pp; English.

XX The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesterol ester transport
 CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of luteinising hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunosuppression; for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
 CC from the measles virus F (VWF) protein and sequences AAY91122-Y91142,
 CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
 CC VWF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
 CC immunogens comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AAY91208 is a
 CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVA Th

CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
 CC infection of T cells. AAY90212 is a modified version of a human IGE
 CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IGE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
 CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVE Th
 CC epitope, and may be used in a malaria vaccine. AAY91228-Y91231 represent
 CC CERP-derived peptides and AAY91232-Y91241 are immunogens comprising a
 CC CERP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
 CC AAY91258-Y91273 are antigenic peptides comprising MVE Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91198 and AAY91199 are respectively an immunostimulatory invasin
 CC protein epitope from Yersinia species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.

SO Sequence 46 AA;

Query Match 100.0%; Score 26; DB 21; Length 46;
 Best Local Similarity 100.0%; Pred. No. 5.1e-17;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLILMDGFGPPEHLVDFIQSLS 26
 21 rdgfilllmdgfgfpehlvdfiqsls 46

DB 21 rdgfilllmdgfgfpehlvdfiqsls 46

RESULT 5
 AAY91233
 ID AAY91233 standard; peptide: 46 AA.

AC AAY91233;
 XX
 XX 22-MAY-2000 (first entry)
 DT
 XX Modified MVE Th epitope/CERP peptide, SEQ ID NO:111.
 DE
 XX Promiscuous T-cell epitope; measles virus F protein; MVE;
 KW hepatitis B virus surface antigen; HBV; Immunogenic; B-cell epitope;
 KW interleukin 6; growth promoting; CD4 receptor; HIV-1; antiviral; FMDV;
 KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
 KW foot and mouth disease virus; immunoglobulin E; IGF; anti-allergic;
 KW plasmodium falciparum; circumsporozoite; antimalarial; CERP;
 KW cholesterol ester transport protein; anti-arteriosclerotic.

XX
 OS Chimeric - Measles virus.
 OS Chimeric - Homo sapiens.
 XX
 PN MO9966957-A2.
 XX
 PD 29-DEC-1999.
 XX
 XX 21-JUN-1999; 99WO-US13975.
 PF
 XX 20-JUN-1998; 98US-0100412.
 PR
 XX (UNBT-) UNITED BIOMEDICAL INC.
 PA
 XX Wang CY;
 PI
 XX WPI; 2000-160564/14.
 DR
 XX New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus
 XX
 XX Claim 11; Page 104-105; 129pp; English.

CC The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesterol ester transport
 CC protein (CERP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumor antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of interleukin hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunosuppression; for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
 CC from the measles virus F (MVE) protein and sequences AAY91122-Y91142,
 CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
 CC MVE Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
 CC peptides comprising somatostatin, and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AAY91208 is a
 CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVE Th
 CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
 CC infection of T cells. AAY90212 is a modified version of a human IGE
 CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IGE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
 CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVE Th
 CC epitope, and may be used in a malaria vaccine. AAY91228-Y91231 represent
 CC CERP-derived peptides and AAY91232-Y91241 are immunogens comprising a
 CC CERP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
 CC AAY91258-Y91273 are antigenic peptides comprising MVE Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91198 and AAY91199 are respectively an immunostimulatory invasin
 CC protein epitope from Yersinia species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.

XX
 SO Sequence 46 AA;

Query Match 100.0%; Score 26; DB 21; Length 46;
 Best Local Similarity 100.0%; Pred. No. 5.1e-17;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLILMDGFGPPEHLVDFIQSLS 26
 21 rdgfilllmdgfgfpehlvdfiqsls 46

DB 21 rdgfilllmdgfgfpehlvdfiqsls 46

RESULT 6
 AAY06127
 ID AAY06127 standard; Protein: 476 AA.

AC AAY06127;
 XX
 XX 07-FEB-1997 (first entry)
 DT
 XX Human cholesterol ester transfer protein.
 DE
 XX

KM		Cholesteryl ester transfer protein; CETP; antigen; vaccine;
KW		cardiovascular disease; atherosclerosis.
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Region	349..367
PT	/label=	B-cell_epitope
FT	Region	461..476
FT	/label=	B-cell_epitope
FT	/note=	"C-terminal epitope involved in neutral lipid binding or a transfer activity of CETP (Claim 5)."
PN	MO634888-A1..	
XX		
PD	07-NOV-1996.	
XX		
PE	01-MAY-1996,	96WO-US06147.
XX		
PR	01-MAY-1995,	95US-0432483.
XX		
PA	(TCEL-) T CEL SCI INC.	
XX		
PI	Rittershaus CM, Thomas LJ:	
DR	WPI; 1996-506103/50.	
XX		
PT	cholesterol ester transfer protein B cell epitope linked to T cell	
PT	epitope - used to generate vaccine to regulate CETP activity for	
PT	decreasing the risk of developing a cardiovascular disease e.g.	
PT	atherosclerosis	
XX		
PS	Claim 2; Page 44-47; 72pp; English.	
CC		
CC	Human liver mature cholesteryl ester transfer protein (CETP) (AAW06127)	
CC	plays a role in altering the relative profile of circulating	
CC	lipoproteins to one associated with an increased risk of	
CC	cardiovascular disease. B-cell epitopes (see also AAW06128) of CETP	
CC	can be used in novel peptide vaccines (see also AAW06129, AAW06131)	
CC	that elicit an immune response against endogenous CETP activity,	
CC	thereby treating or preventing cardiovascular disease, such as	
CC	atherosclerosis.	
XX		
SQ	Sequence 476 AA:	
	Query Match	100.0%; Score 26; DB 17; Length 476;
	Best Local Similarity	100.0%; Pred. No. 3,9e-16;
	Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 RDGFLLDMDFGPEHLVDLFIQSIS 26	
bdb	451 rdgfillqmdfgpehlvdflqsis 476	
RESULT 7		
ID	AAW46446 standard; Peptide: 476 AA.	
AC	AAW46446;	
DT	18-MAY-1998 (first entry)	
XX		
XX	Human mature cholesteryl ester transfer protein (CETP).	
XX		
KW	cholesteryl ester transfer protein; CETP; cholesteryl ester;	
KW	high density lipoprotein; HDL; very low density lipoprotein; VLDL;	
KW	low density lipoprotein; LDL; atherosclerosis; neutral lipid binding;	
KW	transfer activity; immunogenic; B cell epitope; antibody; TP2;	
KW	DNA plasmid-based vaccine; broad range helper T cell epitope;	
KW	treatment; cardiovascular disease.	
XX		

	OS	Homo sapiens.
PX	NN	M09741227-A1.
PD	XX	06-NOV-1997.
PF	XX	01-MAY-1997; 97WO-US07294.
PR	XX	21-FEB-1997; 97US-0802967.
PT	XX	01-MAY-1996; 96DS-0640713.
PA	XX	(?CEL-) T CELL SCI INC.
PI	XX	Thomas LJ;
DR	XX	WPI: 1997-549731/50. N-PDBE: AAVO5127.
PS	XX	DNA plasmid-based vaccine encodes CERP B cell epitope(s) - used for elevating high density lipoprotein levels, and for treating cardiovascular disease
PM	XX	Claim 6; Pages 36-38; 67pp; English.
PB	XX	The present sequence represents a human mature cholesteryl ester transfer protein (CERP). CERPs mediate the transfer of cholesteryl esters from low density lipoprotein (LDL) to very low density lipoprotein (VLDL) and high density lipoprotein (HDL). An increased CERP activity produces an atherogenic lipoprotein profile and induces atherosclerosis. A 13 amino acid stretch in the human CERP (Phe463 to Leu475), and also possibly Asp460, are particularly important for neutral lipid binding and transfer activity. This region has been shown to be immunogenic as a B cell epitope of CERP. And a monoclonal antibody (TP2) directed at this region has been shown to inhibit neutral lipid transfer. A second B cell epitope is defined by Arg349 to Ile367. Antibodies to this second epitope would allow the formation of immune complexes involving CERP, and promote the removal of the complexed CERP. This peptide region was selected for its potential antigenicity and high possibility for surface expression on native CERP. Sequences encoding these 2 epitopes can be used in a DNA plasmid-based vaccine which comprises sequences encoding at least 1 B cell epitope of CERP linked in frame with at least one segment encoding a broad range helper T cell epitope. The vaccines can be used to elevate the ratio of circulating HDL to circulating LDL, VLDL or total cholesterol in a human. It can also be used for decreasing the level of endogenous CERP activity in a human. The vaccine can be used to produce anti-CERP antibodies in vivo and for treating cardiovascular disease.
SQ	XX	Sequence 476 AA:
Query Match	Score 26; DB 18; Length 476; Best Local Similarity 100.0%; Pred. No. 3.9e-16; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	I RDGFLLLQMDFGPENHLVDLFLOSLS 26 Db 45I rdgflllqmdfgfpennlvdffiqsls 476	
RESULT 8	AAY02466	
ID	AAY02466 standard; protein; 476 AA.	
AC	AAY02466;	
DT	14-JUL-1999 (first entry)	
DE	Human cholesteryl ester transfer protein (CERP).	
Vaccine; antilbody; endogenous; cholestery] ester transfer protein; CERP;	KM	high-density lipoprotein-associated cholesterol; metabolism;
low-density lipoprotein-associated cholesterol; atherosclerotic lesion;	KM	cholesterol; atherosclerosis; heart disease.

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XX OS Homo sapiens.
XX PN WO9920302-A1.
XX PD 29-APR-1999.
XX PF 20-OCT-1998; 98WO-US22145.
XX PR 20-OCT-1997; 97US-0954643.
XX PA (AVANT ) AVANT IMMUNOTHERAPEUTICS INC.
XX PI Rittershaus CW, Thomas LJ;
XX DR WPI: 1999-302645/25.
XX DR N-PSDB; AAX35807.
XX PT Vaccine against cholesterol ester transfer protein
XX PS Disclosure: Page 44-46; 61pp; English.
XX CC The specification describes a vaccine that promotes the production of
CC antibodies that bind endogenous cholesterol ester transfer protein
CC (CETP). The vaccines (and equivalent plasmid-based vaccines) are
CC used to increase the ratio of circulating high-density lipoprotein
CC (HDL)-associated cholesterol to low-density lipoprotein (LDL)-associated
CC cholesterol; to decrease the level of endogenous CETP activity in humans
CC or other animals; to alter metabolism of LDL-associated cholesterol, for
CC inhibiting development of atherosclerotic lesions; to lower circulating
CC levels of LDL and total cholesterol; and to treat or prevent
CC atherosclerosis (or more generally heart disease). The present sequence
CC represents human CETP.
XX SQ Sequence 476 AA:

Query Match          100.0%; Score 26; DB 20; Length 476;
Best Local Similarity 100.0%; Pred. No. 3.9e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLQMDFGFPHLLVDFLOSLS 26
DB 451 rdgfillqmdfgfphllvdfllqsls 476

RESULT 9
AAR60342
ID AAR60342 standard; protein; 491 AA.
XX AC AAR60342;
XX DT 01-MAR-1995 (first entry)
XX DE Partial human lipid transfer protein.
XX DE lipid transfer protein; LTP; monoclonal antibody; immunoassay;
KW antigen determining group.
XX OS Homo sapiens.
XX FH Key
XX FT Peptide
XX FT /label= peptide 1
XX FT /note="claim 1; antigen determining group"
XX FT Peptide
XX FT /label= peptide 2
XX FT /note="claim 1; antigen determining group"
XX FT Peptide
XX FT /label= peptide 3
XX FT /note="claim 1; antigen determining group"
XX FT Peptide
XX FT /label= peptide 4

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FT FT Peptide
FT FT /note="claim 1; antigen determining group"
FT FT 360..370
FT FT /label= peptide 5
FT FT /note="claim 1; antigen determining group"
XX PN JP06169793-A.
XX PD 21-JUN-1994.
XX PF 02-DEC-1992; 92JP-0349842.
XX PR 02-DEC-1992; 92JP-0349842.
XX PA (EIKE ) EIKEN KAGAKU KK.
XX DR WPI: 1994-237601/29.
XX DR A monoclonal antibody recognising human lipid transfer protein -
XX PT useful for immunoassay
XX PS Disclosure: Fig 1; 14pp; Japanese.
XX CC This sequence shows a partial human lipid transfer protein,
XX CC containing specific peptide groups that are antigen determining. The
XX CC monoclonal antibody of the invention recognises any of these
XX CC peptides. The Mab can be used in an immunoassay for HLP.
XX SQ Sequence 491 AA:

Query Match          100.0%; Score 26; DB 15; Length 491;
Best Local Similarity 100.0%; Pred. No. 4e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLQMDFGFPHLLVDFLOSLS 26
DB 466 rdgfillqmdfgfphllvdfllqsls 491

RESULT 10
AAV49556
ID AAV49556 standard; Protein; 493 AA.
XX AC AAV49556;
XX DT 13-JAN-2000 (first entry)
XX DE Human cholesterol ester transfer protein sequence.
XX DE Human; coding sequence polymorphism; vascular pathology gene;
KW polymorphic site; phenotype correlation; forensic; paternity testing;
KW medicine; genetic analysis; vascular disease.
XX OS Homo sapiens.
XX PN WO9950454-A2.
XX PD 07-OCT-1999.
XX PF 26-MAR-1999; 99WO-US06473.
XX PR 01-APR-1998; 98US-0054272.
XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX PI Lander ES, Daley GQ, Cargill M, Ireland JS, Rozen SG;
XX DR WPI: 1999-620066/53.
XX DR N-PSDB; AAZ32165.
XX PT Determination of polymorphisms in genes, especially those identifying
XX PT predisposition to vascular disease

```

PS Disclosure: Fig 9; 134pp: English.
 XX
 CC AA232159 to AA232194 represent reference alleles for specifically
 CC claimed nucleic acid sequences from the present invention which comprise
 CC polymorphic sites as given in a table in the specification, selected
 CC from 92 single nucleotide polymorphisms in which the nucleotide at the
 CC polymorphic site is different from a nucleotide at the same site in a
 CC reference allele. The nucleic acids, and primers and probes, are used to
 CC identify polymorphisms, which may predispose an individual to disease,
 CC especially a vascular disease. They can also be used in phenotype
 CC correlations, forensics, paternity testing, medicine or genetic
 CC analysis. AAY49550 to AAY49573 represent the proteins which correspond
 CC to some of the reference alleles.
 CC
 SQ Sequence 493 AA;
 Query Match 100.0%; Score 26; DB 20; Length 493;
 Best Local Similarity 100.0%; Pred. No. 4e-16;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RDGFLLLQMDGFPPEHLVDFLOSL 26
 Db 468 rdgflillqmdfgfpehlvdfllqsls 493
 ||||||||||||||||||||
 ||||||||||||||||||||
 RESULT 11
 AAY49568
 ID AAY49568 standard; Protein; 493 AA.
 XX
 AC AAY49568;
 XX
 DT 13-JAN-2000 (first entry)
 XX
 DE Human cholesterol ester transfer protein sequence.
 XX
 KM Human: coding sequence polymorphism: vascular pathology/ gene;
 KM polymorphic site; phenotype correlation; forensic; paternity testing;
 KM medicine; genetic analysis; vascular disease.
 XX
 OS Homo sapiens.
 XX
 PN WO950454-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 26-MAR-1999; 99WO-US06473.
 XX
 PR 01-APR-1998; 98US-0054272.
 XX
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 XX
 PI Lander ES, Daley GQ, Cargill M, Ireland JS, Rozen SG;
 XX
 DR MPI; 1999-620066/53.
 XX
 DR N-PSDB; AA232188.
 XX
 PT Determination of polymorphisms in genes, especially those identifying
 PT predisposition to vascular disease
 XX
 PS Disclosure: Fig 32; 134pp: English.
 XX
 CC AA232159 to AA232194 represent reference alleles for specifically
 CC claimed nucleic acid sequences from the present invention which comprise
 CC polymorphic sites as given in a table in the specification, selected
 CC from 92 single nucleotide polymorphisms in which the nucleotide at the
 CC polymorphic site is different from a nucleotide at the same site in a
 CC reference allele. The nucleic acids, and primers and probes, are used to
 CC identify polymorphisms, which may predispose an individual to disease,
 CC especially a vascular disease. They can also be used in phenotype
 CC correlations, forensics, paternity testing, medicine or genetic
 CC analysis. AAY49550 to AAY49573 represent the proteins which correspond
 CC to some of the reference alleles.

XX
 SQ Sequence 493 AA;
 Query Match 100.0%; Score 26; DB 20; Length 493;
 Best Local Similarity 100.0%; Pred. No. 4e-16;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RDGFLLLQMDGFPPEHLVDFLOSL 26
 Db 468 rdgflillqmdfgfpehlvdfllqsls 493
 ||||||||||||||||||||
 ||||||||||||||||||||
 RESULT 12
 AAG5636
 ID AAG5636 standard; Protein; 493 AA.
 XX
 AC AAG5636;
 XX
 DT 07-JAN-2002 (first entry)
 XX
 DE Human cholesterol ester transfer protein (CETP).
 XX
 KM CETP; arteriosclerosis; cholesterol ester transfer protein; HDL;
 KM high density lipoprotein; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..17
 FT /note= "signal peptide"
 FT 18..493
 FT /note= "mature protein indicated as Seq Id No. 2"
 XX
 PN WO200171032-A1.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-JP02327.
 XX
 PR 24-MAR-2000; 2000JP-0084264.
 XX
 PA (BMLB-) BML INC.
 XX
 PI Nagano M, Ito M, Sageshashi Y, Hattori H, Egashira T, Yamashita S;
 PI Matsuzawa Y;
 XX
 DR MPI; 2001-611516/70.
 XX
 DR N-PSDB; AAI6654.
 XX
 PT Determining a risk factor for arteriosclerosis comprises detecting
 PT mutations in genes for cholesterol ester transfer protein.
 XX
 PS Disclosure: Page 43-47; 58pp: Japanese.
 XX
 CC The invention relates to detecting the risk factor for arteriosclerosis
 CC in a subject that involves detecting mutations in the gene for
 CC cholesterol ester transfer protein (CETP) related to the degree of risk
 CC of arteriosclerosis. The mutant proteins alter the level of HDL in the
 CC blood. The high frequency mutations can be detected for prevention and
 CC treatment of arteriosclerosis. The present sequence represents a
 CC human CETP.
 CC
 SQ Sequence 493 AA;
 Query Match 100.0%; Score 26; DB 22; Length 493;
 Best Local Similarity 100.0%; Pred. No. 4e-16;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RDGFLLLQMDGFPPEHLVDFLOSL 26
 Db 468 rdgflillqmdfgfpehlvdfllqsls 493
 ||||||||||||||||||||
 ||||||||||||||||||||

```

RESULT 13
AA13815
ID AAY13815 standard; peptide; 22 AA.
XX
AC AAY13815;
XX
DT 08-JUL-1999 (first entry)
XX
DE Rabbit CERP immunogenic fragment.
XX
KW CERP; cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;
KW antibody production; cholesteryl ester transfer; therapy;
KW high density lipoprotein; HDL cholesterol concentration;
KW pro-atherogenic dyslipoproteinaemia.
XX
OS Oryctolagus sp.
XX
PN WO915655-A1.
XX
PD 01-APR-1999.
XX
PF 17-SEP-1998; 98WO-US19366.
XX
PR 19-SEP-1997; 97US-0934367.
XX
PA (MONS ) MONSANTO CO.
XX
PI Glenn K, Needleman P;
XX
DR WPI; 1999-276984/23.
XX
PT New recombinant DNA vaccines
PS
SQ Sequence 22 AA;

CC This sequence represents an immunogenic fragment of the rabbit
CC cholesteryl ester transferase protein (CERP).
CC The invention relates to recombinant DNA vaccines that contain DNA
CC encoding CERP, which can be used for producing antibodies to lessen the
CC transfer of cholesteryl esters from high density lipoprotein (HDL). The
CC method can provide an autogenic immunological process for lessening the
CC transfer of cholesteryl esters from HDL particles and for increasing the
CC HDL cholesterol concentration of a mammal whose blood also contains
CC CERP. The method may be useful in treating human pro-atherogenic
CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
CC method can have an effect that lasts for months as compared to the
CC short-term effects of the small molecule drugs now available.
XX
SQ Sequence 22 AA;

Query Match 84.6%; Score 22; DB 20; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.2e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 LLLQMDGFPFHLVDPIQSLIS 26
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 lllqmdgfpfhlhldflqsls 22

RESULT 14
AA13821
ID AAY13821 standard; peptide; 22 AA.
XX
AC AAY13821;
XX
DT 08-JUL-1999 (first entry)
XX
DE Human CERP immunogenic fragment.
KW CERP; cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;

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KW antibody production; cholesteryl ester transfer; therapy;
KW high density lipoprotein; HDL cholesterol concentration;
KW pro-atherogenic dyslipoproteinaemia.
XX
OS Homo sapiens.
XX
PN WO915655-A1.
XX
PD 01-APR-1999.
XX
PF 17-SEP-1998; 98WO-US19366.
XX
PR 19-SEP-1997; 97US-0934367.
XX
PA (MONS ) MONSANTO CO.
XX
PI Glenn K, Needleman P;
XX
DR WPI; 1999-276984/23.
XX
PT New recombinant DNA vaccines
PS
SQ Sequence 22 AA;

CC This sequence represents an immunogenic fragment of the human
CC cholesteryl ester transferase protein (CERP).
CC The invention relates to recombinant DNA vaccines that contain DNA
CC encoding CERP, which can be used for producing antibodies to lessen the
CC transfer of cholesteryl esters from high density lipoprotein (HDL). The
CC method can provide an autogenic immunological process for lessening the
CC transfer of cholesteryl esters from HDL particles and for increasing the
CC HDL cholesterol concentration of a mammal whose blood also contains
CC CERP. The method may be useful in treating human pro-atherogenic
CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
CC method can have an effect that lasts for months as compared to the
CC short-term effects of the small molecule drugs now available.
XX
SQ Sequence 22 AA;

Query Match 84.6%; Score 22; DB 20; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.2e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 LLLQMDGFPFHLVDPIQSLIS 26
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 lllqmdgfpfhlhldflqsls 22

RESULT 15
AA02469
ID AAY02469 standard; protein; 496 AA.
XX
AC AAY02469;
XX
DT 14-JUL-1999 (first entry)
XX
DE Humanised rabbit cholesteryl ester transfer protein (CERP).
XX
KW Vaccine; antibody; endogenous; cholesteryl ester transfer protein; CERP;
KW high-density lipoprotein-associated cholesterol; metabolism;
KW low-density lipoprotein-associated cholesterol; atherosclerotic lesion;
KW cholesterol; atherosclerosis; heart disease.
XX
OS Synthetic.
OS Oryctolagus sp.
XX
PN WO9920302-A1.
XX
PD 29-APR-1999.
XX
PF 20-OCT-1998; 98WO-US22145.
XX

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PR 20-OCT-1997; 97US-0954643.
 PA (AVANT-) AVANT IMMUNOTHERAPEUTICS INC.
 XX
 XX
 PI Rittershaus CW, Thomas LJ;
 XX
 XX WPI: 1999-302645/25.
 DR
 XX
 XX
 PT Vaccine against cholesterol ester transfer protein
 PS
 XX Disclosure: Page 53-54; 61pp; English.
 CC The specification describes a vaccine that promotes the production of
 CC antibodies that bind endogenous cholesterol ester transfer protein
 CC (CETP). The vaccines (and equivalent plasmid-based vaccines) are
 CC used to increase the ratio of circulating high-density lipoprotein
 CC (HDL)-associated cholesterol to low-density lipoprotein (LDL)-associated
 CC cholesterol; to decrease the level of endogenous CETP activity in humans
 CC or other animals; to alter metabolism of LDL-associated cholesterol; for
 CC inhibiting development of atherosclerotic lesions; to lower circulating
 CC levels of LDL and total cholesterol; and to treat or prevent
 CC atherosclerosis (or more generally heart disease). The present sequence
 CC represents a humanised rabbit CETP.
 CC
 SQ Sequence 496 AA:
 50
 Query Match 84.6%; Score 22; DB 20; Length 496;
 Best Local Similarity 100.0%; Pred. No. 1.8e-12;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 50
 QY 5 LLLQMDGFPEHLVDFLOSL 26
 |||||||
 Db 475 LLLQMDGFPEHLVDFLOSL 496
 |||||||
 RESULT 16
 AAY91229
 ID AAY91229 standard; peptide; 16 AA.
 XX
 XX AAY91229;
 AC
 XX
 DT 22-MAY-2000 (first entry)
 DE Human cholesterol transport protein (CETP) peptide, SEQ ID NO:107.
 XX
 XX promiscuous T-cell epitope; measles virus F protein; MvF;
 KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
 KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; PMDV;
 KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 KW Plasmodium falciparum; circumsporozoite; antimalarial; CETP;
 KW cholesterol ester transport protein; anti-arteriosclerotic.
 XX
 OS Homo sapiens.
 XX
 PN WO9966957-A2.
 PD 29-DEC-1999.
 XX
 XX 21-JUN-1999; 99WO-US13975.
 PF
 XX 20-JUN-1998; 98US-0100412.
 PR
 XX
 PA (UNBI-) UNITED BIOMEDICAL INC.
 PI Wang CY;
 XX
 XX WPI: 2000-160564/14.
 DR
 XX New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 or human immune deficiency virus -
 PT

XX Claim 10; Page 50; 129pp; English.
 PS
 XX
 CC The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesterol ester transport
 CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of luteinising hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunocastration; for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
 CC from the measles virus F (MvF) protein and sequences AAY91122-Y91142,
 CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
 CC MvF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
 CC peptides comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AAY91208 is a
 CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MvF Th
 CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
 CC infection of T cells. AAY90212 is a modified version of a human IgE
 CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IgE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
 CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MvF Th
 CC epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent
 CC CETP-derived peptides and AAY91232-Y91241 are immunogens comprising a
 CC CETP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
 CC AAY91258-Y91273 are antigenic peptides comprising MvF Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91198 and AAY91199 are respectively an immunostimulatory invasive
 CC protein epitope from Yersinia species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.
 CC
 XX
 SO Sequence 16 AA:
 50
 Query Match 61.5%; Score 16; DB 21; Length 16;
 Best Local Similarity 100.0%; Pred. No. 2.8e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 50
 QY 11 FGPEHLVDFLOSL 26
 |||||||
 Db 1 fgfpehlvdflosls 16
 |||||||
 RESULT 17
 AAW06129
 ID AAW06129 standard; Peptide; 31 AA.
 XX
 XX AAW06129;
 AC
 XX 07-FEB-1997 (first entry)
 DT

XX PF 21-JUN-1999; 99WO-US13975.
 XX PR 20-JUN-1998; 98US-0100412.
 XX (UNBI-) UNITED BIOMEDICAL INC.
 XX Wang CY;
 XX WPI: 2000-160564/14.
 DR XX
 PT New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus -
 XX
 PS Claim 11: Page 106; 129pp; English.

CC The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesterol ester transport
 CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of interleukin hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunocastration); for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
 CC from the measles virus F (MVF) protein and sequences AAY91122-Y91142,
 CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
 CC MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
 CC peptides comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AAY91208 is a
 CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVH Th
 CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
 CC infection of T cells. AAY90212 is a modified version of a human IGE
 CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IGE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
 CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th
 CC epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent
 CC CETP-derived peptides and AAY91232-Y91241 are immunogens comprising a
 CC CETP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
 CC AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91188 and AAY91189 are respectively an immunostimulatory invasin
 CC protein epitope from *Yersinia* species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.
 XX
 XX Sequence 35 AA;

Query Match 61.5%; Score 16; DB 21; Length 35;
 Best Local Similarity 100.0%; Pred. No. 5.6e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 RGFPEHLVDFLOSLS 26
 Db 20 fgfpehlvdfldfsgs 35

RESULT 20
 AAY91234
 ID AAY91234 standard; peptide: 36 AA.
 XX
 AC AAY91234;
 XX
 DT 22-MAY-2000 (first entry)
 DE
 DE Modified MVF Th epitope/CETP peptide, SEQ ID NO:112.
 XX
 KW Promiscuous T-cell epitope; measles virus F protein; MVF;
 KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KW interleukin hormone releasing hormone; LHRH; contraceptive; anticancer;
 KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
 KW foot and mouth disease virus; immunoglobulin E; IGE; anti-allergic;
 KW Plasmodium falciparum; circumsporozoite; anti-malaria; CETP;
 KW cholesterol ester transport protein; anti-arteriosclerotic.
 OS Chimeric - Measles virus.
 OS Chimeric - Homo sapiens.
 XX
 PN M09966957-A2.
 XX
 PD 29-DEC-1999.
 XX
 PF 21-JUN-1999; 99WO-US13975.
 XX
 PR 20-JUN-1998; 98US-0100412.
 XX (UNBI-) UNITED BIOMEDICAL INC.
 XX Wang CY;
 XX WPI: 2000-160564/14.
 DR XX
 PT New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus -
 XX
 PS Claim 11: Page 105; 129pp; English.

CC The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesterol ester transport
 CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of interleukin hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunocastration); for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
 CC from the measles virus F (MVF) protein and sequences AAY91122-Y91142,
 CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
 CC MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides

CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
CC is the LHRH target antigenic peptide used in these LHRH antigenic
CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
CC peptides comprising somatostatin and a Th epitope. Somatostatin
CC immunogens may be used to promote growth in livestock. Somatostatin
CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVH Th
CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
CC infection of T cells. AAY90212 is a modified version of a human IgE
CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IgE CH3
CC antigenic peptides which may be used in the treatment of allergies.
CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVE Th
CC epitope, and may be used in a malaria vaccine. AAY91228-Y91231 represent
CC CERP-derived peptides and AAY91232-Y91241 are immunogens comprising a
CC CERP peptide and a Th epitope which may be used to prevent or treat
CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
CC AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell
CC epitope which may be used as a component in an anti-HIV-1 vaccine.
CC AAY91198 and AAY91199 are respectively an immunostimulatory invasin
CC protein epitope from Yersinia species, and hinge spacer peptide, both of
CC which may optionally be used in the antigenic peptides of the
CC invention.

XX Sequence 36 AA;

Query Match 61.5%; Score 16; DB 21; Length 36;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 FGPEHLVDFLOSLS 26
|||||
Db 21 fgfpehllyvdfiqsls 36

RESULT 21
AAY91235
ID AAY91235 standard; peptide: 36 AA.

XX AAY91235;

XX 22-MAY-2000 (first entry)

DE Modified MVE Th epitope/CERP peptide, SEQ ID NO:113.

XX Promiscuous T-cell epitope; measles virus F protein; MVE;
KM hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KM luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
KM somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
KM foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KM Plasmodium falciparum; circumsporozoite; antimalarial; CERP;
KM cholesterol ester transport protein; anti-arteriosclerotic.

OS Chimeric - Measles virus.
OS Chimeric - Homo sapiens.

PN WO966957-A2.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US13975.

XX 20-JUN-1998; 98US-0100412.

XX (UNBT-) UNITED BIOMEDICAL INC.

PA Wang CY;

XX WPI; 2000-160564/14.

PT New artificial T helper cell epitope and derived immunogens with target
PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT or human immune deficiency virus
XX
XX
PS Claim 11: Page 105; 129pp; English.

XX The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response.
CC specifically against Plasmodium falciparum, cholesterol ester transport
CC protein (CERP) or HIV epitopes, but more generally against any pathogen,
CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC peptide immunogens may be used for prevention and/or treatment of
CC infections (HIV, foot-and-mouth disease or malaria); for cancer
CC immunotherapy; for inhibition of the action of luteinising hormone
CC releasing hormone (LHRH) for contraception, treatment of hormone-
CC dependent cancer, prevention of boar taint in meat, and
CC immunocastration; for promoting the growth of animals; or for
CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
CC Th (functional in genetically diverse subjects) into an immunogen
CC improves capacity to induce a strong T helper cell-mediated immune
CC response, resulting in production of antibodies against a target
CC antigen. Th can replace carrier proteins and pathogen-derived T helper
CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
CC from the measles virus F (MVE) protein and sequences AAY91122-Y91142,
CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
CC MVE Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
CC from hepatitis B virus (HBV) surface antigen, and sequences
CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
CC is the LHRH target antigenic peptide used in these LHRH antigenic
CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
CC peptides comprising somatostatin and a Th epitope. Somatostatin
CC immunogens may be used to promote growth in livestock. AAY91208 is a
CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVH Th
CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
CC infection of T cells. AAY90212 is a modified version of a human IgE
CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IgE CH3
CC antigenic peptides which may be used in the treatment of allergies.
CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVE Th
CC epitope, and may be used in a malaria vaccine. AAY91228-Y91231 represent
CC CERP-derived peptides and AAY91232-Y91241 are immunogens comprising a
CC CERP peptide and a Th epitope which may be used to prevent or treat
CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
CC AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell
CC epitope which may be used as a component in an anti-HIV-1 vaccine.
CC AAY91198 and AAY91199 are respectively an immunostimulatory invasin
CC protein epitope from Yersinia species, and hinge spacer peptide, both of
CC which may optionally be used in the antigenic peptides of the
CC invention.

XX Sequence 36 AA;

Query Match 61.5%; Score 16; DB 21; Length 36;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 FGPEHLVDFLOSLS 26
|||||
Db 21 fgfpehllyvdfiqsls 36

RESULT 22
AAY91237
ID AAY91237 standard; peptide: 36 AA.

AC	AAV91237;
XX	
DT	22-MAY-2000 (first entry)
XX	
DE	Modified MVF Th epitope/CETP peptide, SEQ ID NO:115.
XX	
KW	Promiscuous T-cell epitope; measles virus F protein; MVF;
KW	hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KW	lutealising hormone releasing hormone; LHRH; contraceptive; anticancer;
KW	somatostatin; growth promotion; CD4 receptor; HIV-1; artiviral; FMDV;
KW	foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KW	Plasmodium falciparum; circumporozoite; antimalarial; CETP;
KM	cholesteryl ester transport protein; anti-arteriosclerotic.
XX	
OS	Chimeric - Measles virus.
OS	Chimeric - Homo sapiens.
XX	
PN	MO9966957-A2.
PD	
PD	29-DEC-1999.
PF	
PR	21-JUN-1999; 99MO-US13975.
XX	
PR	20-JUN-1998; 98US-0100412.
PA	(UNBI-) UNITED BIOMEDICAL INC.
PS	
PT	Mang CY;
XX	
DR	WPJ: 2000-160564/14.
XX	
PT	New artificial T helper cell epitope and derived immunogens with target
PT	antigenic site, for immunization against e.g. malaria, arteriosclerosis
XX	or human immune deficiency virus
XX	
PS	Claim 11: Page 106; 129pp; English.
XX	
CC	The invention relates to novel promiscuous T helper cell epitopes (Th),
CC	and immunogenic peptides comprising the Th epitopes of the invention
CC	along with B cell epitopes. The Th epitopes and peptide immunogens
CC	containing them, are used to induce a T helper cell response,
CC	specifically against Plasmodium falciparum, cholesteryl ester transport
CC	protein (CETP) or HIV epitopes, but more generally against any pathogen,
CC	immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC	peptide immunogens may be used for prevention and/or treatment of
CC	infections (HIV, foot-and-mouth disease or malaria); for cancer
CC	immunotherapy; for inhibition of the action of lutealising hormone
CC	releasing hormone (LHRH) for contraception, treatment of hormone-
CC	dependent cancer, prevention of boar taint in meat, and
CC	immunoconstrastion); for promoting the growth of animals; or for
CC	treating allergies or arteriosclerosis. Incorporation of a promiscuous
CC	Th (functional in genetically diverse subjects) into an immunogen
CC	improves capacity to induce a strong T helper cell-mediated immune
CC	response, resulting in production of antibodies against a target
CC	antigen. Th can replace carrier proteins and pathogen-derived T helper
CC	epitopes. Sequence AAV91121 represents a promiscuous T helper epitope
CC	from the measles virus F (MVF) protein and sequences AAV91122-V91142,
CC	AAV91226 and AAV91245-Y91246 represent synthetic Th epitopes based on
CC	MVF Th epitope. Sequence AAV91143 represents a promiscuous Th epitope
CC	from hepatitis B virus (HBV) surface antigen, and sequences
CC	AAV91144-Y91155 are synthetic epitopes derived from this HBV epitope.
CC	AAV91156-Y91196, AAV91227 and AAV91242-Y91244 are antigenic peptides
CC	comprising an LHRH sequence joined to a promiscuous Th epitope. AAV91197
CC	is the LHRH target antigenic peptide used in these LHRH antigenic
CC	peptides. AAV91200 is somatostatin, and AAV91201-Y90219 are antigenic
CC	peptides comprising somatostatin and a Th epitope. Somatostatin
CC	immunogens may be used to promote growth in livestock. AAV91208 is a
CC	human CD4 CD82-like domain antigenic site, and AAV91209-Y90211 are MVH Th
CC	epitope/CD4 CD82 antigenic peptides which may be used to prevent HIV
CC	infection of T cells. AAV90212 is a modified version of a human IGE
CC	(immunoglobulin E) CH3 domain, and AAV90213-Y90215 are Th epitope/IgE
CC	antigenic peptides which may be used in the treatment of allergies.
CC	AAV91220 is a peptide derived from foot and mouth disease virus (FMDV).

DR WPI; 1996-506103/50.
 XX Cholesteryl ester transfer protein B cell epitope linked to T cell
 PT epitope - used to generate vaccine to regulate CERP activity for
 PT decreasing the risk of developing a cardiovascular disease e.g.
 PT atherosclerosis
 XX
 XX Disclosure; Page 7; 72pp; English.
 XX
 CC A multivalent vaccine comprises an immunogenic helper T-cell
 CC epitope of tetanus toxoid protein covalently linked to the B-cell
 CC epitopes of human cholesteryl ester transfer protein (CERP) (see
 CC also AAM061277). The vaccine elicits an immune response against
 CC endogenous CERP activity, and is used to treat or prevent a
 CC cardiovascular disease, such as atherosclerosis.
 CC
 XX
 SO Sequence 50 AA;
 .
 Query Match 61.5%; Score 16; DB 17; Length 50;
 Best Local Similarity 100.0%; Pred. No. 7.6e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 11 EGPEHLLVDFLOSLS 26
 Db 35 fgtfphllvdfllqsls 50
 .
 RESULT 24
 ID AAM24294 standard; peptide; 11 AA.
 XX AAM24294;
 AC
 XX 17-OCT-1997 (first entry)
 DT
 XX Human/Rabbit CERP common peptide.
 DE
 XX Immune response; high density lipoprotein; HDL; cholesterol; human;
 KW serum; epitope; cholesteryl ester transfer protein; CERP; rabbit.
 XX
 OS Oryctolagus cuniculus.
 OS Homo sapiens.
 XX
 PN WO9639168-A1.
 XX
 PD 12-DEC-1996.
 XX
 PF 05-JUN-1996; 96WO-US09143.
 XX
 PR 06-JUN-1995; 95US-0482454.
 XX
 PA (IMMU-) IMMUNE RESPONSE CORP.
 XX
 PI Brostoff SM, Carlo DJ, Kwoh DY;
 DR WPI; 1997-042849/04.
 XX
 PT Stimulating an immune response to increase high density lipoprotein
 PT - avoids repeated administration of toxic drugs to lower cholesteryl
 PT ester transfer protein levels
 XX
 XX Claim 5; Page 16; 26pp; English.
 .
 The sequences given in AAM24292-94 were used in the method of the
 CC invention to stimulate an immune response to increase high density
 CC lipoprotein (HDL) cholesterol in a mammal exhibiting low levels of
 CC serum HDL. These peptides represent immunogenic epitopes of
 CC cholesteryl ester transfer protein (CERP). The method utilizes
 CC the body's own immune system to lower CERP levels, thereby increasing
 CC the level of beneficial HDL cholesterol, preferably in serum. The
 CC method avoids the problems associated with the repeated administration
 CC of drugs which have undesirable side effects. This peptide represents

CC a region of CERP which is common to both human and rabbit proteins.
 XX
 SO Sequence 11 AA;
 .
 Query Match 42.3%; Score 11; DB 18; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00076;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 16 HLLVDFLOSLS 26
 Db 1 hllvdfllqsls 11
 .
 RESULT 25
 ID AAY91230 standard; peptide; 16 AA.
 XX AAY91230;
 AC
 XX 22-MAY-2000 (first entry)
 DT
 XX Human cholesteryl transport protein (CERP) peptide, SEQ ID NO:108.
 DE
 XX Promiscuous T-cell epitope; measles virus F protein; MZF;
 KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KW interleukin-6; growth hormone releasing hormone; LHRH; contraceptive; anticancer;
 KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
 KW foot and mouth disease virus; immunoglobulin E; IGE; anti-allergic;
 KW Plasmodium falciparum; circumporozoite; anti-malarial; CERP;
 KW cholesteryl ester transport protein; anti-arteriosclerotic.
 XX
 OS Homo sapiens.
 XX
 PN WO966957-A2.
 XX
 PD 29-DEC-1999.
 XX
 PF 21-JUN-1999; 99WO-US13975.
 XX
 PR 20-JUN-1998; 98US-0100412.
 XX
 PA (UNDI-) UNITED BIOMEDICAL INC.
 XX
 PI Wang CY;
 DR WPI; 2000-160564/14.
 XX
 PT New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus
 XX
 PS Claim 10; Page 62; 129pp; English.
 XX
 CC The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesteryl ester transport
 CC protein (CERP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of interleukin hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunocastration; for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope

CC from the measles virus F (MVF) protein and sequences AAY91122-Y91142, the
 CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
 CC MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
 CC peptides comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AAY91208 is a
 CC human CD4 CD82-like domain antigenic site, and AAY91203-Y90211 are MVH Th
 CC epitope/CD4 CD82 antigenic peptides which may be used to prevent HIV
 CC infection of T cells. AAY90212 is a modified version of a human IGE
 CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IGE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VPI capsid protein and AAY91221-Y91222 comprise this peptide and a Th
 CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th
 CC epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent
 CC CERP-derived peptides and AAY91232-Y91241 are immunogens comprising a
 CC CERP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
 CC AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91198 and AAY91199 are respectively an immunostimulatory invasion
 CC protein epitope from Yersinia species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.

SQ Sequence 16 AA;

Query Match 42.3%; Score 11; DB 21; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HLVDFFLOSLS 26
 |||||
 Db 6 hllvdfflgs 16

RESULT 26
 AAY13809
 ID AAY13809 standard; peptide: 22 AA.

XX AAY13809;

DT 08-JUL-1999 (first entry)

DE Rabbit CERP immunogenic fragment.

XX CERP, cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;
 KW antibody production; cholesteryl ester transfer; therapy;
 KM high density lipoprotein; HDL cholesterol concentration;
 KM pro-atherogenic dyslipoproteinaemia.

XX Oryctolagus sp.

PN WO915655-A1.

PD 01-APR-1999.

PP 17-SEP-1998; 98WO-US19366.

PR 19-SEP-1997; 97US-0934367.

PA (MONS) MONSANTO CO.

PI Glenn K, Needleman P;

XX

DR WPI: 1999-276984/23.
 XX New recombinant DNA vaccines
 PT Example 1; Page 73; 99pp; English.
 PS This sequence represents an immunogenic fragment of the rabbit
 CC cholesteryl ester transferase protein (CERP).
 CC The invention relates to recombinant DNA vaccines that contain the
 CC encoding CERP, which can be used for producing antibodies to lessen the
 CC transfer of cholesteryl esters from high density lipoprotein (HDL). The
 CC method can provide an autogenic immunological process for lessening the
 CC transfer of cholesteryl esters from HDL particles and for increasing the
 CC HDL cholesterol concentration of a mammal whose blood also contains
 CC CERP. The method may be useful in treating human pro-atherogenic
 CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
 CC method can have an effect that lasts for months as compared to the
 CC short-term effects of the small molecule drugs now available.

SQ Sequence 22 AA;

Query Match 42.3%; Score 11; DB 20; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.0014;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HLVDFFLOSLS 26
 |||||
 Db 12 hllvdfflgs 22

RESULT 27
 AAY13802
 ID AAY13802 standard; peptide: 26 AA.

XX AAY13802;

DT 08-JUL-1999 (first entry)

DE Rabbit CERP immunogenic fragment.

XX CERP, cholesteryl-ester transfer protein; recombinant DNA vaccine; HDL;
 KW antibody production; cholesteryl ester transfer; therapy;
 KM high density lipoprotein; HDL cholesterol concentration;
 KM pro-atherogenic dyslipoproteinaemia.

XX Oryctolagus sp.

PN WO915655-A1.

PD 01-APR-1999.

PP 17-SEP-1998; 98WO-US19366.

PR 19-SEP-1997; 97US-0934367.

PA (MONS) MONSANTO CO.

PI Glenn K, Needleman P;

DR WPI: 1999-276984/23.

XX New recombinant DNA vaccines

PS Claim 15; Page 94; 99pp; English.

CC This sequence represents an immunogenic fragment of the rabbit
 CC cholesteryl ester transferase protein (CERP).
 CC The invention relates to recombinant DNA vaccines that contain the
 CC encoding CERP, which can be used for producing antibodies to lessen the
 CC transfer of cholesteryl esters from high density lipoprotein (HDL). The
 CC method can provide an autogenic immunological process for lessening the
 CC transfer of cholesteryl esters from HDL particles and for increasing the

CC HDL cholesterol concentration of a mammal whose blood also contains
 CC CEMP. The method may be useful in treating human pro-atherogenic
 CC dyslipoproteinaemias characterised by low HDL/LDL cholesterol ratios. The
 CC method can have an effect that lasts for months as compared to the
 CC short-term effects of the small molecule drugs now available.

XX Sequence 26 AA;

Query Match 42.3%; Score 11; DB 20; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.0016;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HLIVDFLOSLS 26
 |||||
 Db 16 hllivdflosls 26

RESULT 28
 ID AAY91231 standard; peptide; 26 AA.
 AC AAY91231;

XX 22-MAY-2000 (first entry)

DE Human cholesterol transport protein (CEMP) peptide, SEQ ID NO:109.

XX Promiscuous T-cell epitope; measles virus F protein; MVF;
 KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KW interleukin hormone releasing hormone; LHRH; contraceptive; anticancer;
 KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
 KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 KW Plasmodium falciparum; circumsporozoite; antimalarial; CEMP;
 KW cholesterol ester transport protein; anti-arteriosclerotic.

XX Homo sapiens.

OS WO966957-A2.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US13975.

XX 20-JUN-1998; 98US-0100412.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY;

DR WPI; 2000-160564/14.

PT New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus
 PS Claim 10; Page 62; 129pp; English.

XX The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesterol ester transport
 CC protein (CEMP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of interleukin hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunosuppression; for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 Th (functional in genetically diverse subjects) into an immunogen

CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
 CC from the measles virus F (MVF) protein and sequences AAY91122-Y91142,
 CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
 CC MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
 CC peptides comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AAY91208 is a
 CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVA Th
 CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
 CC infection of T cells. AAY90212 is a modified version of a human IgE
 CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IgE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VPI capsid protein and AAY91221-Y91222 comprise this peptide and a Th
 CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th
 CC epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent
 CC CEMP-derived peptides and AAY91232-Y91241 are immunogens comprising a
 CC CEMP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
 CC AAY91258-Y91273 are antigenic peptides comprising MVA Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91198 and AAY91199 are respectively an immunostimulatory invasion
 CC protein epitope from Yersinia species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.

XX Sequence 26 AA;

Query Match 42.3%; Score 11; DB 21; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.0016;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HLIVDFLOSLS 26
 |||||
 Db 16 hllivdflosls 26

RESULT 29

ID AAY91238 standard; peptide; 36 AA.

AC AAY91238;

XX 22-MAY-2000 (first entry)

DE Modified MVF Th epitope/CEMP peptide, SEQ ID NO:116.

XX Promiscuous T-cell epitope; measles virus F protein; MVF;
 KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KW interleukin hormone releasing hormone; LHRH; contraceptive; anticancer;
 KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
 KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
 KW Plasmodium falciparum; circumsporozoite; antimalarial; CEMP;
 KW cholesterol ester transport protein; anti-arteriosclerotic.

OS Chimeric - Measles virus.

OS Chimeric - Homo sapiens.

XX WO966957-A2.
 XX 29-DEC-1999.

PF 21-JUN-1999: 99WO-US13975.
 XX 20-JUN-1998: 98US-0100412.
 PR (UNBI-) UNITED BIOMEDICAL INC.
 XX
 PA Wang CY:
 XX MPI: 2000-160564/14.
 DR
 XX New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus
 PS Claim 11: Page 106; 129pp; English.
 XX
 XX The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesterol, ester transport
 CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of interleukin hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunocastration; for promoting the growth of animals, or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
 CC from the measles virus F (MVF) protein and sequences AAY91122-Y91142,
 CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
 CC MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
 CC peptides comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. Somatostatin
 CC human CD4 CDR2 antigenic peptides which may be used to prevent HIV
 CC infection of T cells. AAY90212 is a modified version of a human IGE
 CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitopes/IGe CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
 CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th
 CC epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent
 CC CETP-derived peptides and AAY91232-Y91241 are immunogens comprising a
 CC CETP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
 CC AAY91258-Y91273 are antigenic peptides comprising MVF Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91198 and AAY91199 are respectively an immunostimulatory Invasin
 CC protein epitope from Yersinia species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.
 XX
 XX Sequence 36 AA:
 SO

QY 16 HLLVDFLOSLS 26
 |||||
 DB 26 hllvdflosgls 36
 RESULT 30
 AAY91239
 ID AAY91239 standard; peptide: 36 AA.
 XX
 AC AAY91239;
 XX
 DT 22-MAY-2000 (first entry)
 XX
 DE Modified MVF Th epitope/CETP peptide, SEQ ID NO:117.
 XX
 XX Promiscuous T-cell epitope: measles virus F protein; MVF;
 KM hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KM interleukin hormone releasing hormone; LHRH; contraceptive; anticancer;
 KM somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
 KM foot and mouth disease virus; immunoglobulin E; IGE; anti-allergic;
 KM Plasmodium falciparum; circumsporozoite; antimalarial; CETP;
 KM cholesterol ester transport protein; anti-arteriosclerotic.
 XX
 OS Chimeric - Measles virus.
 OS Chimeric - Homo sapiens.
 OS
 PN WO966957-A2.
 XX
 PD 29-DEC-1999.
 XX
 PF 21-JUN-1999: 99WO-US13975.
 XX
 PR 20-JUN-1998: 98US-0100412.
 XX
 PA (UNBI-) UNITED BIOMEDICAL INC.
 XX
 PI Wang CY:
 XX MPI: 2000-160564/14.
 DR
 XX New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus
 PS Claim 11: Page 107; 129pp; English.
 XX
 XX The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesterol, ester transport
 CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of interleukin hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunocastration; for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
 CC from the measles virus F (MVF) protein and sequences AAY91122-Y91142,
 CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
 CC MVF Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197

CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAY91200 is somatostatin and a Th epitope. Somatostatin
 CC immunogens comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AAY91208 is a
 CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVA Th
 CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
 CC infection of T cells. AAY90212 is a modified version of a human IGE
 CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IGE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
 CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVA Th
 CC epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent
 CC CERP-derived peptides and AAY91232-Y91241 are immunogens comprising a
 CC CERP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
 CC AAY91258-Y91273 are antigenic peptides comprising MVA Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91198 and AAY91199 are respectively an immunostimulatory invasin
 CC protein epitope from *Yersinia* species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.

CC Sequence 36 AA;

Query Match 42.3%; Score 11; DB 21; Length 36;

Best Local Similarity 100.0%; Pred. No. 0.0021;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HLLVDFLOSLTS 26
 |||||
 Db 26 hllvdfllgsls 36

RESULT 31

ID AAY91240 standard; peptide; 46 AA.

AC AAY91240;

DT 22-MAY-2000 (first entry)

DE Modified MVA Th epitope/CERP peptide, SEQ ID NO:118.

KM Promiscuous T-cell epitope; measles virus F protein; MVA;
 KM hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KM interleukin-6 growth promoting hormone; LHRH; contraceptive; anticancer;
 KM somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
 KM foot and mouth disease virus; immunoglobulin E; IGE; anti-allergic;
 KM Plasmodium falciparum; circumsporozoite; antimalarial; CERP;
 KM cholesterol ester transport protein; anti-arteriosclerotic.

OS Chimeric - Measles virus.

OS Chimeric - Homo sapiens.

PN WO966957-A2.

PD 29-DEC-1999.

PF 21-JUN-1999; 99WO-US13975.

PR 20-JUN-1998; 98US-0100412.

PA (UNBI-) UNITED BIOMEDICAL INC.

PI Wang CY;

DR WPI; 2000-160564/14.

PT New artificial T helper cell epitope and derived immunogens with target

PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus
 XX
 XX
 PS Claim 11; Page 107; 129pp; English.

CC The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogen
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesterol ester transport
 CC protein (CERP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of interleukin hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunocastration); for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
 CC from the measles virus F (MVA) protein and sequences AAY91122-Y91142,
 CC AAY91226 and AAY91245-Y91246 represent synthetic Th epitopes based on the
 CC MVA Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
 CC peptides comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AAY91208 is a
 CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVA Th
 CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
 CC infection of T cells. AAY90212 is a modified version of a human IGE
 CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IGE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th
 CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVA Th
 CC epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent
 CC CERP-derived peptides and AAY91232-Y91241 are immunogens comprising a
 CC CERP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
 CC AAY91258-Y91273 are antigenic peptides comprising MVA Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91198 and AAY91199 are respectively an immunostimulatory invasin
 CC protein epitope from *Yersinia* species, and hinge spacer peptide, both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.

CC Sequence 46 AA;

Query Match 42.3%; Score 11; DB 21; Length 46;

Best Local Similarity 100.0%; Pred. No. 0.0026;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HLLVDFLOSLTS 26
 |||||
 Db 36 hllvdfllgsls 46

RESULT 32

ID AAY91241 standard; peptide; 46 AA.

AC AAY91241;

XX 22-MAY-2000 (first entry)
 DT Modified MVE Th epitope/CETP peptide, SEQ ID NO:119.
 DE
 XX
 KM Promiscuous T-cell epitope; measles virus F protein; MVE;
 KM hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
 KM interleukin-6 releasing hormone; LHRH; contraceptive; anticancer;
 KM somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
 KM foot and mouth disease virus; immunoglobulin E; IGE; anti-allergic;
 KM Plasmodium falciparum; circumsporozoite; antimalarial; CETP;
 KM cholesterol ester transport protein; anti-arteriosclerotic.
 XX
 OS Chimeric - Measles virus.
 OS Chimeric - Homo sapiens.
 XX
 PN MO9966957-A2.
 XX
 PD 29-DEC-1999.
 XX
 PF 21-JUN-1999; 99WO-US13975.
 XX
 PR 20-JUN-1998; 98US-0100412.
 XX
 PA (UNB1-) UNITED BIOMEDICAL INC.
 XX
 PI Wang CY;
 XX
 DR MPI; 2000-160564/14.
 XX
 PT New artificial T helper cell epitope and derived immunogens with target
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
 PT or human immune deficiency virus
 XX
 PS Claim 11; Page 107-108; 129pp; English.

CC The invention relates to novel promiscuous T helper cell epitopes (Th),
 CC and immunogenic peptides comprising the Th epitopes of the invention
 CC along with B cell epitopes. The Th epitopes and peptide immunogens
 CC containing them, are used to induce a T helper cell response,
 CC specifically against Plasmodium falciparum, cholesterol ester transport
 CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
 CC peptide immunogens may be used for prevention and/or treatment of
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer
 CC immunotherapy; for inhibition of the action of interleukin hormone
 CC releasing hormone (LHRH) for contraception, treatment of hormone-
 CC dependent cancer, prevention of boar taint in meat, and
 CC immunosuppression; for promoting the growth of animals; or for
 CC treating allergies or arteriosclerosis. Incorporation of a promiscuous
 CC Th (functional in genetically diverse subjects) into an immunogen
 CC improves capacity to induce a strong T helper cell-mediated immune
 CC response, resulting in production of antibodies against a target
 CC antigen. Th can replace carrier proteins and pathogen-derived T helper
 CC epitopes. Sequence AAY91121 represents a promiscuous T helper epitope
 CC from the measles virus F (MVE) protein and sequences AAY91122-Y91142,
 CC AAY91226 and AAY91243-Y91246 represent synthetic Th epitopes based on the
 CC MVE Th epitope. Sequence AAY91143 represents a promiscuous Th epitope
 CC from hepatitis B virus (HBV) surface antigen, and sequences
 CC AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope.
 CC AAY91156-Y91196, AAY91227 and AAY91247-Y91244 are antigenic peptides
 CC comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197
 CC is the LHRH target antigenic peptide used in these LHRH antigenic
 CC peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic
 CC peptides comprising somatostatin and a Th epitope. Somatostatin
 CC immunogens may be used to promote growth in livestock. AAY91208 is a
 CC human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVE Th
 CC epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV
 CC infection of T cells. AAY90212 is a modified version of a human IGE
 CC (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IGE CH3
 CC antigenic peptides which may be used in the treatment of allergies.
 CC AAY91220 is a peptide derived from foot and mouth disease virus (FMDV)
 CC VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th

CC epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target
 CC antigen, and AAY91224-Y91225 comprise the CS antigen and an MVE Th
 CC epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent
 CC CETP-derived peptides and AAY91232-Y91241 are immunogens comprising a
 CC CETP peptide and a Th epitope which may be used to prevent or treat
 CC arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257
 CC are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and
 CC AAY91258-Y91273 are antigenic peptides comprising MVE Th and HIV-1 B-cell
 CC epitope which may be used as a component in an anti-HIV-1 vaccine.
 CC AAY91198 and AAY91199 are respectively an immunostimulatory invasive
 CC protein epitope from Yersinia species, and hinge spacer peptide. Both of
 CC which may optionally be used in the antigenic peptides of the
 CC invention.
 CC
 XX
 SQ Sequence 46 AA:
 XX

Query Match 42.3%; Score 11; DB 21; Length 46;
 Best Local Similarity 100.0%; Pred. No. 0.0026;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 HLLVDFLOSLS 26
 Db 36 HLLVDFLGS 46

RESULT 33
 AAM06132
 ID AAM06132 standard; Peptide; 50 AA.
 XX
 AC AAM06132;
 XX
 DT 07-FEB-1997 (first entry)
 XX
 DE Anti-cholesterol ester transfer multivalent vaccine peptide.
 XX
 KW Cholesterol ester transfer protein; CETP; antigen; vaccine;
 KW cardiovascular disease; atherosclerosis.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT 2..15
 FT Region /label= "T-cell epitope
 FT /note= "T-cell epitope comprises amino acids
 FT 830-843 of tetanus toxoid protein"
 FT 16..34
 FT Region /label= "B-cell epitope
 FT /note= "B-cell epitope comprises amino acids
 FT 350-368 of rabbit CETP"
 FT 35..50
 FT Region /label= "B-cell epitope
 FT /note= "B-cell epitope comprises the C-terminal 16
 FT amino acids of rabbit CETP, involved in
 FT neutral lipid binding or transfer activity"
 FT

WO9634888-A1.
 07-NOV-1996.
 01-MAY-1996; 96WO-US06147.
 01-MAY-1995; 95US-0432483.
 (TCCL-) T CELL SCI INC.
 Rittershaus CW, Thomas LJ;
 MPI; 1996-506103/50.
 Cholesterol ester transfer protein B cell epitope linked to T cell
 epitope used to generate vaccine to regulate CETP activity for
 decreasing the risk of developing a cardiovascular disease e.g.

Pt for treating cardiovascular disease
Xx

Ps Claim 8; Page 22; 67pp; English.

Cc The present sequence represents a construct containing a helper T cell epitope from the toxoid leatus protein, and 2 B cell epitopes of rabbit CCE mature cholesteryl ester transfer protein (CETP). CETPs mediate the CC transfer of cholesterol esters from high density lipoprotein (HDL) to CC very low density lipoprotein (VLDL), and low density lipoprotein (IDL), CC and vice versa. An increased CETP activity produces an atherogenic CC lipoprotein profile and induces atherosclerosis. A 13 amino acid stretch CC in the rabbit CETP (AAW46445) (Phe463 to Leu495) is important for CC neutral lipid binding and transfer activity. This region has been shown CC to be immunogenic as a B cell epitope of CETP. A second B cell epitope CC is defined by Arg350 to Ile368. Antibodies to this second epitope would allow the formation of immune complexes involving CETP, and promote CC the removal of the complexed CETP. The present sequence is encoded by a CC DNA plasmid-based vaccine which comprises sequences encoding at least 1 CC B cell epitope of CETP linked in frame with at least one segment CC encoding a broad range helper T cell epitope. The vaccines can be used to CC elevate the ratio of circulating HDL to circulating LDL, VLDL or total CC cholesterol in a human. It can also be used for decreasing the level of CC endogenous CETP activity in vivo and for treating cardiovascular disease.
CC anti-CETP antibodies in vivo and for treating cardiovascular disease.
Cc XX

SQ Sequence 50 AA:

Query Match Best Local Similarity 42.3%; Score 11; DB 18; Length 50;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 HLLVDLFLOSLS 26
|||
Db 40 hllvdlfqlsls 50

RESULT 35
AAAY02468
ID ID AAY02468 standard; protein; 477 AA.
XX
AC AAY02468;
XX
DT 14-JUL-1999 (first entry)
DE Modified rabbit cholesteryl ester transfer protein (CETP).
Xx KW Vaccine; antibody; endogenous; cholesteryl ester transfer protein; CETP;
KW high-density lipoprotein-associated cholesterol; metabolism;
KM low-density lipoprotein-associated cholesterol; atherosclerotic lesion;
KV cholesterol; atherosclerosis; heart disease.
Xx OS Synthetic.
OS Oryctolagus sp.
XX
PN WO9920302-A1.
XX
PD 29-APR-1999.
XP 20-OCT-1998; 98WO-US22145.
XF 20-OCT-1997; 97US-0954643.
XX
PA (AVANT-) AVANT IMMUNOTHERAPEUTICS INC.
PI Rittershaus CW, Thomas LJ;
XX WPI: 1999-302645/25.
DR Vaccine against cholesteryl ester transfer protein
PT Claim 5; Page 50-52; 61pp; English.
XS

CC The specification describes a vaccine that promotes the production of
 CC antibodies that bind endogenous cholesteryl ester transfer protein
 CC (CETP). The vaccines (and equivalent plasmid-based vaccines) are
 CC used to increase the ratio of circulating high-density lipoprotein
 CC (HDL)-associated cholesterol to low-density lipoprotein (LDL)-associated
 CC cholesterol; to decrease the level of endogenous CETP activity in humans
 CC or other animals; to alter metabolism of LDL-associated cholesterol, for
 CC inhibiting development of atherosclerotic lesions; to lower circulating
 CC levels of LDL and total cholesterol; and to treat or prevent
 CC atherosclerosis (or more generally heart disease). The present sequence
 CC represents a modified rabbit CETP.

SQ Sequence 477 AA:

Query Match 42.3%; Score 11; DB 20; Length 477;
 Best Local Similarity 100.0%; Pred. No. 0.02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 HLLVDFLOSLS 26
 |||||
 Db 467 hllvdflosls 477

RESULT 36

AAW06133
 ID AAW06133 standard; Protein; 496 AA.

AC AAW06133;

DT 07-FEB-1997 (first entry)

DE Rabbit cholesteryl ester transfer protein.

KW Cholesteryl ester transfer protein; CETP; antigen; vaccine;
 KM cardiovascular disease; atherosclerosis.

OS Oryctolagus cuniculus.

PH Key Location/Qualifiers

FT Region 350..368

FT Region /label=B-cell_epitope

FT Region 481..496

FT /label=B-cell_epitope

FT /note="C-terminal epitope involved in neutral

FT lipid binding or a transfer activity of

FT CETP"

PA (TCEL-) T CELL SCI INC.

PI Rittershaus CW, Thomas LJ;

DR WPI; 1996-506103/50.

PT Cholesteryl ester transfer protein B cell epitope linked to T cell

PT epitope used to generate vaccine to regulate CETP activity for

PT decreasing the risk of developing a cardiovascular disease e.g.

PT atherosclerosis

PS Disclosure; Page 51-54; 72pp; English.

CC Rabbit mature cholesteryl ester transfer protein (CETP) (AAW06127)

CC plays a role in altering the relative profile of circulating

CC lipoproteins. It shows approx. 80% amino acid homology to

CC human CETP (AAW06127), raised levels of which have been linked to an

CC increased risk of cardiovascular disease. B-cell epitopes of the
 CC rabbit or human CETP can be used in novel peptide vaccines (see
 CC also AAW06129, AAW06131-32) that elicit an immune response against
 CC endogenous CETP activity, thereby treating or preventing
 CC cardiovascular disease, such as atherosclerosis.

SQ Sequence 496 AA:

Query Match 42.3%; Score 11; DB 17; Length 496;
 Best Local Similarity 100.0%; Pred. No. 0.021;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 HLLVDFLOSLS 26
 |||||
 Db 486 hllvdflosls 496

RESULT 37

AAW46445
 ID AAW46445 standard; Protein; 496 AA.

AC AAW46445;

DT 18-MAY-1998 (first entry)

DE Mature rabbit cholesteryl ester transfer protein (CETP).

KW Cholesteryl ester transfer protein; CETP; rabbit; cholesteryl ester;

KM high density lipoprotein; HDL; very low density lipoprotein; VLDL;

KW low density lipoprotein; LDL; atherosclerosis; neutral lipid binding;

KW transfer activity; immunogenic; B cell epitope; antibody; TP2;

KW DNA plasmid-based vaccine; broad range helper T cell epitope;

KW treatment; cardiovascular disease.

OS Oryctolagus sp.

PH Key Location/Qualifiers

FT Region 350..368

FT Region /label=B-cell_epitope

FT Region 481..496

FT /label=B-cell_epitope

FT /note="C-terminal epitope involved in neutral

FT lipid binding or a transfer activity of

FT CETP"

PA (TCEL-) T CELL SCI INC.

PI Thomas LJ;

DR WPI; 1997-549731/50.

PT DNA plasmid-based vaccine encodes CETP B cell and helper T cell

PT epitope(s) - used for elevating high density lipoprotein levels, and

PT for treating cardiovascular disease

PS Disclosure; Pages 32-34; 67pp; English.

CC The present sequence represents the mature rabbit cholesteryl ester

CC transfer protein (CETP). CETPs mediate the transfer of cholesteryl esters

CC from high density lipoprotein (HDL) to very low density lipoprotein

CC (VLDL) and low density lipoprotein (LDL). An increased CETP activity

CC produces an atherogenic lipoprotein profile and induces atherosclerosis.

CC A 13 amino acid stretch in the rabbit CETP (Phe483 to Leu495), and also

CC possibly Asp480, are particularly important for neutral lipid binding and

CC transfer activity. This region has been shown to be immunogenic as a B

CC cell epitope of CETP, and a monoclonal antibody (TP2) directed at this

CC region has been shown to inhibit neutral lipid transfer. A second B cell

CC epitope is defined by Arg350 to Ile368. Antibodies to this second epitope

CC would allow the formation of immune complexes involving CETP, and promote

CC the removal of the complexed CETP. This peptide region was selected for

CC its potential antigenicity and high possibility for surface expression
 CC on native CERP. Sequences encoding these 2 epitopes can be used in a DNA
 CC plasmid-based vaccine which comprises sequences encoding at least 1 B
 CC cell epitope of CERP linked in frame with at least one segment encoding
 CC a broad range helper T cell epitope. The vaccines can be used to elevate
 CC the ratio of circulating HDL to circulating LDL, VLDL or total
 CC cholesterol in a human. It can also be used for decreasing the level of
 CC endogenous CERP activity in a human. The vaccine can be used to produce
 CC anti-CERP antibodies in vivo and for treating cardiovascular disease.
 CC
 SQ Sequence 496 AA;

Query Match 42.3%; Score 11; DB 18; Length 496;
 Best Local Similarity 100.0%; Pred. No. 0.021;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 HLVDPLQSLG 26
 |||||
 DB 486 hllvdflqsls 496

RESULT 38

AY02467
 ID AAY02467 standard; protein; 496 AA.
 XX
 AC AAY02467;

DT 14-JUL-1999 (first entry)

DE Rabbit cholesteryl ester transfer protein (CETP).

XX Vaccine; antibody; endogenous; cholesteryl ester transfer protein; CETP;

KW high-density lipoprotein-associated cholesterol; metabolism;

KM low-density lipoprotein-associated cholesterol; atherosclerotic lesion;

KW cholesterol; atherosclerosis; heart disease.

XX Oryctolagus sp.

PN W09920302-A1.

PD 29-APR-1999.

PE 20-OCT-1998; 98WO-US22145.

PR 20-OCT-1997; 97US-0954643.

XX (AVANT) IMMUNOTHERAPEUTICS INC.

PI Rittershaus CW, Thomas LJ;

DR WPI: 1999-302645/25.

XX N-PSDB; AAX35808.

PT Vaccine against cholesteryl ester transfer protein

PS Disclosure; Page 47-49; 61pp; English.

CC The specification describes a vaccine that promotes the production of
 CC antibodies that bind endogenous cholesteryl ester transfer protein
 CC (CETP). The vaccines (and equivalent plasmid-based vaccines) are
 CC used to increase the ratio of circulating high-density lipoprotein
 CC (HDL)-associated cholesterol to low-density lipoprotein (LDL)-associated
 CC cholesterol; to decrease the level of endogenous CETP activity in humans
 CC or other animals; to alter metabolism of LDL-associated cholesterol, for
 CC inhibiting development of atherosclerotic lesions; to lower circulating
 CC levels of LDL and total cholesterol; and to treat or prevent
 CC atherosclerosis (or more generally heart disease). The present sequence
 CC represents rabbit CETP.

SQ Sequence 496 AA;

Query Match 42.3%; Score 11; DB 20; Length 496;
 Best Local Similarity 100.0%; Pred. No. 0.021;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 HLVDPLQSLG 26
 |||||
 DB 486 hllvdflqsls 496

RESULT 39

AAM31066
 ID AAM31066 standard; Protein; 51 AA.
 XX
 AC AAM31066;

DT 17-OCT-2001 (first entry)

DE Peptide #5103 encoded by probe for measuring placental gene expression.

XX Probe; microarray; human; placenta; antenatal diagnosis;

KW genetic disorder.

XX Homo sapiens.

FN W0200157272-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00663.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA Penn SG, Hanzel DK, Chen W, Rank DR;

PI WPI: 2001-488897/53.

DR Human genome-derived single exon nucleic acid probes useful for

PT analyzing gene expression in human placenta -

XX Claim 27; SEQ ID No 31335; 654pp; English.

CC The present invention relates to single exon nucleic acid probes (SENP;

CC see A131315-A131346). The present sequence is a peptide encoded by one

CC such probe. The probes are useful for producing a microarray for

CC predicting, measuring and displaying gene expression in samples derived

CC from human placenta. The probes are useful for antenatal diagnosis of

CC human genetic disorders.

SQ Sequence 51 AA;

Query Match 26.9%; Score 7; DB 22; Length 51;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGFLLQ 8
 |||||
 DB 18 dgflilq 24

RESULT 40

AAU17886
 ID AAU17886 standard; Protein; 69 AA.
 XX
 AC AAU17886;

XX 07-NOV-2001 (first entry)
XX
DE Novel human respiratory antigen #202.
XX
KW Human; respiratory antigen; respiratory disorder; throat disorder;
lung disorder; nose disorder; lung cancer; gene therapy; cytostatic;
anti allergic; anti asthmatic; anti inflammatory; olfactory;
respiratory active.
XX
OS Homo sapiens.
XX
PN WO20015548-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01333.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-022557.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 23-AUG-2000; 2000US-0227182.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.

PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0246417.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.

PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM.
XX
DR WPI; 2001-476224/51.
DR N-PSDB; AAS28070.
XX
XX
PT Isolated polypeptide for treating, preventing and/or prognosing
PT disorders related to the respiratory system including respiratory
PT cancers and also for testing and detection e.g. diagnosis -
XX
PS Claim 11; SEQ ID No 504; 546bp; English.
XX
CC The present invention relates to the isolation of novel human
CC respiratory antigens, and cDNA (AA527869-AA528159) and genomic
CC sequences encoding for these polypeptides. The sequences of the
CC invention are useful for preventing, treating and/or prognosing
CC disorders related to the respiratory system including throat
CC disorders (e.g. vocal cord paralysis, tonsillitis, and laryngitis),
CC lung disorders e.g. pneumonia, allergic disorders e.g. asthma,
CC pleurisy, cystic fibrosis, emphysema, nose disorders and cancers of
CC the respiratory tissues e.g. lung cancer. The polynucleotide sequences
CC of the invention are useful in gene therapy and antisense therapy.
CC AAU1683-AAU17575 represent novel human respiratory antigens.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 69 AA;
XX
Query Match 26.9%; Score 7; DB 22; Length 69;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 LLDMDRG 12
Db 43 lldmdrg 49
XX
RESULT 41
ABG07716
ID ABG07716 standard; Protein: 186 AA.
XX
AC ABG07716;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #7707.
XX
KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX

PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS71903.
XX
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 38075; 103bp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 186 AA;
XX
Query Match 26.9%; Score 7; DB 22; Length 186;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DGFLLQ 8
Db 93 dgfllq 99
XX
RESULT 42
ABG17572
ID ABG17572 standard; Protein: 401 AA.
XX
AC ABG17572;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #17563.
XX
KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;
XX
XX MPI: 2001-639362/73.
DR N-PSDB: AAS81759.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX Claim 20; SEQ ID No 47931; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 401 AA:
SO

Query Match 26.9%; Score 7; DB 22; Length 401;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGFLLIQ 8
| | | | | | |
DB 308 dgfillq 314

RESULT 43
ABG07733
ID ABG07733 standard; Protein: 417 AA.
XX
XX ABG07733;
XX
XX 13-FEB-2002 (first entry)
DT
XX
XX Novel human diagnostic protein #7724.
DE
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
OS
XX
XX WO200175067-A2.
PN
XX
XX 11-OCT-2001.
PD
XX
XX 30-MAR-2001; 2001WO-US08631.
PF
XX
XX 31-MAR-2000; 2000US-0540217.
PR
XX
XX 23-AUG-2000; 2000US-0649167.
PA
XX
XX (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;
XX
XX MPI: 2001-639362/73.
DR N-PSDB: AAS71920.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX Claim 20; SEQ ID No 38092; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 417 AA:
SO

Query Match 26.9%; Score 7; DB 22; Length 417;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGFLLIQ 8
| | | | | | |
DB 329 dgfillq 335

RESULT 44
AAR54202
ID AAR54202 standard; Protein: 422 AA.
XX
XX AAR54202;
XX
XX 18-NOV-1994 (first entry)
DT
XX
XX snaf gene product involved in streptogramin biosynthetic pathway.
DE
XX
XX Antibiotic; streptogramin; snaf; snab; snac; biosynthesis; enzyme;
KW biosynthetic pathway; Streptomyces pristinaespiralis.
XX
XX Streptomyces pristinaespiralis.
OS
XX
XX FR2696189-A.
PN
XX
XX 01-APR-1994.
PD
XX
XX 25-SEP-1992; 92FR-0011441.
PF
XX
XX 25-SEP-1992; 92FR-0011441.
PR
XX
XX (RHON) RHONE-POULENC RORER SA.
PA
XX
XX Blanc V, Blanche F, Crouzet J, Jacques N, Lacroix P;
PI Thibaut D, Zagorec M;

XX WPI; 1994-128286/16.
 DR N-PSDB; AAO64202.
 XX
 PT DNA involved in streptogramin antibiotic biosynthesis - for
 PT prodn. or bio-conversion of streptogramin(s) or prodn. of
 PT streptogramin intermediates, derivs. or hybrid antibiotics
 XX
 PS Claim 21: Page 49-51; 83pp; French.
 XX
 CC The snaz gene product is involved in the biosynthesis of
 CC streptogramins, antibiotics active against Gram positive bacteria.
 CC The identification of the sequences encoding the enzymes involved
 CC in the biosynthetic pathway means that they can be isolated and
 CC manipulated. Mutant microorganisms in which a step in the
 CC streptogramin biosynthetic pathway is blocked can be cultured to
 CC produce streptogramin intermediates, which may later be converted
 CC to streptogramin derivatives. Recombinant cells may also be used
 CC for the bioconversion of streptogramins from one form to another or
 CC for the production of hybrid antibiotics.
 XX
 SQ Sequence 422 AA;

Query Match 26.9%; Score 7; DB 15; Length 422;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 11 FGFEHL 17
 |||||
 Db 143 fgfhl 149

RESULT 45
 ID ABG16251
 XX ABG16251 standard; Protein; 466 AA.
 AC
 XX ABG16251;
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #16242.
 XX
 KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KM food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 OS
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS80438.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 XX
 PS Claim 20; SEQ ID No 46610; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,

CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 XX
 SQ Sequence 466 AA;

Query Match 26.9%; Score 7; DB 22; Length 466;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2 DGFILIQ 8
 |||||
 Db 373 dgflllq 379

RESULT 46
 ID ABG15687
 XX ABG15687 standard; Protein; 478 AA.
 AC
 XX ABG15687;
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #15678.
 XX
 KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KM food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 OS
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS79874.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 XX
 PS Claim 20; SEQ ID No 46046; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

and gen mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG3037 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct-sequences](http://wipo.int/pub/published_pct-sequences).

Query Match	26.9%	Score 7:	DB 22:	Length 478:
Best Local Similarity	100.0%	Pred. No. 91:		
Matches 7, Conservative	0:	Mismatches	0:	Gaps 0:

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QY      2 DGFLLQ 8
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Db      151 dgfllq 157
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RESULT	47
AAG82878	
ID	AAG82878 standard; Protein: 1501 AA.

AC AAG82878;

DT 03-SEP-2001 (first entry)

S. epidermidis open reading frame protein sequence SEQ ID NO:2850.

Staphylococcus epidermidis SRI strain; infection; diagnosis; vaccination; endocarditis

05 Staphylococcus epidermidis.

PN WO200134809-A2

PD 17-MAY-2001.

PF 09-NOV-2000; 2000WO-US30782.
VY

PR 09-NOV-1999; 99US-0164258.
XX

PA (GLAA) GLAXO GROUP LTD.
XX

XX

DR N-PSDB; AAH53728.

PT Nucleic acids encoding polypeptides from *Staphylococcus epidermidis*,
nucA1, for use in the preparation of a vaccine

PS Claim 18: Page 742-743: 2188cc: English
XX

AA
CC
AAH52304 to AAH53970 represent nucleic acids (T) associated with polypeptides

(I) and (II) can have antibacterial activity and therefore can be used

S. epidermidis polypeptides (II) via the production of vectors

polypeptides. The polypeptides (II) (and/or nucleic acids) may then be

CC used to vaccinate subjects and to raise antibodies against the bacteria.
CC The polypeptides may also be used to assay for other inhibitors of their
CC activity and therefore identify compounds that may be used for the
CC treatment of *S. epidermidis* infections, e.g. endocarditis. AAH53971 to
CC AAH55090 represent specifically claimed *S. epidermidis* genomic DNA
CC polynucleotide sequences from the present invention. AAH55091 to
CC AAH55098 represent oligonucleotide sequences and primers which are used
CC in the exemplification of the present invention.
CC N.B. The present invention specifically claims all the polynucleotide
CC sequences given in the sequence listing of the present specification,
CC however the sequence listing only goes up to SEQ ID NO:4454 so even
CC though sequences are given in the disclosure for SEQ ID NO:4455 to 4472,
CC no sequences are present for SEQ ID NO:4455 to 4464.
XX
XX Sequence 1501 AA;

Query Match	26.9%	Score 7	DB 22	Length 1501
Best Local Similarity	100.0%	Pred. No.	2.5e+02	
Matches	7	Conservative	0	Mismatches 0
				Indels 0
				Gaps 0

QY	17	LLVDFLQ	23
Db	404	llvdfiq	410

RESULT 48
AAY27814
ID AAY27814 standard; Protein; 14 AA.

... AC AAY27814;

DT 30-JUL-1999 (first entry)

Human secreted protein encoded by gene No. 84

KW Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumor; tumor marker

KW immune system: asthma: lymphocytic disease: brain: heart: lymphoma: developmental abnormality; foetal deficiency; blood; allergy; renal; KW

cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus.
 KW

KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

OS Homo sapiens.

PN WO9924836-A1.
XX

PD 20-MAY-1999
XX

04 NOV 1990, 38NW-0523433.
XX

PR 07-NOV-1997; 97US-0064900.

PR	07-NOV-1997;	97US-0064911.
DE	07-NOV-1997	07US-0064911

PR	07-NOV-1997;	97US-0064983.
PR	07-NOV-1997.	97US-0064984

PR	07-NOV-1997;	97US-0064985.
PR	07-NOV-1997:	97US-0064987.

PR	17-NOV-1997;	97US-0066090.
----	--------------	---------------

PR 17-NOV-1997; 97US-0066095.

[illegible]

XX
XX
Cartier KC
Ehonor D
Enriquez CA
Fest C
Fitz J
Fitz J

PI Ruben SM, Shi Y, Soppet DR, Wei Y:
ayaw H, Lallieur DW, Moore PA, Ni J, Olsen HS, Rosen CA

XX	WP1: 1999-337740/28.
DR	N-PSDB; AAX85016.
XX	
PT	New human secreted proteins and coding sequences useful for treating
PT	disorders of the immune system and hyperproliferative disorders
XX	
PS	Disclosure; Page 119; 507pp; English.
XX	
CC	This sequence represents a secreted human protein encoded by the gene
CC	clone detailed in the descriptor line. The gene can be used to generate
CC	fusion proteins by linking to the gene to a human immunoglobulin Fc
CC	portion (e.g. AAX84924) for increasing the stability of the fused
CC	protein as compared to the human protein only.
CC	The invention relates to 125 novel genes and their fragments (nucleic
CC	acid sequences: AAX84933-X85057; amino acid sequences AAX27567-Y27933)
CC	which are useful for preventing, treating or ameliorating medical
CC	conditions e.g. by protein or gene therapy. Also, pathological
CC	conditions can be diagnosed by determining the amount of the new
CC	polypeptides in a sample or by determining the presence of mutations in
CC	the new polynucleotides. Specific uses are described for each of the 125
CC	polynucleotides, based on which tissues they are most highly expressed in
CC	(see AAX84933 for described uses).
XX	
SO	Sequence 14 AA:
QY	21 FLSLS 26
DB	8 fllslls 13
XX	
XX	RESULT 49
XX	AAB51836
ID	AAB51836 standard; Protein; 31 AA.
XX	
AC	AAB51836;
DT	16-FEB-2001 (first entry)
XX	
DE	Human secreted protein sequence encoded by gene 10 SEQ ID NO:69.
XX	
KW	Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;
KW	antiproliferative; cytostatic; cardiact; vasotrophic; cerebroprotective;
KW	neotropic; neuroprotective; antibacterial; virucide; fungicide;
KW	ophthalmological; vulnery; autoimmune disease; rheumatoid arthritis;
KW	hyperproliferative disorders; cancer; cardiovascular disorder;
KW	cardiac arrest; cerebrovascular disorder; nervous system disorder;
KW	Alzheimer's disease; ocular disorder; wound healing; skin aging.
XX	
OS	Homo sapiens.
PN	WO2000061626-A1.
XX	
PD	19-OCT-2000.
XX	
PF	06-APR-2000; 2000WO-US09066.
XX	
PR	09-APR-1999; 99US-0128698.
PR	20-JAN-2000; 2000US-0176926.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	(ROSE/) ROSEN C A.
PI	Rosen CA, Ruben SM, Komatsoulis G;
XX	
DR	WP1, 2000-619227/59.
DR	N-PSDB; AAC93468.
XX	

PT	New nucleic acid molecules encoding 49 human secreted proteins for
PT	diagnosing, preventing or ameliorating medical conditions and used for
PT	food additives or preservatives -
PS	Claim 11; Page 466; 516pp; English.
XX	
CC	Polynucleotide sequences AAC934479 - AAC93527 represent cDNA encoding
CC	human secreted proteins AAB51827 - AAB51875. Sequences AAB51876 -
CC	AAB51927 represent alternative polypeptides encoded by the genes, and
CC	amino acid sequences with which they share homology. The genes and
CC	proteins have activities dependent on the tissues and cells in which they
CC	are expressed. Examples of their activities include immunosuppressive;
CC	antiarthritic; antineumatic; antiproliferative; cytostatic; cardiant;
CC	vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial;
CC	virucide; fungicide; ophthalmological; and vulnerary. The secreted
CC	proteins, polynucleotides, antagonists and agonists may be useful in
CC	treating, preventing and/or diagnosing diseases and disorders such as
CC	autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC	disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC	e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC	angiogenesis, nervous system disorders e.g. Alzheimer's disease,
CC	infections caused by bacteria, viruses and fungi and ocular disorders
CC	e.g. corneal infection. The polypeptides can also be used to aid wound
CC	healing and epithelial cell proliferation, to prevent skin aging due to
CC	sunburn, to maintain organs before transplantation, for supporting cell
CC	culture of primary tissues, to regenerate tissues and in chemotaxis. The
CC	polypeptides can also be used as a food additive or preservative to
CC	increase or decrease storage capabilities, fat content, lipid, protein,
CC	carbohydrate, vitamins, minerals, cofactors and other nutritional
CC	components. Oligonucleotides AAC93470 - AAC93478 and peptide AAB51826 are
CC	used in the isolation and characterisation of the proteins and
CC	polynucleotides of the invention.
SQ	
XX	
SQ	Sequence 31 AA:
QY	17 LTVDFL 22
DB	9 LTVDFL 14
QY	23.1%; Score 6; DB 21; Length 31;
DB	Best Local Similarity 100.0%; Pred. No. 69;
Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 50	
AAB38991	
ID	AAB38991 standard; Protein; 42 AA.
AC	
AC	AAB38991;
DT	02-FEB-2001 (first entry)
DE	
XX	Human secreted protein #8.
XX	
XX	Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
XX	antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
KW	vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW	cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW	neurological disease; infection; human; secreted protein.
OS	
XX	Homo sapiens.
PN	WO200056880-A1.
XX	
PD	28-SEP-2000.
XX	
PF	16-MAR-2000; 2000MO-US06781.
XX	
XX	19-MAR-1999; 99US-0125363.
PR	08-DEC-1999; 99US-0169617.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM, Komatsoulis G;
PI WPI: 2000-602220/57.
DR N-PSDB; AAC59699.
XX
PT Nucleic acid molecules encoding human secreted proteins, used in
PT preventing, treating or ameliorating disorders such as Parkinson's and
PT Alzheimer's diseases, cancers and infections -
XX
PS Claim 11; Page 377; 422pp; English.
XX
CC Sequences AAB38971-B39020 represent the amino acid sequences of 50
CC human secreted proteins encoded by the genes AAC59679-C59728. The genes
CC and proteins are useful for preventing, ameliorating or treating medical
CC conditions, e.g. by protein or gene therapy. The genes are isolated from
CC a range of human tissues disclosed in the specification. The nucleic
CC acids, proteins, antibodies and (ant)agonists are useful in the
CC diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer, and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
XX
SQ Sequence 42 AA;

Query Match 23.1%; Score 6; DB 21; Length 42;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DGFLL 7
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Db 11 dgfl 11 16

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Job time: 124 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 19, 2002, 11:06:51 ; Search time 104.14 Seconds
(without alignments)
87.624 Million cell updates/sec

Title: US-09-943-334-1

Perfect score: 26

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	26	100.0	26	1	PCT-US99-139758-106
2	26	100.0	26	8	US-08-432-483-1
3	26	100.0	26	8	US-08-432-483A-1
4	26	100.0	26	11	US-08-785-997-29
5	26	100.0	26	11	US-08-788-882-29
6	26	100.0	26	13	US-08-934-367-29
7	26	100.0	26	13	US-08-945-289-1

8	26	100.0	26	17	US-09-386-591-29	Sequence 29, Appl
9	26	100.0	26	17	US-09-387-340-29	Sequence 29, Appl
10	26	100.0	26	21	US-09-701-588-106	Sequence 106, App
11	26	100.0	26	23	US-09-943-334-1	Sequence 1, Appl1
12	26	100.0	26	23	US-09-943-548-1	Sequence 1, Appl1
13	26	100.0	26	23	PCT-US99-139758-110	Sequence 110, App
14	26	100.0	46	1	PCT-US99-139758-111	Sequence 111, App
15	26	100.0	46	21	US-09-701-588-110	Sequence 110, App
16	26	100.0	46	21	US-09-701-588-111	Sequence 111, App
17	26	100.0	46	21	US-09-701-588-111	Sequence 111, App
18	26	100.0	470	22	US-09-518-598-14	Sequence 111, App
19	26	100.0	476	10	US-08-640-713-4	Sequence 14, Appl
20	26	100.0	476	11	US-08-640-713-4	Sequence 14, Appl
21	26	100.0	476	11	US-08-785-997-28	Sequence 28, Appl
22	26	100.0	476	11	US-08-788-882-28	Sequence 28, Appl
23	26	100.0	476	12	US-08-802-967A-4	Sequence 28, Appl
24	26	100.0	476	13	US-08-834-367-28	Sequence 4, Appl1
25	26	100.0	476	13	US-08-945-289-4	Sequence 4, Appl1
26	26	100.0	476	13	US-08-954-643-1	Sequence 1, Appl1
27	26	100.0	476	17	US-09-386-591-28	Sequence 28, Appl
28	26	100.0	476	17	US-09-387-340-28	Sequence 28, Appl
29	26	100.0	476	19	US-09-529-762-1	Sequence 1, Appl1
30	26	100.0	476	23	US-09-943-334-4	Sequence 4, Appl1
31	26	100.0	493	11	US-08-785-997-30	Sequence 30, Appl
32	26	100.0	493	11	US-08-788-882-30	Sequence 30, Appl
33	26	100.0	493	13	US-08-934-367-30	Sequence 30, Appl
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35	26	100.0	493	14	US-09-054-272-48	Sequence 10, Appl
36	26	100.0	493	17	US-09-386-591-30	Sequence 30, Appl
37	26	100.0	493	17	US-09-387-340-30	Sequence 30, Appl
38	26	100.0	493	22	US-09-802-640-12	Sequence 12, Appl
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41	22	84.6	22	11	US-08-788-882-10	Sequence 10, Appl
42	22	84.6	22	11	US-08-788-882-34	Sequence 10, Appl
43	22	84.6	22	13	US-08-934-367-10	Sequence 10, Appl
44	22	84.6	22	13	US-08-934-367-34	Sequence 10, Appl
45	22	84.6	22	17	US-09-386-591-10	Sequence 10, Appl
46	22	84.6	22	17	US-09-386-591-34	Sequence 10, Appl
47	22	84.6	22	17	US-09-387-340-10	Sequence 10, Appl
48	22	84.6	22	17	US-09-387-340-34	Sequence 10, Appl
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52	16	61.5	16	21	US-09-701-588-107	Sequence 107, App
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55	16	61.5	31	13	US-08-945-289-2	Sequence 2, Appl1
56	16	61.5	31	13	US-08-954-643-7	Sequence 7, Appl1
57	16	61.5	31	19	US-09-529-762-7	Sequence 7, Appl1
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59	16	61.5	31	23	US-09-943-334-2	Sequence 2, Appl1
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61	16	61.5	35	21	US-09-701-588-112	Sequence 112, App
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70	16	61.5	50	23	US-09-943-548-8	Sequence 8, Appl1
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72	11	42.3	16	1	PCT-US99-139758-108	Sequence 108, App
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75	11	42.3	22	11	US-08-788-882-4	Sequence 4, Appl1

ALIGNMENTS

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; Sequence 106, Application PC/RTUS9913975B
; GENERAL INFORMATION:
; APPLICANT: UNITED BIOMEDICAL INC., FT AL.
; TITLE OF INVENTION: ARTIFICIAL T HELPER CELL
; TITLE OF INVENTION: EPITOPES AS IMMUNE STIMULATORS FOR SYNTHETIC
; NUMBER OF SEQUENCES: 151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US99/13975B
; FILING DATE: 21-JUNE-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,412
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4158PCT1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US99-13975B-106
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Query Match 100.0%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RDGFLLLQMDGFPPEHLVDPLQSL 26
Db 1 RDGFLLLQMDGFPPEHLVDPLQSL 26
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RESULT 2
US-08-432-483-1
; Sequence 1, Application US/08432483
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
; TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: Ten South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-7407
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
```

```
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/432,483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Leon R. Yankwich
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: 95,179(TCS-95179)
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL:
; ANTI-SENSE:
; FEATURE:
; NAME/KEY: Carboxyl terminal 26 amino acids of
; NAME/KEY: human CETP
; LOCATION:
; PUBLICATION INFORMATION:
; AUTHORS: Drayna, Dennis, et al.
; TITLE: Cloning and sequencing of human
; JOURNAL: Nature
; VOLUME: 327
; ISSUE:
; PAGES: 632-634
; DATE: 18-JUN-1987
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 26
US-08-432-483-1
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Query Match 100.0%; Score 26; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RDGFLLLQMDGFPPEHLVDPLQSL 26
Db 1 RDGFLLLQMDGFPPEHLVDPLQSL 26
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RESULT 3
US-08-432-483A-1
; Sequence 1, Application US/08432483A
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
; TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: Ten South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-7407
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/432,483A
; FILING DATE: 1-May-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Leon R. Yankwich
```

REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: 95,179(TCS-95179)
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL:
ANTI-SENSE:
FEATURE:
NAME/KEY: Carboxyl terminal 26 amino acids of
NAME/KEY: human CETP
LOCATION:
PUBLICATION INFORMATION:
AUTHORS: Drayna, Dennis, et al.
TITLE: Cloning and sequencing of human
TITLE: cholesterol ester transfer CDNA
JOURNAL: Nature
VOLUME: 327
ISSUE:
PAGES: 632-634
DATE: 18-JUN-1987
RELEVANT RESIDUES IN SEQ ID NO: 1:FROM 1 TO 26
US-08-432-483A-1

Query Match 100.0%; Score 26; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RDGFLLQMDGFGPPEHLVDPLQSL 26
DB 1 RDGFLLQMDGFGPPEHLVDPLQSL 26

RESULT 4
US-08-785-997-29
Sequence 29, Application US/08785997
GENERAL INFORMATION:
APPLICANT: Needleman, Philip
APPLICANT: Glenn, Kevin
TITLE OF INVENTION: An Immunological Process for Increasing
TITLE OF INVENTION: the HDL Cholesterol Concentration
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,997
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gamsen Ph.D., Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-101.0 6018/68346
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1500
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
PUBLICATION INFORMATION:
AUTHORS: Swenson, T. L.
AUTHORS: et al.,
JOURNAL: J. Biol. Chem.
VOLUME: 264
PAGES: 14318-14326
DATE: 1989
US-08-785-997-29

Query Match 100.0%; Score 26; DB 11; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RDGFLLQMDGFGPPEHLVDPLQSL 26
DB 1 RDGFLLQMDGFGPPEHLVDPLQSL 26

RESULT 5
US-08-788-882-29
Sequence 29, Application US/08788882
GENERAL INFORMATION:
APPLICANT: Needleman, Philip
APPLICANT: Glenn, Kevin
APPLICANT: Krul, Elaine
APPLICANT: Gamsen, Edward P.
TITLE OF INVENTION: An Immunological Process and Constructs
TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,882
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gamsen, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1500
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PUBLICATION INFORMATION:
AUTHORS: Swenson, T. L.
AUTHORS: et al.,
JOURNAL: J. Biol. Chem.
VOLUME: 264
PAGES: 14318-14326
DATE: 1989
US-08-788-882-29

Query Match 100.0%; Score 26; DB 11; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLQMDGFPEPHLVDFLOSLS 26
|||||
Db 1 RDGFLLQMDGFPEPHLVDFLOSLS 26

RESULT 6
US-08-934-367-29

; Sequence 29, Application US/08934367
; GENERAL INFORMATION:
; APPLICANT: Needleman, Philip
; TITLE OF INVENTION: An Immunological Process and Constructs
; TITLE OF INVENTION: for increasing the HDL Cholesterol Concentration by DNA
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 120 South Riverside Plaza, 22nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,367
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamsen Ph.D., Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)655-1500
; TELEFAX: (312)655-1501
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PUBLICATION INFORMATION:
; AUTHORS: Swenson, T. L.
; JOURNAL: et al.,
; VOLUME: 264
; PAGES: 14318-14326
; DATE: 1989
; US-08-934-367-29

Query Match 100.0%; Score 26; DB 13; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLQMDGFPEPHLVDFLOSLS 26
|||||
Db 1 RDGFLLQMDGFPEPHLVDFLOSLS 26

RESULT 7
US-08-945-289-1
; Sequence 1, Application US/08945289
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles, W.
; APPLICANT: Thomas, Lawrence J.
;

; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
; TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/945,289
; FILING DATE: October 17, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/432,483
; FILING DATE: May 1, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Leon R. Yankwich
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: TCS-411.1P US

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL:
; ANTI-SENSE:
; FEATURE:
; NAME/KEY: Carboxyl terminal 26 amino
; NAME/KEY: acids of human CETP
; LOCATION:
; PUBLICATION INFORMATION:
; AUTHORS: Drayna, Dennis, et al.
; TITLE: Cloning and sequencing of human cholesterol ester transfer cDNA
; JOURNAL: Nature
; VOLUME: 327
; ISSUE:
; PAGES: 632-634
; DATE: 18-JUN-1987
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 26
; US-08-945-289-1

Query Match 100.0%; Score 26; DB 13; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLQMDGFPEPHLVDFLOSLS 26
|||||
Db 1 RDGFLLQMDGFPEPHLVDFLOSLS 26

RESULT 8
US-09-386-591-29
; Sequence 29, Application US/09386591
; GENERAL INFORMATION:
; APPLICANT: Needleman, Philip
; APPLICANT: Glenn, Kevin
; TITLE OF INVENTION: An Immunological Process and Constructs
; TITLE OF INVENTION: for increasing the HDL Cholesterol Concentration by DNA
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 120 South Riverside Plaza, 22nd Floor
; CITY: Chicago

STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: #1.0, Version #1.30
APPLICATION NUMBER: US/09/386,591
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gamson Ph.D., Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1500
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PUBLICATION INFORMATION:
AUTHORS: Swenson, T. L.
JOURNAL: J. Biol. Chem.
VOLUME: 264
PAGES: 14318-14326
DATE: 1989
US-09-386-591-29

Query Match 100.0%; Score 26; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDFGFPEHLLVDFLOSL 26
DB 1 RDGFLLLQMDFGFPEHLLVDFLOSL 26

RESULT 9
US-09-387-340-29
Sequence 29, Application US/09387340
GENERAL INFORMATION:
APPLICANT: Needleman, Phillip
APPLICANT: Glenn, Kevin
APPLICANT: Krul, Elaine
APPLICANT: Gamson, Edward P.
TITLE OF INVENTION: An Immunological Process and Constructs
TITLE OF INVENTION: for increasing the HDL Cholesterol Concentration
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,340
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1500
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PUBLICATION INFORMATION:
AUTHORS: Swenson, T. L.
JOURNAL: J. Biol. Chem.
VOLUME: 264
PAGES: 14318-14326
DATE: 1989
US-09-387-340-29

Query Match 100.0%; Score 26; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDFGFPEHLLVDFLOSL 26
DB 1 RDGFLLLQMDFGFPEHLLVDFLOSL 26

RESULT 10
US-09-701-588-106
Sequence 106, Application US/09701588
GENERAL INFORMATION:
APPLICANT: Wang, Chang YI
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Flinnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/701,588
FILING DATE: 29-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-1580S1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6649
INFORMATION FOR SEQ ID NO: 106
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 106

US-09-701-588-106

Query Match	100.0%;	Score 26;	DB 21;	Length 26;
Best Local Similarity	100.0%;	Pred. No. 1.7e-16;		
Matches	26;	Conservative	0;	Mismatches 0;
				Indels

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QY      1 RDGFEILLQMDFGFEPPEHLLVDFLQSLS    26  
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DB      1 RDGFELLQMDFEGFPPEHLLVDFLQSLS    26
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RESULT 11
US-09-943-334-1
; Sequence 1, Application US/09943334
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; APPLICANT: Thomas, Lawrence J.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVITY
; FILE REFERENCE: TCS-411.1P US-1: TCS-411.1P US-2
; CURRENT APPLICATION NUMBER: US/09/943,334
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 08/432,483
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: PCT/US96/06147
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/945,289
; PRIOR FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: C - terminal 26 amino acids of Human CETP
; US-09-943-334-1

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Query Match	100.0%	Score 26;	DB 23;	length 26;					
Best Local Similarity	100.0%	Pred. No. 1.7e-16;							
Matches	26;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;

QY	1	RDGFLLLOMDFGFPEHLLVDFLOSLTS	26
Db	1	RDGFLLLQMDFGFPHEHLLVDFLOSLTS	26

```

RESULT 12
US-09-943-548-1
; Sequence 1, Application US/09943548
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; APPLICANT: Thomas, Lawrence J.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVITY
; FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
; CURRENT APPLICATION NUMBER: US/09/943,548
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 08/432,483
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: PCT/US96/06147
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/945,289
; PRIOR FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: C - terminal 26 amino acids of Human CETP
US-09-943-548-1

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Query Match	100.0%;	Score 26;	DB 23;	length 26;
Best Local Similarity	100.0%;	Pred. NO. 1.7e-16;		
Matches 26;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

[illegible]

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Query Match	100.0%;	Score 26;	DB 1;	Length 46;
Best Local Similarity	100.0%;	Pred. No. 2.6e-16;		
Matches	26;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0

QY	1	RDGFLLLQMDGEGPEHLLVDFLOSL	26
Db	21	RDGFLLLQMDGEGPEHLLVDFLOSL	46

RESULT 14
PCT-US99-13975B-111
; Sequence 111, Application PC/TUS9913975B
; GENERAL INFORMATION:
; APPLICANT: UNITED BIOMEDICAL INC., ET AL.
; TITLE OF INVENTION: ARTIFICIAL T HELPER CELL
; TITLE OF INVENTION: EPITOPE AS IMMUNE STIMULATORS FOR SYNTHETIC
; TITLE OF INVENTION: PEPTIDE IMMUNOGENS
; NUMBER OF SEQUENCES: 151

```

CORRESPONDENCE ADDRESS:
ADDRESS: Morgan & Flinnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US99/13975B
FILING DATE: 21-JUNE-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,412
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4158PCL
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-751-6849
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US99-13975B-111

Query Match      100.0%; Score 26; DB 1; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDFGFPEHLVDFLQSL 26
DB 21 RDGFLLLQMDFGFPEHLVDFLQSL 46

RESULT 15
US-09-701-588-110
Sequence 110, Application US/09701588
GENERAL INFORMATION:
APPLICANT: Wang, Chang YI
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESS: Morgan & Flinnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/701,588
FILING DATE: 29-NOV-2000
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
```

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REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-1580S1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-751-6849
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 110
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 110
US-09-701-588-110

Query Match      100.0%; Score 26; DB 21; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDFGFPEHLVDFLQSL 26
DB 21 RDGFLLLQMDFGFPEHLVDFLQSL 46

RESULT 16
US-09-701-588-111
Sequence 111, Application US/09701588
GENERAL INFORMATION:
APPLICANT: Wang, Chang YI
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESS: Morgan & Flinnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/701,588
FILING DATE: 29-NOV-2000
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-1580S1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-751-6849
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 111
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 111
US-09-701-588-111

Query Match      100.0%; Score 26; DB 21; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDFGFPEHLVDFLQSL 26
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Db 21 RDGFLLLQMDGFPPEHLVDFLQSL 46
|||||

RESULT 17
US-09-518-598-14

; Sequence 14, Application US/09518598

; GENERAL INFORMATION:

; APPLICANT: Beamer, Lesa J.

; APPLICANT: Carroll, Stephen F.

; TITLE OF INVENTION: BACTERICIDAL/PERMEABILITY-INCREASING PROTEIN:

; TITLE OF INVENTION: CRYSTALLIZATION, X-RAY DIFFRACTION, THREE-DIMENSIONAL

; TITLE OF INVENTION: STRUCTURE DETERMINATION, RATIONAL DRUG DESIGN AND

; FILE REFERENCE: 1103/11034US03

; CURRENT APPLICATION NUMBER: US/09/518.598

; EARLIER FILING DATE: 2000-03-03

; EARLIER FILING DATE: 1997-06-20

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 14

; LENGTH: 470

; TYPE: PRT

; ORGANISM: Human

; FEATURE:

; OTHER INFORMATION: cholesterol ester transfer protein (CETP) (Figure

; US-09-518-598-14

Query Match 100.0%; Score 26; DB 19; Length 470;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RDGFLLLQMDGFPPEHLVDFLQSL 26
|||||

Db 445 RDGFLLLQMDGFPPEHLVDFLQSL 470

RESULT 18
US-09-872-128-14

; Sequence 14, Application US/09872128

; GENERAL INFORMATION:

; APPLICANT: Beamer, Lesa J.

; APPLICANT: Carroll, Stephen F.

; TITLE OF INVENTION: BACTERICIDAL/PERMEABILITY-INCREASING PROTEIN:

; TITLE OF INVENTION: CRYSTALLIZATION, X-RAY DIFFRACTION, THREE-DIMENSIONAL

; TITLE OF INVENTION: STRUCTURE DETERMINATION, RATIONAL DRUG DESIGN AND

; FILE REFERENCE: 1103/11034US03

; CURRENT APPLICATION NUMBER: US/09/872.128

; CURRENT FILING DATE: 2001-05-31

; PRIOR APPLICATION NUMBER: US/09/518.598

; PRIOR FILING DATE: 2000-03-03

; PRIOR APPLICATION NUMBER: 08/879,565

; PRIOR FILING DATE: 1997-06-20

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 14

; LENGTH: 470

; TYPE: PRT

; ORGANISM: Human

; FEATURE:

; OTHER INFORMATION: cholesterol ester transfer protein (CETP) (Figure

; US-09-872-128-14

Query Match 100.0%; Score 26; DB 22; Length 470;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RDGFLLLQMDGFPPEHLVDFLQSL 26
|||||
Db 445 RDGFLLLQMDGFPPEHLVDFLQSL 470

RESULT 19
US-08-640-713-4

; Sequence 4, Application US/08640713

; GENERAL INFORMATION:

; APPLICANT: Thomas, Lawrence J.

; TITLE OF INVENTION: PLASMIID-BASED VACCINE FOR TREATING

; TITLE OF INVENTION: ATHEROSCLEROSIS

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Banner & Allogreth, Ltd.

; STREET: 75 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Wordperfect 6.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/640.713

; FILING DATE: May 1, 1996

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Leon R. Yankwich

; REGISTRATION NUMBER: 30,237

; REFERENCE/DOCKET NUMBER: 95,1102(TCS-205-999)

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 476 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHEetical:

; ANTI-SENSE:

; FEATURE:

; NAME/KEY: Amino acid sequence of mature human CETP

; LOCATION:

; PUBLICATION INFORMATION:

; AUTHORS: Dayna, Dennis, et al.

; TITLE: Cloning and sequencing of human

; TITLE: cholesterol ester transfer cDNA

; JOURNAL: Nature

; VOLUME: 327

; ISSUE: 632-634

; PAGES: 632-634

; DATE: 18-JUN-1987

; RELEVANT RESIDUES IN SEQ ID NO: 4: FROM 1 TO

; RELEVANT RESIDUES IN SEQ ID NO: 476

; US-08-640-713-4

Query Match 100.0%; Score 26; DB 10; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RDGFLLLQMDGFPPEHLVDFLQSL 26
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Db 451 RDGFLLLQMDGFPPEHLVDFLQSL 476

RESULT 20

US-08-785-997-28

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; Sequence 28, Application US/08785997
; GENERAL INFORMATION:
; APPLICANT: Needleman, Philip
; APPLICANT: Glenn, Kevin
; TITLE OF INVENTION: An Immunological Process for Increasing
; TITLE OF INVENTION: The HDL Cholesterol Concentration
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 120 South Riverside Plaza, 22nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/785,997
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson Ph.D., Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: MON-101.0 6018/68346
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)655-1500
; TELEFAX: (312)655-1501
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PUBLICATION INFORMATION:
; AUTHORS: Drayna, Dennis
; AUTHORS: Jarnagin, Alisha Stephens
; AUTHORS: McLean, John
; AUTHORS: Henzel, William
; AUTHORS: Kohr, William
; AUTHORS: Fielding, Christopher
; AUTHORS: Lawn, Richard
; TITLE: Cloning and sequencing of human cholesterol
; TITLE: ester transfer protein cDNA
; JOURNAL: Nature
; VOLUME: 327
; PAGES: 632-634
; DATE: June 18-1987
;
US-08-785-997-28

Query Match          100.0%; Score 26; DB 11; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RDGFLLLQMDFGPEHLVDFLOSLS 26
DB      451 RDGFLLLQMDFGPEHLVDFLOSLS 476

RESULT 21
; Sequence 28, Application US/08788882
; GENERAL INFORMATION:
; APPLICANT: Needleman, Philip
; APPLICANT: Glenn, Kevin
; APPLICANT: Krul, Elaine
; APPLICANT: Gamson, Edward P.
; TITLE OF INVENTION: An Immunological Process and Constructs
; TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration
```

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; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 120 South Riverside Plaza, 22nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,882
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)655-1500
; TELEFAX: (312)655-1501
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PUBLICATION INFORMATION:
; AUTHORS: Drayna, Dennis
; AUTHORS: Jarnagin, Alisha Stephens
; AUTHORS: McLean, John
; AUTHORS: Henzel, William
; AUTHORS: Kohr, William
; AUTHORS: Fielding, Christopher
; AUTHORS: Lawn, Richard
; TITLE: Cloning and sequencing of human cholesterol
; TITLE: ester transfer protein cDNA
; JOURNAL: Nature
; VOLUME: 327
; PAGES: 632-634
; DATE: June 18-1987
;
US-08-788-882-28

Query Match          100.0%; Score 26; DB 11; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RDGFLLLQMDFGPEHLVDFLOSLS 26
DB      451 RDGFLLLQMDFGPEHLVDFLOSLS 476

RESULT 22
; Sequence 4, Application US/08802967A
; GENERAL INFORMATION:
; APPLICANT: Thomas, Lawrence J.
; TITLE OF INVENTION: PLASMID-BASED VACCINE FOR
; TITLE OF INVENTION: TREATING ATHEROSCLEROSIS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
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: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Word 7
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/802,967A
: FILING DATE: 21-FEB-1997
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/640,713
: FILING DATE: 01-MAY-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Leon R. Yankwich
: REGISTRATION NUMBER: 30,237
: REFERENCE/DOCKET NUMBER: TCS 414.1 US
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 476 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: HYPOTHEICAL:
: ANTI-SENSE:
: FEATURE:
: NAME/KEY: Amino acid sequence of mature human
: NAME/KEY: CETP
: LOCATION:
: PUBLICATION INFORMATION:
: AUTHORS: Drayna, Dennis, et al.
: TITLE: Cloning and sequencing of human
: TITLE: cholesterol ester transfer CDNA
: JOURNAL: Nature
: VOLUME: 327
: ISSUE:
: PAGES: 632 - 634
: DATE: 18-JUN-1987
: RELEVANT RESIDUES IN SEQ ID NO: 4: FROM 1 TO 476
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: US-08-802-967A-4
:
: Query Match 100.0%; Score 26; DB 12; Length 476;
: Best Local Similarity 100.0%; Pred. NO. 1.7e-15;
: Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY 1 RDGFLLLQMDFGFPEHLVDFLQSL 26
: DB 451 RDGFLLLQMDFGFPEHLVDFLQSL 476
:
: RESULT 23
: US-08-934-367-28
: Sequence 28, Application US/08934367
: GENERAL INFORMATION:
: APPLICANT: Needleman, Philip
: APPLICANT: Glenn, Kevin
: TITLE OF INVENTION: An Immunological Process and Constructs
: TITLE OF INVENTION: for increasing the HDL Cholesterol Concentration by DNA
: NUMBER OF SEQUENCES: 52
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Welsh & Katz, Ltd.
: STREET: 120 South Riverside Plaza, 22nd Floor
: CITY: Chicago
: STATE: IL
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/934,367

```

```

: FILING DATE:
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Gamsen Ph.D., Edward P.
: REGISTRATION NUMBER: 29,381
: REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312)655-1500
: TELEFAX: (312)655-1501
: INFORMATION FOR SEQ ID NO: 28:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 476 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: PUBLICATION INFORMATION:
: AUTHORS: Drayna, Dennis
: AUTHORS: Jarnagin, Alisha Stephens
: AUTHORS: McLean, John
: AUTHORS: Henzel, William
: AUTHORS: Kohr, William
: AUTHORS: Fielding, Christopher
: TITLE: Cloning and sequencing of human cholesterolyl
: TITLE: ester transfer protein CDNA
: JOURNAL: Nature
: VOLUME: 327
: PAGES: 632-634
: DATE: June 18-1987
:
: US-08-934-367-28
:
: Query Match 100.0%; Score 26; DB 13; Length 476;
: Best Local Similarity 100.0%; Pred. NO. 1.7e-15;
: Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY 1 RDGFLLLQMDFGFPEHLVDFLQSL 26
: DB 451 RDGFLLLQMDFGFPEHLVDFLQSL 476
:
: RESULT 24
: US-08-945-289-4
: Sequence 4, Application US/08945289
: GENERAL INFORMATION:
: APPLICANT: Rittershaus, Charles, W.
: APPLICANT: Thomas, Lawrence J.
: TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
: TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Yankwich & Associates
: STREET: 130 Bishop Allen Drive
: CITY: Cambridge
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02139
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: Windows 95
: SOFTWARE: Word 97
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/945,289
: FILING DATE: October 17, 1997
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/432,483
: FILING DATE: May 1, 1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Leon R. Yankwich
: REGISTRATION NUMBER: 30,237

```

REFERENCE/DOCKET NUMBER: TCS-411.1P US
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL:
FEATURE:
ANTI-SENSE:
NAME/KEY: Amino acid sequence of mature
NAME/KEY: human CETP
LOCATION:
PUBLICATION INFORMATION:
AUTHORS: Drayna, Dennis, et al.
TITLE: Cloning and sequencing of human cholesterol ester transfer CDNA
JOURNAL: Nature
VOLUME: 327
ISSUE:
PAGES: 632-634
DATE: 18-JUN-1987
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 476
US-08-945-289-4

Query Match 100.0%; Score 26; DB 13; Length: 476;
Best Local Similarity 100.0%; Pred. No. 1,7e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGFLLLQMDFGFPEHLVDFLQSL 26
Db 451 RDGFLLLQMDFGFPEHLVDFLQSL 476

RESULT 25
US-08-954-643-1
Sequence 1, Application US/08954643
GENERAL INFORMATION:
APPLICANT: Rittershaus, Charles, W.
TITLE OF INVENTION: XENOGENEIC CHOLESTERYL ESTER
TITLE OF INVENTION: TRANSFER PROTEIN (CETP) FOR MODULATION OF CETP ACTIVITY
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: TCS-420.0 US
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:

NAME/KEY: amino acid sequence of mature human CETP
LOCATION:
PUBLICATION INFORMATION:
AUTHORS: Drayna, Dennis, et al.
TITLE: Cloning and sequencing of human cholesterol
TITLE: ester transfer CDNA
JOURNAL: Nature
VOLUME: 327
PAGES: 632-634
DATE: 18-JUN-1987
RELEVANT RESIDUES IN SEQ ID NO: 1: 1 to 476
US-08-954-643-1

Query Match 100.0%; Score 26; DB 13; Length 476;
Best Local Similarity 100.0%; Pred. No. 1,7e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGFLLLQMDFGFPEHLVDFLQSL 26
Db 451 RDGFLLLQMDFGFPEHLVDFLQSL 476

RESULT 26
US-09-386-591-28
Sequence 28, Application US/09386591
GENERAL INFORMATION:
APPLICANT: Needleman, Phillip
TITLE OF INVENTION: An Immunological Process and Constructs
TITLE OF INVENTION: for increasing the HDL Cholesterol Concentration by DNA
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/386,591
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gamson Ph.D., Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1501
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PUBLICATION INFORMATION:
AUTHORS: Drayna, Dennis
AUTHORS: Jarnagin, Alisha Stephens
AUTHORS: McLean, John
AUTHORS: Henzel, William
AUTHORS: Kohr, William
AUTHORS: Fielding, Christopher
AUTHORS: Lawn, Richard
TITLE: Cloning and sequencing of human cholesterol
TITLE: ester transfer protein CDNA

JOURNAL: Nature
VOLUME: 327
PAGES: 632-634
DATE: June 18-1987
US-09-386-591-28

Query Match 100.0%; Score 26; DB 17; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDFGFPPEHLVDFLQSL 26
DB 451 RDGFLLLQMDFGFPPEHLVDFLQSL 476

RESULT 27
US-09-387-340-28
Sequence 28, Application US/09387340
GENERAL INFORMATION:
APPLICANT: Needleman, Philip
APPLICANT: Glenn, Kevin
APPLICANT: Krul, Elaine
TITLE OF INVENTION: An Immunological Process and Constructs
TITLE OF INVENTION: For Increasing the HDL Cholesterol Concentration
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Melsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/387,340
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1500
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PUBLICATION INFORMATION:
AUTHORS: Drayna, Dennis
AUTHORS: Jarnagin, Alisha Stephens
AUTHORS: McLean, John
AUTHORS: Henzel, William
AUTHORS: Kohr, William
AUTHORS: Fielding, Christopher
AUTHORS: Lawn, Richard
TITLE: Cloning and sequencing of human cholesteryl
TITLE: ester transfer protein CDNA
JOURNAL: Nature
VOLUME: 327
PAGES: 632-634
DATE: June 18-1987
US-09-387-340-28

Query Match 100.0%; Score 26; DB 17; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDFGFPPEHLVDFLQSL 26
DB 451 RDGFLLLQMDFGFPPEHLVDFLQSL 476

RESULT 28
US-09-529-762-1
Sequence 1, Application US/09529762
GENERAL INFORMATION:
APPLICANT: AVANT Immunotherapeutics, Inc.
APPLICANT: Rittershaus, Charles
APPLICANT: Thomas, Lawrence
TITLE OF INVENTION: Xenogeneic Cholesteryl Ester Transfer Protein (CETP) for
TITLE OF INVENTION: Modulation of CETP Activity
FILE REFERENCE: sequence listing for TCS-420.1 PCT
CURRENT APPLICATION NUMBER: US/09/529,762
CURRENT FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: USSN 08/954,643
PRIOR FILING DATE: 1997-10-20
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 476
TYPE: PRT
ORGANISM: Homo sapiens
US-09-529-762-1

Query Match 100.0%; Score 26; DB 19; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDFGFPPEHLVDFLQSL 26
DB 451 RDGFLLLQMDFGFPPEHLVDFLQSL 476

RESULT 29
US-09-943-334-4
Sequence 4, Application US/09943334
GENERAL INFORMATION:
APPLICANT: Rittershaus, Charles W.
APPLICANT: Thomas, Lawrence J.
TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVI
FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
CURRENT APPLICATION NUMBER: US/09/943,334
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: 08/432,483
PRIOR FILING DATE: 1995-05-01
PRIOR APPLICATION NUMBER: PCT/US96/06147
PRIOR FILING DATE: 1996-05-01
PRIOR APPLICATION NUMBER: 08/945,289
PRIOR FILING DATE: 1997-10-17
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 476
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-943-334-4

Query Match 100.0%; Score 26; DB 23; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.7e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDFGFPPEHLVDFLQSL 26
DB 451 RDGFLLLQMDFGFPPEHLVDFLQSL 476

Db 451 RDGFLLLQMDGFGPPEHLVDFLQSL 476

RESULT 30
US-09-943-548-4
; Sequence 4, Application US/09943548
; GENERAL INFORMATION:
; APPLICANT: Riteghaus, Charles W.
; APPLICANT: Thomas, Lawrence J.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVITY
; FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
; CURRENT APPLICATION NUMBER: US/09/943,548
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 08/432,483
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: PCT/US96/06147
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/945,289
; PRIOR FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-943-548-4

Query Match 100.0%; Score 26; DB 23; Length 476;
Best Local Similarity 100.0%; Pred. NO. 1.7e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGFLLLQMDGFGPPEHLVDFLQSL 26
Db 451 RDGFLLLQMDGFGPPEHLVDFLQSL 476

RESULT 31
US-08-785-997-30
; Sequence 30, Application US/08785997
; GENERAL INFORMATION:
; APPLICANT: Needleman, Phillip
; APPLICANT: Glenn, Kevin
; TITLE OF INVENTION: An Immunological Process for Increasing
; TITLE OF INVENTION: the HDL Cholesterol Concentration
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 120 South Riverside Plaza, 22nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/785,997
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamsen Ph.D., Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: MON-101.0 6018/68346
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)655-1500
; TELEFAX: (312)655-1501
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 493 amino acids
; TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PUBLICATION INFORMATION:
AUTHORS: Pape, Michael E.
AUTHORS: Rehberg, Edward F.
AUTHORS: Marotli, Keith R.
AUTHORS: Melchior, George W.
TITLE: Molecular Cloning, Sequence, and Expression
TITLE: of Cynomolgus Monkey Cholesteryl Ester Transfer
PROTEIN
JOURNAL: Arteriosclerosis and Thrombosis
VOLUME: 11
ISSUE: 6
PAGES: 1759-1771
DATE: Nov/Dec-1991
US-08-785-997-30

Query Match 100.0%; Score 26; DB 11; Length 493;
Best Local Similarity 100.0%; Pred. NO. 1.8e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGFLLLQMDGFGPPEHLVDFLQSL 26
Db 468 RDGFLLLQMDGFGPPEHLVDFLQSL 493

RESULT 32
US-08-788-882-30
; Sequence 30, Application US/08788882
; GENERAL INFORMATION:
; APPLICANT: Needleman, Phillip
; APPLICANT: Glenn, Kevin
; APPLICANT: Krul, Elaine
; APPLICANT: Gamsen, Edward P.
; TITLE OF INVENTION: An Immunological Process and Constructs
; TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 120 South Riverside Plaza, 22nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,882
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamsen, Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)655-1500
; TELEFAX: (312)655-1501
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 493 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PUBLICATION INFORMATION:
; AUTHORS: Pape, Michael E.
; AUTHORS: Rehberg, Edward F.
; AUTHORS: Marotli, Keith R.

;;
; AUTHORS: Melchior, George W.
; TITLE: Molecular Cloning, Sequence, and Expression
; of Cynomolgus Monkey Cholesteryl Ester Transfer
; TITLE: Protein
; JOURNAL: Arteriosclerosis and Thrombosis
; VOLUME: 11
; ISSUE: 6
; PAGES: 1759-1771
; DATE: Nov/Dec-1991
; US-08-788-882-30

Query Match 100.0%; Score 26; DB 11; Length 493;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDGFPPEHLVDFLOSLS 26
DB 468 RDGFLLLQMDGFPPEHLVDFLOSLS 493

RESULT 33
US-08-934-367-30
; Sequence 30, Application US/08934367
; GENERAL INFORMATION:
; APPLICANT: Needleman, Philip
; APPLICANT: Glenn, Kevin
; TITLE OF INVENTION: An Immunological Process and Constructs
; TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration by DNA
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 120 South Riverside Plaza, 22nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,367
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson Ph.D., Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)655-1500
; TELEFAX: (312)655-1501
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 493 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PUBLICATION INFORMATION:
; AUTHORS: Pape, Michael E.
; AUTHORS: Reiberg, Edward F.
; AUTHORS: Marotti, Keith R.
; AUTHORS: Melchior, George W.
; TITLE: Molecular Cloning, Sequence, and Expression
; of Cynomolgus Monkey Cholesteryl Ester Transfer
; TITLE: Protein
; JOURNAL: Arteriosclerosis and Thrombosis
; VOLUME: 11
; ISSUE: 6
; PAGES: 1759-1771

;;
; DATE: Nov/Dec-1991
; US-08-934-367-30

Query Match 100.0%; Score 26; DB 13; Length 493;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDGFPPEHLVDFLOSLS 26
DB 468 RDGFLLLQMDGFPPEHLVDFLOSLS 493

RESULT 34
US-09-054-272-14
; Sequence 14, Application US/09054272
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Daley, George O.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Rozen, Steven G.
; TITLE OF INVENTION: CODING SEQUENCE POLYMORPHISMS
; TITLE OF INVENTION: IN VASCULAR PATHOLOGY GENES
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,272
; FILING DATE: 01-APR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WHI98-05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 493 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-054-272-14

Query Match 100.0%; Score 26; DB 14; Length 493;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDGFPPEHLVDFLOSLS 26
DB 468 RDGFLLLQMDGFPPEHLVDFLOSLS 493

RESULT 35
US-09-054-272-48

```
; Sequence 48, Application US/09054272
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Daley, George O.
; APPLICANT: Carell, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Rozen, Steven G.
; TITLE OF INVENTION: CODING SEQUENCE POLYMORPHISMS
; TITLE OF INVENTION: IN VASCULAR PATHOLOGY GENES
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESS: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,272
; FILING DATE: 01-APR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WH198-05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 493 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
; US-09-054-272-48

Query Match          100.0%; Score 26; DB 14; Length 493;
Best Local Similarity 100.0%; Pred. NO. 1.8e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDFGFPHLLVDFLQSL 26
DB 468 RDGFLLLQMDFGFPHLLVDFLQSL 493

RESULT 36
US-09-386-591-30
; Sequence 30, Application US/09386591
; GENERAL INFORMATION:
; APPLICANT: Needleman, Phillip
; APPLICANT: Glenn, Kevin
; TITLE OF INVENTION: An Immunological Process and Constructs
; TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration by DNA
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 120 South Riverside Plaza, 22nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
```

```
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/386,591
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson Ph.D., Edward P.
; REGISTRATION NUMBER: 29,381
; REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)655-1500
; TELEFAX: (312)655-1501
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 493 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PUBLICATION INFORMATION:
; AUTHORS: Pape, Michael E.
; AUTHORS: Rehberg, Edward F.
; AUTHORS: Marottil, Keith R.
; AUTHORS: Melchior, George W.
; TITLE: Molecular Cloning, Sequence, and Expression
; TITLE: of Cynomolgus Monkey Cholesteryl Ester Transfer
; TITLE: Protein
; JOURNAL: Arteriosclerosis and Thrombosis
; VOLUME: 11
; ISSUE: 6
; PAGES: 1759-1771
; DATE: Nov/Dec-1991
; US-09-386-591-30

Query Match          100.0%; Score 26; DB 17; Length 493;
Best Local Similarity 100.0%; Pred. NO. 1.8e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDFGFPHLLVDFLQSL 26
DB 468 RDGFLLLQMDFGFPHLLVDFLQSL 493

RESULT 37
US-09-387-340-30
; Sequence 30, Application US/09387340
; GENERAL INFORMATION:
; APPLICANT: Needleman, Phillip
; APPLICANT: Glenn, Kevin
; APPLICANT: Krul, Elaine
; APPLICANT: Gamson, Edward P.
; TITLE OF INVENTION: An Immunological Process and Constructs
; TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 120 South Riverside Plaza, 22nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/09/387,340
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Gansson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1500
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 493 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PUBLICATION INFORMATION:
AUTHORS: Pape, Michael E.
AUTHORS: Reinberg, Edward F.
AUTHORS: Marotti, Keith R.
AUTHORS: Melchior, George W.
TITLE: Molecular Cloning, Sequence, and Expression
TITLE: of Cynomolgus Monkey Cholesteryl Ester Transfer
PROTEIN:
JOURNAL: Arteriosclerosis and Thrombosis
VOLUME: 11
ISSUE: 6
PAGES: 1759-1771
DATE: Nov/Dec-1991
US-09-387-340-30

Query Match 100.0%; Score 26; DB 17; Length 493;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDFGFPEHLVDFLOSL 26
|||||
DB 468 RDGFLLLQMDFGFPEHLVDFLOSL 493

RESULT 38
US-09-802-640-12
Sequence 12, Application US/09802640
GENERAL INFORMATION:
APPLICANT: Braun, Andreas
APPLICANT: Bonsal Aruna
APPLICANT: Kleya Patrick
TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
FILE REFERENCE: 24736-2048
CURRENT APPLICATION NUMBER: US/09/802,640
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 12
LENGTH: 493
TYPE: prp
ORGANISM: Homo sapien
US-09-802-640-12

Query Match 100.0%; Score 26; DB 22; Length 493;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLLQMDFGFPEHLVDFLOSL 26
|||||
DB 468 RDGFLLLQMDFGFPEHLVDFLOSL 493

RESULT 39

US-08-785-997-10
Sequence 10, Application US/08785997
GENERAL INFORMATION:
APPLICANT: Needleman, Phillip
APPLICANT: Glenn, Kevin
TITLE OF INVENTION: An Immunological Process for Increasing
TITLE OF INVENTION: the HDL Cholesterol Concentration
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,997
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gansson Ph.D., Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-101.0 6018/68346
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1500
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-785-997-10

Query Match 84.6%; Score 22; DB 11; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.8e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LLLQMDFGFPEHLVDFLOSL 26
|||||
DB 1 LLLQMDFGFPEHLVDFLOSL 22

RESULT 40
US-08-785-997-34
Sequence 34, Application US/08785997
GENERAL INFORMATION:
APPLICANT: Needleman, Phillip
APPLICANT: Glenn, Kevin
TITLE OF INVENTION: An Immunological Process for Increasing
TITLE OF INVENTION: the HDL Cholesterol Concentration
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,997

FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gamsen Ph.D., Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-101.0 6018/68346
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1501
TELEFAX: (312)655-1500
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-785-997-34

Query Match 84.6%; Score 22; DB 11; Length 22;
Best Local Similarity 100.0%; Pred. No. 6,8e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LLLQMDGFPEHLVDLQSLSS 26
|||||
DB 1 LLLQMDGFPEHLVDLQSLSS 22

RESULT 41
US-08-788-882-10
Sequence 10, Application US/08788882
GENERAL INFORMATION:
APPLICANT: Needleman, Philip
APPLICANT: Glenn, Kevin
APPLICANT: Krul, Elaine
TITLE OF INVENTION: An Immunological Process and Constructs
TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,882
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gamsen, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1501
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-788-882-10

Query Match 84.6%; Score 22; DB 11; Length 22;

Best Local Similarity 100.0%; Pred. No. 6,8e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LLLQMDGFPEHLVDLQSLSS 26
|||||
DB 1 LLLQMDGFPEHLVDLQSLSS 22

RESULT 42
US-08-788-882-34
Sequence 34, Application US/08788882
GENERAL INFORMATION:
APPLICANT: Needleman, Philip
APPLICANT: Glenn, Kevin
APPLICANT: Krul, Elaine
APPLICANT: Gamsen, Edward P.
TITLE OF INVENTION: An Immunological Process and Constructs
TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,882
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gamsen, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1501
TELEFAX: (312)655-1500
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-788-882-34

Query Match 84.6%; Score 22; DB 11; Length 22;
Best Local Similarity 100.0%; Pred. No. 6,8e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LLLQMDGFPEHLVDLQSLSS 26
|||||
DB 1 LLLQMDGFPEHLVDLQSLSS 22

RESULT 43
US-08-934-367-10
Sequence 10, Application US/08934367
GENERAL INFORMATION:
APPLICANT: Needleman, Philip
APPLICANT: Glenn, Kevin
APPLICANT: Krul, Elaine
TITLE OF INVENTION: An Immunological Process and Constructs
TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration by DNA
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.

```
STREET: 120 South Riverside Plaza, 22nd Floor
City: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,367
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ganson Ph.D., Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1500
TELEFAX: (312)655-1501
SEQUENCE CHARACTERISTICS:
SEQUENCE FOR SEQ ID NO: 10:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-367-10

Query Match      84.6%; Score 22; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.8e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LLLQMDGFFPHLLVDFLOSL 26
Db 1 LLLQMDGFFPHLLVDFLOSL 22

RESULT 44
US-08-934-367-34
Sequence 34, Application US/08934367
GENERAL INFORMATION:
APPLICANT: Needleman, Philip
TITLE OF INVENTION: An Immunological Process and Constructs
TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration by DNA
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
City: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,367
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ganson Ph.D., Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1500
TELEFAX: (312)655-1501
```

```
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-367-34

Query Match      84.6%; Score 22; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.8e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LLLQMDGFFPHLLVDFLOSL 26
Db 1 LLLQMDGFFPHLLVDFLOSL 22

RESULT 45
US-09-386-591-10
Sequence 10, Application US/09386591
GENERAL INFORMATION:
APPLICANT: Needleman, Philip
TITLE OF INVENTION: An Immunological Process and Constructs
TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration by DNA
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 South Riverside Plaza, 22nd Floor
City: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/386,591
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Ganson Ph.D., Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)655-1500
TELEFAX: (312)655-1501
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-386-591-10

Query Match      84.6%; Score 22; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.8e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LLLQMDGFFPHLLVDFLOSL 26
Db 1 LLLQMDGFFPHLLVDFLOSL 22

RESULT 46
US-09-386-591-34
```

```
: Sequence 34, Application US/09386591
: GENERAL INFORMATION:
: APPLICANT: Needleman, Philip
: APPLICANT: Glenn, Kevin
: TITLE OF INVENTION: An Immunological Process and Constructs
: TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration by DNA
: NUMBER OF SEQUENCES: 52
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Welsh & Katz, Ltd.
: STREET: 120 South Riverside Plaza, 22nd Floor
: CITY: Chicago
: STATE: IL
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/386,591
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Gamsen Ph.D., Edward P.
: REGISTRATION NUMBER: 29,381
: REFERENCE/DOCKET NUMBER: MON-103.0 6221/69666
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312)655-1500
: TELEFAX: (312)655-1501
: INFORMATION FOR SEQ ID NO: 34:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 22 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-09-386-591-34

Query Match      84.6%; Score 22; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 6,8e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 LLLQMDFGFPHLLVDFLQSLS 26
DB      1 LLLQMDFGFPHLLVDFLQSLS 22

RESULT 47
US-09-387-340-10
: Sequence 10, Application US/09387340
: GENERAL INFORMATION:
: APPLICANT: Needleman, Philip
: APPLICANT: Glenn, Kevin
: APPLICANT: Krul, Elaine
: APPLICANT: Gamsen, Edward P.
: TITLE OF INVENTION: An Immunological Process and Constructs
: TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration
: NUMBER OF SEQUENCES: 50
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Welsh & Katz, Ltd.
: STREET: 120 South Riverside Plaza, 22nd Floor
: CITY: Chicago
: STATE: IL
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/387,340
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Gamsen, Edward P.
: REGISTRATION NUMBER: 29,381
: REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312)655-1500
: TELEFAX: (312)655-1501
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 22 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-09-387-340-10

Query Match      84.6%; Score 22; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 6,8e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 LLLQMDFGFPHLLVDFLQSLS 26
DB      1 LLLQMDFGFPHLLVDFLQSLS 22

RESULT 48
US-09-387-340-34
: Sequence 34, Application US/09387340
: GENERAL INFORMATION:
: APPLICANT: Needleman, Philip
: APPLICANT: Glenn, Kevin
: APPLICANT: Krul, Elaine
: APPLICANT: Gamsen, Edward P.
: TITLE OF INVENTION: An Immunological Process and Constructs
: TITLE OF INVENTION: for Increasing the HDL Cholesterol Concentration
: NUMBER OF SEQUENCES: 50
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Welsh & Katz, Ltd.
: STREET: 120 South Riverside Plaza, 22nd Floor
: CITY: Chicago
: STATE: IL
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/387,340
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Gamsen, Edward P.
: REGISTRATION NUMBER: 29,381
: REFERENCE/DOCKET NUMBER: MON-102.0 6018/69242
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312)655-1500
: TELEFAX: (312)655-1501
: INFORMATION FOR SEQ ID NO: 34:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 22 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-09-387-340-34
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Query Match 84.6%; Score 22; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.8e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LLLQMDGFPPEHLVDFLOSL 26
|||||
DB 1 LLLQMDGFPPEHLVDFLOSL 22

RESULT 49
US-08-954-643-6
; Sequence 6, Application US/08954643
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles, W.
; APPLICANT: Thomas, Lawrence J.
; TITLE OF INVENTION: XENOGENEIC CHOLESTERYL ESTER
; TITLE OF INVENTION: TRANSFER PROTEIN (CTP) FOR MODULATION OF CTP ACTIVITY
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,643
; FILING DATE: concurrently herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Leon R. Yankwich
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: TCS-420.0 US
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: amino acid sequence for a humanized
; NAME/KEY: rabbit CTP protein
US-08-954-643-6

Query Match 84.6%; Score 22; DB 13; Length 496;
Best Local Similarity 100.0%; Pred. No. 8.5e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LLLQMDGFPPEHLVDFLOSL 26
|||||
DB 475 LLLQMDGFPPEHLVDFLOSL 496

RESULT 50
US-09-529-762-6
; Sequence 6, Application US/09529762
; GENERAL INFORMATION:
; APPLICANT: AVANT Immunotherapeutics, Inc.
; APPLICANT: Rittershaus, Charles
; APPLICANT: Thomas, Lawrence
; TITLE OF INVENTION: Xenogeneic Cholesteryl Ester Transfer Protein (CTP) for
; TITLE OF INVENTION: Modulation of CTP Activity
; FILE REFERENCE: sequence listing for TCS-420.1 PCT

; CURRENT APPLICATION NUMBER: US/09/529,762
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: USSN 08/954,643
; PRIOR FILING DATE: 1997-10-20
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-529-762-6

Query Match 84.6%; Score 22; DB 19; Length 496;
Best Local Similarity 100.0%; Pred. No. 8.5e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LLLQMDGFPPEHLVDFLOSL 26
|||||
DB 475 LLLQMDGFPPEHLVDFLOSL 496

Search completed: June 19, 2002, 11:10:11
Job time: 200 sec

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OM protein - protein search, using sw model

Run on: June 19, 2002, 11:07:06 ; Search time 14.77 Seconds
(without alignments)
152,226 Million cell updates/sec

Title: US-09-943-334-1

Perfect score: 26

Sequence: 1 RDGFLLQMDGFPEHLVDFLQSL 26

Scoring table:
OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 262238 seqs, 86476186 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262238

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 75 summaries

Database :

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3: /cgn2_6/pdata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/pdata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/pdata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/pdata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/pdata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	470	5	US-09-446-415B-6
2	11	42.3	11	5	US-09-523-033A-3
3	7	26.9	405	5	US-09-935-625-15267
4	6	23.1	42	6	US-10-105-299-4676
5	6	23.1	69	6	US-10-106-698-4318
6	6	23.1	97	6	US-10-144-850-423
7	6	23.1	193	7	US-09-360-039-20191
8	6	23.1	259	7	US-09-360-039-16488
9	6	23.1	260	7	US-09-360-039-17364
10	6	23.1	261	7	US-09-360-039-13333
11	6	23.1	269	7	US-09-360-039-17696
12	6	23.1	364	7	US-09-360-039-16535
13	6	23.1	370	5	US-09-895-913A-210
14	6	23.1	397	5	US-09-540-209B-5750
15	6	23.1	430	6	US-10-145-415-8
16	6	23.1	430	6	US-10-145-415-12
17	6	23.1	430	6	US-10-145-415-20
18	6	23.1	430	6	US-10-145-415-30
19	6	23.1	442	6	US-10-106-698-6383
20	6	23.1	481	7	US-09-360-039-4831
21	6	23.1	484	7	US-09-360-039-7590
22	6	23.1	487	7	US-09-360-039-8897
23	6	23.1	892	7	US-09-360-039-22811
24	6	23.1	903	6	US-10-104-047-2951
25	6	23.1	911	7	US-09-360-039-12464
26	6	23.1	1340	7	US-09-360-039-19485

27	5	19.2	7	6	US-10-105-299-3886	Sequence 3886, Ap
28	5	19.2	9	6	US-10-117-937-269	Sequence 269, Ap
29	5	19.2	9	6	US-10-014-340-19	Sequence 19, Ap
30	5	19.2	10	6	US-10-117-937-270	Sequence 270, Ap
31	5	19.2	13	1	PCT-US02-09135-151	Sequence 151, Ap
32	5	19.2	13	1	PCT-US02-09105-221	Sequence 221, Ap
33	5	19.2	13	1	PCT-US02-09257-299	Sequence 299, Ap
34	5	19.2	13	1	PCT-US02-09922-285	Sequence 285, Ap
35	5	19.2	13	6	US-10-105-299-3814	Sequence 3814, Ap
36	5	19.2	22	6	US-10-105-299-5535	Sequence 5535, Ap
37	5	19.2	24	6	US-10-143-775-636	Sequence 636, Ap
38	5	19.2	28	6	US-10-105-299-4607	Sequence 4607, Ap
39	5	19.2	34	6	US-10-105-299-5561	Sequence 5561, Ap
40	5	19.2	35	6	US-10-106-698-5700	Sequence 5700, Ap
41	5	19.2	37	6	US-10-105-299-4199	Sequence 4199, Ap
42	5	19.2	41	6	US-10-143-922-216	Sequence 216, Ap
43	5	19.2	44	1	PCT-US02-01109-100	Sequence 100, Ap
44	5	19.2	44	6	US-10-137-337-750	Sequence 750, Ap
45	5	19.2	46	6	US-10-105-299-5159	Sequence 5159, Ap
46	5	19.2	46	6	US-10-105-299-5161	Sequence 5161, Ap
47	5	19.2	48	1	PCT-US02-09921-928	Sequence 928, Ap
48	5	19.2	50	6	US-10-105-299-5308	Sequence 5308, Ap
49	5	19.2	52	6	US-10-143-788-680	Sequence 680, Ap
50	5	19.2	56	6	US-10-105-299-6077	Sequence 6077, Ap
51	5	19.2	60	6	US-10-106-698-7059	Sequence 7059, Ap
52	5	19.2	60	6	US-10-152-780-462	Sequence 462, Ap
53	5	19.2	60	6	US-10-152-780-466	Sequence 466, Ap
54	5	19.2	61	5	US-09-380-693A-55	Sequence 55, Ap
55	5	19.2	62	5	US-09-380-693A-57	Sequence 57, Ap
56	5	19.2	62	5	US-09-380-693A-54	Sequence 54, Ap
57	5	19.2	63	5	US-09-540-209B-9390	Sequence 9390, Ap
58	5	19.2	63	6	US-10-106-698-6030	Sequence 6030, Ap
59	5	19.2	63	6	US-10-144-860-281	Sequence 281, Ap
60	5	19.2	64	6	US-10-143-090-253	Sequence 253, Ap
61	5	19.2	65	5	US-09-620-393B-5812	Sequence 5812, Ap
62	5	19.2	69	5	US-09-380-693A-56	Sequence 56, Ap
63	5	19.2	72	6	US-10-144-702-537	Sequence 537, Ap
64	5	19.2	74	6	US-09-935-625-8321	Sequence 8321, Ap
65	5	19.2	74	6	US-10-105-299-4472	Sequence 4472, Ap
66	5	19.2	78	6	US-10-106-698-8410	Sequence 8410, Ap
67	5	19.2	80	5	US-09-620-393B-4183	Sequence 4183, Ap
68	5	19.2	80	5	US-09-620-393B-8965	Sequence 8965, Ap
69	5	19.2	87	5	US-09-991-150-175	Sequence 175, Ap
70	5	19.2	87	5	US-09-935-625-9319	Sequence 9319, Ap
71	5	19.2	88	1	PCT-US02-09921-991	Sequence 991, Ap
72	5	19.2	89	5	US-09-620-393B-548	Sequence 548, Ap
73	5	19.2	91	5	US-09-620-393B-547	Sequence 547, Ap
74	5	19.2	91	5	US-09-935-625-9036	Sequence 9036, Ap
75	5	19.2	93	5	US-09-620-393B-5781	Sequence 5781, Ap

ALIGNMENTS

RESULT 1
US-09-446-415B-6
Sequence 6, Applicant US/09446415B
GENERAL INFORMATION:
APPLICANT: Beamer, Lisa J.
APPLICANT: Eisenberg, David
TITLE OF INVENTION: BACTERIAL/PERMEABILITY-INCREASING PROTEIN:
TITLE OF INVENTION: CRYSTALLIZATION, X-RAY DIFFRACTION, THREE-DIMENSIONAL
TITLE OF INVENTION: STRUCTURE DETERMINATION, RATIONAL DRUG DESIGN AND
TITLE OF INVENTION: MOLECULAR MODELING OF RELATED PROTEINS
FILE REFERENCE: 110340502
CURRENT APPLICATION NUMBER: US/09/446,415B
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 08/879,565
PRIOR FILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6

LENGTH: 470
TYPE: PRT
ORGANISM: Human
FEATURE:
OTHER INFORMATION: cholesterol ester transfer protein (CETP) (Figure
US-09-446-415B-6

Query Match 100.0%; Score 26; DB 5; Length 470;
Best Local Similarity 100.0%; Pred. No. 3.7e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGFLLLQMDGFEPEHLVDFLOSL 26
DB 445 RDGFLLLQMDGFEPEHLVDFLOSL 470

RESULT 2
US-09-523-033A-3
; Sequence 3, Application US/09523033A
; GENERAL INFORMATION:
; APPLICANT: Kwok, Deborah Y.
; APPLICANT: Brostoff, Steven W.
; APPLICANT: Carlo, Dennis J.
; TITLE OF INVENTION: METHOD FOR INCREASING HDL CHOLESTEROL LEVEL
; FILE REFERENCE: TCS-428.0 US-1
; CURRENT APPLICATION NUMBER: US/09/523,033A
; CURRENT FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 08/482,454
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-523-033A-3

Query Match 42.3%; Score 11; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 HLLVDFLOSL 26
DB 1 HLLVDFLOSL 11

RESULT 3
US-09-935-625-15267
; Sequence 15267, Application US/099355625
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE
; FILE REFERENCE: 2750-1481P
; CURRENT APPLICATION NUMBER: US/09/935,625
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 33136
; SEQ ID NO 15267
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: 1..405
; OTHER INFORMATION: Ceres Seq. ID no. 3440036
US-09-935-625-15267

Query Match 26.9%; Score 7; DB 5; Length 405;
Best Local Similarity 100.0%; Pred. No. 24;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 19 VDFLOSL 25
DB 37 VDFLOSL 43

RESULT 4
US-10-105-299-4676
; Sequence 4676, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4676
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-299-4676

Query Match 23.1%; Score 6; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGFLL 7
DB 11 DGFLL 16

RESULT 5
US-10-106-698-4318
; Sequence 4318, Application US/10106698
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 4318
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-106-698-4318

Query Match 23.1%; Score 6; DB 6; Length 69;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 FLOSL 26
DB 8 FLOSL 13

RESULT 6
US-10-144-850-423
; Sequence 423, Application US/10144850
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

```
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM039CIN
; CURRENT APPLICATION NUMBER: US/10/144,850
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 09/758,443
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 432
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 423
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-144-850-423
```

```
Query Match          23.1%; Score 6; DB 6; Length 97;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 17 LVVFL 22
    |||||
Db 41 LVVFL 46
```

```
RESULT 7
US-60-360-039-20191
; Sequence 20191, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 20191
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Nostoc punctiforme
US-60-360-039-20191
```

```
Query Match          23.1%; Score 6; DB 7; Length 193;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 20 DFLQSL 25
    |||||
Db 78 DFLQSL 83
```

```
RESULT 8
US-60-360-039-16488
; Sequence 16488, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
```

```
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 16488
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-60-360-039-16488
```

```
Query Match          23.1%; Score 6; DB 7; Length 259;
Best Local Similarity 100.0%; Pred. No. 1.15e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 RDGFLL 6
    |||||
Db 116 RDGFLL 121
```

```
RESULT 9
US-60-360-039-17364
; Sequence 17364, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 17364
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Bacillus halodurans
US-60-360-039-17364
```

```
Query Match          23.1%; Score 6; DB 7; Length 260;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 RDGFLL 6
    |||||
Db 113 RDGFLL 118
```

```
RESULT 10
US-60-360-039-13333
; Sequence 13333, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 13333
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Aspergillus nidulans
; FEATURE:
; NAME/KEY: unsure
```

```
; LOCATION: (1)-(261)
; OTHER INFORMATION: unsure at all xaa locations
US-60-360-039-13333

Query Match          23.1%; Score 6; DB 7; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 FLOSLIS 26
    |||||
Db 109 FLOSLIS 114

RESULT 11
US-60-360-039-17696
; Sequence 17696, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 17696
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-60-360-039-17696

Query Match          23.1%; Score 6; DB 7; Length 269;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFL 6
    |||||
Db 123 RDGFL 128

RESULT 12
US-60-360-039-16535
; Sequence 16535, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 16535
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-60-360-039-16535

Query Match          23.1%; Score 6; DB 7; Length 364;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 FLOSLIS 26
    |||||
```

```
Db 292 FLOSLIS 297

RESULT 13
US-09-895-913A-210
; Sequence 210, Application US/09895913A
; GENERAL INFORMATION:
; APPLICANT: Kleantous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean Francois
; APPLICANT: Comen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding Novel Helicobacter Polypeptides in the Helicobacter
; FILE REFERENCE: 06132/043002
; CURRENT APPLICATION NUMBER: US/09/895,913A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 08/881,227
; PRIOR FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 210
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-895-913A-210

Query Match          23.1%; Score 6; DB 5; Length 370;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LLOQMF 11
    |||||
Db 240 LLOQMF 245

RESULT 14
US-09-540-209B-5750
; Sequence 5750, Application US/09540209B
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES
; FILE REFERENCE: 2709,1001-001
; CURRENT APPLICATION NUMBER: US/09/540,209B
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 5750
; LENGTH: 397
; TYPE: PRT
; ORGANISM: B. fragilis
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (44)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are un
US-09-540-209B-5750

Query Match          23.1%; Score 6; DB 5; Length 397;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LLYDFL 22
    |||||
Db 298 LLYDFL 303

RESULT 15
US-10-145-415-8
; Sequence 8, Application US/10145415
; GENERAL INFORMATION:
```

```
; APPLICANT: Buckel, Thomas Gunter
; APPLICANT: Hammer, Philip Eugene
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ligon, James Madison
; APPLICANT: Molnar, Istvan
; APPLICANT: Pachlatko, Johannes Paul
; APPLICANT: Zirkle, Ross Eric
; TITLE OF INVENTION: Methods and Compositions for Making Emamectin
; FILE REFERENCE: SYN-117 109846.312
; CURRENT APPLICATION NUMBER: US/10/145,415
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US 60/291,149
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Streptomyces lydicus
US-10-145-415-8
```

```
Query Match          23.1%; Score 6; DB 6; Length 430;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 12 GPEHL 17
    |||||
Db 99 GPEHL 104
```

```
RESULT 16
US-10-145-415-12
; Sequence 12, Application US/10145415
; GENERAL INFORMATION:
; APPLICANT: Buckel, Thomas Gunter
; APPLICANT: Hammer, Philip Eugene
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ligon, James Madison
; APPLICANT: Molnar, Istvan
; APPLICANT: Pachlatko, Johannes Paul
; APPLICANT: Zirkle, Ross Eric
; TITLE OF INVENTION: Methods and Compositions for Making Emamectin
; FILE REFERENCE: SYN-117 109846.312
; CURRENT APPLICATION NUMBER: US/10/145,415
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US 60/291,149
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Streptomyces chattanoogensis
US-10-145-415-12
```

```
Query Match          23.1%; Score 6; DB 6; Length 430;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 12 GPEHL 17
    |||||
Db 99 GPEHL 104
```

```
RESULT 17
US-10-145-415-20
; Sequence 20, Application US/10145415
; GENERAL INFORMATION:
; APPLICANT: Buckel, Thomas Gunter
; APPLICANT: Hammer, Philip Eugene
; APPLICANT: Hill, Dwight Steven
```

```
; APPLICANT: Ligon, James Madison
; APPLICANT: Molnar, Istvan
; APPLICANT: Pachlatko, Johannes Paul
; APPLICANT: Zirkle, Ross Eric
; TITLE OF INVENTION: Methods and Compositions for Making Emamectin
; FILE REFERENCE: SYN-117 109846.312
; CURRENT APPLICATION NUMBER: US/10/145,415
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US 60/291,149
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Streptomyces kasugaensis
US-10-145-415-20
```

```
Query Match          23.1%; Score 6; DB 6; Length 430;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 12 GPEHL 17
    |||||
Db 99 GPEHL 104
```

```
RESULT 18
US-10-145-415-30
; Sequence 30, Application US/10145415
; GENERAL INFORMATION:
; APPLICANT: Buckel, Thomas Gunter
; APPLICANT: Hammer, Philip Eugene
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ligon, James Madison
; APPLICANT: Molnar, Istvan
; APPLICANT: Pachlatko, Johannes Paul
; APPLICANT: Zirkle, Ross Eric
; TITLE OF INVENTION: Methods and Compositions for Making Emamectin
; FILE REFERENCE: SYN-117 109846.312
; CURRENT APPLICATION NUMBER: US/10/145,415
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: US 60/291,149
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Streptomyces lydicus
US-10-145-415-30
```

```
Query Match          23.1%; Score 6; DB 6; Length 430;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 12 GPEHL 17
    |||||
Db 99 GPEHL 104
```

```
RESULT 19
US-10-106-698-6383
; Sequence 6383, Application US/10106698
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
; FILE REFERENCE: PA005PI
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
```

```
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 6383
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (2)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (144)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; US-10-106-698-6383
```

```
Query Match          23.1%; Score 6; DB 6; Length 442;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 9 LLLQMD 14
    |||||
Db 137 LLLQMD 142
```

```
RESULT 20
US-60-360-039-4831
; Sequence 4831, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4831
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-60-360-039-4831
```

```
Query Match          23.1%; Score 6; DB 7; Length 481;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 5 LLLQMD 10
    |||||
Db 83 LLLQMD 88
```

```
RESULT 21
US-60-360-039-7590
; Sequence 7590, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; FILE REFERENCE: 38-10(52052)A
```

```
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 7590
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Burkholderia cepacia
US-60-360-039-7590
```

```
Query Match          23.1%; Score 6; DB 7; Length 484;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 5 LLLQMD 10
    |||||
Db 83 LLLQMD 88
```

```
RESULT 22
US-60-360-039-8897
; Sequence 8897, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 8897
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Chloroflexus aurantiacus
US-60-360-039-8897
```

```
Query Match          23.1%; Score 6; DB 7; Length 487;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 5 LLLQMD 10
    |||||
Db 171 LLLQMD 176
```

```
RESULT 23
US-60-360-039-22811
; Sequence 22811, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 22811
; LENGTH: 892
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-60-360-039-22811
```

```
Query Match          23.1%; Score 6; DB 7; Length 892;
```

Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 FLOSL 26
DB 405 FLOSL 410

RESULT 24
US-10-104-047-2951
; Sequence 2951, Application US/10104047
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentia Ver. 2.1
; SEQ ID NO 2951
; LENGTH: 903
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2951

Query Match 23.1%; Score 6; DB 6; Length 903;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DFLOSL 25
DB 210 DFLOSL 215

RESULT 25
US-60-360-039-12464
; Sequence 12464, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 12464
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Aspergillus nidulans
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(911)
; OTHER INFORMATION: unsure at all Xaa locations
US-60-360-039-12464

Query Match 23.1%; Score 6; DB 7; Length 911;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 FLOSL 26
DB 400 FLOSL 405

RESULT 26

US-60-360-039-19485
; Sequence 19485, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 19485
; LENGTH: 1340
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-60-360-039-19485

Query Match 23.1%; Score 6; DB 7; Length 1340;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LVDPL 22
DB 572 LVDPL 577

RESULT 27
US-10-105-299-3886
; Sequence 3886, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: Patentia Ver. 2.0
; SEQ ID NO 3886
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-299-3886

Query Match 19.2%; Score 5; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFLL 7
DB 2 GFLL 6

RESULT 28
US-10-117-937-269
; Sequence 269, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPILOPE SEQUENCES
; FILE REFERENCE: CTLIM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06

; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 269
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-269

Query Match 19.2% Score 5; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFULL 7
|||||
DB 5 GFULL 9

RESULT 29
US-10-014-340-19
; Sequence 19, Application US/10014340
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
; FILE REFERENCE: 9195-078
; CURRENT APPLICATION NUMBER: US/10/014,340
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-340-19

Query Match 19.2% Score 5; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 FPEHL 17
|||||
DB 2 FPEHL 6

RESULT 30
US-10-117-937-270
; Sequence 270, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CytImm.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 270
; LENGTH: 10

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-270

Query Match 19.2% Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFULL 7
|||||
DB 6 GFULL 10

RESULT 31
PCT-US02-09135-151
; Sequence 151, Application PC/TUS0209135
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS956PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09135
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/950,082
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 09/950,083
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 151
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09135-151

Query Match 19.2% Score 5; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFULL 7
|||||
DB 5 GFULL 9

RESULT 32
PCT-US02-09105-221
; Sequence 221, Application PC/TUS0209105
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS951PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09105
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/278,650
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 09/950,082
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 09/950,083
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 779
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 221
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09105-221

Query Match 19.2% Score 5; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFULL 7
|||||

Db 5 GFULL 9

RESULT 33

PCT-US02-09257-299

; Sequence 299, Application PC/TUS0209257

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc.

; TITLE OF INVENTION: Human Secreted Proteins

; FILE REFERENCE: PS957PCT

; CURRENT APPLICATION NUMBER: PCT/US02/09257

; CURRENT FILING DATE: 2002-03-26

; PRIOR APPLICATION NUMBER: US 60/278,650

; PRIOR FILING DATE: 2001-03-27

; PRIOR APPLICATION NUMBER: US 09/950,082

; PRIOR FILING DATE: 2001-09-12

; PRIOR APPLICATION NUMBER: US 09/950,083

; PRIOR FILING DATE: 2001-09-12

; NUMBER OF SEQ ID NOS: 994

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 299

; LENGTH: 13

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US02-09257-299

Query Match 19.2%; Score 5; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 1e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFULL 7
|||||

Db 5 GFULL 9

RESULT 34

PCT-US02-09922-285

; Sequence 285, Application PC/TUS0209922

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc.

; TITLE OF INVENTION: Human Secreted Proteins

; FILE REFERENCE: PS955PCT

; CURRENT APPLICATION NUMBER: PCT/US02/09922

; CURRENT FILING DATE: 2002-03-26

; PRIOR APPLICATION NUMBER: US 60/278,650

; PRIOR FILING DATE: 2001-03-27

; PRIOR APPLICATION NUMBER: US 09/950,082

; PRIOR FILING DATE: 2001-09-12

; PRIOR APPLICATION NUMBER: US 09/950,083

; PRIOR FILING DATE: 2001-09-12

; NUMBER OF SEQ ID NOS: 1117

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 285

; LENGTH: 13

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US02-09922-285

Query Match 19.2%; Score 5; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 1e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFULL 7
|||||

Db 5 GFULL 9

RESULT 35

US-10-105-299-3814

; Sequence 3814, Application US/10105299

; GENERAL INFORMATION:

; APPLICANT: Rosen, et. al

; TITLE OF INVENTION: Human Secreted Proteins

; FILE REFERENCE: PS950

; CURRENT APPLICATION NUMBER: US/10/105,299

; CURRENT FILING DATE: 2002-03-26

; NUMBER OF SEQ ID NOS: 15197

; Prior Application removed - See File Wrapper or Palm

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3814

; LENGTH: 13

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-105-299-3814

Query Match 19.2%; Score 5; DB 6; Length 13;

Best Local Similarity 100.0%; Pred. No. 1e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFULL 7
|||||

Db 5 GFULL 9

RESULT 36

US-10-105-299-5635

; Sequence 5635, Application US/10105299

; GENERAL INFORMATION:

; APPLICANT: Rosen, et. al

; TITLE OF INVENTION: Human Secreted Proteins

; FILE REFERENCE: PS950

; CURRENT APPLICATION NUMBER: US/10/105,299

; CURRENT FILING DATE: 2002-03-26

; NUMBER OF SEQ ID NOS: 15197

; Prior Application removed - See File Wrapper or Palm

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 5635

; LENGTH: 22

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-105-299-5635

Query Match 19.2%; Score 5; DB 6; Length 22;

Best Local Similarity 100.0%; Pred. No. 1e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 FLOSL 25
|||||

Db 11 FLOSL 15

RESULT 37

US-10-143-775-636

; Sequence 636, Application US/10143775

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PC021CIN

; CURRENT APPLICATION NUMBER: US/10/143,775

; CURRENT FILING DATE: 2002-05-14

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 1064

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 636

; LENGTH: 24

; TYPE: PRT

; ORGANISM: Homo sapiens

FEATURE:

```
; NAME/KEY: misc_feature
; LOCATION: (14)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-10-143-775-636
```

```
Query Match          19.2%: Score 5; DB 6; Length 24;
Best Local Similarity 100.0%: Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 19 VDFLLQ 23
    |||||
Db 8 VDFLLQ 12
```

```
RESULT 38
; Sequence 4607, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4607
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-299-4607
```

```
Query Match          19.2%: Score 5; DB 6; Length 28;
Best Local Similarity 100.0%: Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 4 FLLIQ 8
    |||||
Db 18 FLLIQ 22
```

```
RESULT 39
; US-10-105-299-5561
; Sequence 5561, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5561
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-299-5561
```

```
Query Match          19.2%: Score 5; DB 6; Length 34;
Best Local Similarity 100.0%: Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 3 GFLLL 7
    |||||
Db 17 GFLLL 21
```

```
RESULT 40
US-10-106-698-5700
```

```
; Sequence 5700, Application US/10106698
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 5700
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-106-698-5700
```

```
Query Match          19.2%: Score 5; DB 6; Length 35;
Best Local Similarity 100.0%: Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 18 LVDFLL 22
    |||||
Db 3 LVDFLL 7
```

```
RESULT 41
; US-10-105-299-4199
; Sequence 4199, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4199
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-299-4199
```

```
Query Match          19.2%: Score 5; DB 6; Length 37;
Best Local Similarity 100.0%: Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 3 GFLLL 7
    |||||
Db 18 GFLLL 22
```

```
RESULT 42
; US-10-143-922-216
; Sequence 216, Application US/10143922
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC022C1N
; CURRENT APPLICATION NUMBER: US/10/143,922
; CURRENT FILING DATE: 2002-05-14
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 216
; LENGTH: 41
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-143-922-216
```

```
Query Match          19.2%; Score 5; DB 6; Length 41;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      13 FPEHL 17
        |||||
Db       8 FPEHL 12
```

```
RESULT 43
PCT-US02-01109-100
; Sequence 100, Application PC/TUS0201109
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: 50 Human Secreted Proteins
; FILE REFERENCE: P2016PCT2
; CURRENT APPLICATION NUMBER: PCT/US02/01109
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: US 60/262,066
; PRIOR FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 100
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-01109-100
```

```
Query Match          19.2%; Score 5; DB 1; Length 44;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      3 GFLLL 7
        |||||
Db       12 GFLLL 16
```

```
RESULT 44
US-10-137-337-750
; Sequence 750, Application US/10137337
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM028C1N
; CURRENT APPLICATION NUMBER: US/10/137,337
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 09/758,447
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 812
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 750
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
```

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; NAME/KEY: misc_feature
; LOCATION: (27)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-137-337-750
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Query Match          19.2%; Score 5; DB 6; Length 44;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      18 LVDFL 22
        |||||
Db       19 LVDFL 23
```

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RESULT 45
US-10-105-299-5159
; Sequence 5159, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5159
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-299-5159
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Query Match          19.2%; Score 5; DB 6; Length 46;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      3 GFLLL 7
        |||||
Db       5 GFLLL 9
```

```
RESULT 46
US-10-105-299-5161
; Sequence 5161, Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5161
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-299-5161
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Query Match          19.2%; Score 5; DB 6; Length 46;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY      15 EHLVL 19
        |||||
Db       34 EHLVL 38
```

```
RESULT 47
PCT-US02-09921-928
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; Sequence 928, Application PC/TUS0209921
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DAFRO, Abel
; APPLICANT: JONES, Anissa L.
; APPLICANT: TRAN, Alanna-Phung B.
; APPLICANT: DAHL, Christopher R.
; APPLICANT: GIETZEN, Darryl
; APPLICANT: CHINN, Joyce
; APPLICANT: DUPOUR, Gerard E.
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: YU, Jimmy Y.
; APPLICANT: TUASON, Olivia
; APPLICANT: YAP, Pierre E.
; APPLICANT: AMSHEY, Stefan R.
; APPLICANT: DAUGHERTY, Sean C.
; APPLICANT: DAM, Tam C.
; APPLICANT: LIU, Tommy F.
; APPLICANT: NGUYEN, Duy-Viet An
; APPLICANT: KLEEFELD, Yael
; APPLICANT: GERSTIN JR., Edward H.
; APPLICANT: PERALTA, Careyna H.
; APPLICANT: DAVID, Marie H.
; APPLICANT: LEWIS, Samantha A.
; APPLICANT: CHEN, Alice J.
; APPLICANT: PANZER, Scott R.
; APPLICANT: HARRIS, Bernard
; APPLICANT: FLORES, Vincent
; APPLICANT: MARMAN, Rakesh
; APPLICANT: LO, Audrey
; APPLICANT: LAN, Ruth Y.
; APPLICANT: URASHKA, Michael
; FILE OF INVENTION: SECRETORY MOLECULES
; FILE REFERENCE: PT-1232 PCF
; CURRENT FILING DATE: 2002-03-27
; CURRENT APPLICATION NUMBER: PCT/US02/09921
; PRIOR APPLICATION NUMBER: 60/280,067; 60/280,068; 60/291,280; 60/291,849;
; 60/291,829; 60/299,428; 60/300,001; 60/299,776
; PRIOR FILING DATE: 2001-03-29; 2001-03-29; 2001-05-16; 2001-05-17;
; 2001-05-17; 2001-06-19; 2001-06-20; 2001-06-20
; NUMBER OF SEQ ID NOS: 1146
; SOFTWARE: PERL Program
; SEQ ID NO 928
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: LI:260629.7.orfi:2001MAY17
; PCT-US02-09921-928

Query Match          19.2%; Score 5; DB 1; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      21 FLOSL 25
        |||||
Db      22 FLOSL 26

RESULT 48
US-10-105-299-5308
; Sequence 5308, Application US/10105239
; GENERAL INFORMATION:
; APPLICANT: ROSEN, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
```

```
; SEQ ID NO 5308
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-299-5308

Query Match          19.2%; Score 5; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      17 LLYDF 21
        |||||
Db      1 LLYDF 5

RESULT 49
US-10-143-788-680
; Sequence 680, Application US/10143788
; GENERAL INFORMATION:
; APPLICANT: ROSEN et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC017C1N
; CURRENT APPLICATION NUMBER: US/10/143,788
; CURRENT FILING DATE: 2002-05-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 930
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 680
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (52)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-143-788-680

Query Match          19.2%; Score 5; DB 6; Length 52;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 MDEGF 13
        |||||
Db      10 MDEGF 14

RESULT 50
US-10-105-299-6077
; Sequence 6077, Application US/10105239
; GENERAL INFORMATION:
; APPLICANT: ROSEN, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6077
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-299-6077

Query Match          19.2%; Score 5; DB 6; Length 56;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GFLLL 7
        |||||
```

Wed Jun 19 11:12:08 2002

us-09-943-334-1.oligo.rapn

Page 13

Db 36 GFULL 40

Search completed: June 19, 2002, 11:10:33
Job time: 207 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 19, 2002, 11:05:55 ; Search time 13.15 seconds
(without alignments)

48.294 Million cell updates/sec

Title: US-09-943-334-1

Sequence: 1 RDGFLLQMDPFPPEHLVDFLOSLS 26

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 231628 seqs, 24425594 residues

Word size : 0

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 75 summaries

Database :

- 1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/2/1aa/PCPUS.COMB.pep.*
- 6: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	470	3	US-08-879-565-14
2	26	100.0	476	4	US-09-171-969-4
3	11	42.3	50	4	US-09-171-969-7
4	11	42.3	496	4	US-09-171-969-2
5	7	26.9	422	2	US-08-403-852D-17
6	7	26.9	422	2	US-08-510-646B-18
7	7	26.9	422	4	US-09-231-818-17
8	6	23.1	166	4	US-09-339-813B-79
9	6	23.1	166	4	US-09-339-804A-79
10	6	23.1	166	4	US-08-769-062B-79
11	6	23.1	166	4	US-09-344-002B-79
12	6	23.1	189	1	US-08-026-758-11
13	6	23.1	189	1	US-08-026-758-20
14	6	23.1	189	4	US-09-206-935-10
15	6	23.1	189	4	US-09-206-936-10
16	6	23.1	464	6	5463025-1
17	6	23.1	911	2	US-08-928-692-59
18	6	23.1	2539	2	US-09-413-814-42
19	6	23.1	7257	3	US-09-335-409-5
20	6	23.1	7257	4	US-09-568-102-5
21	6	23.1	7257	4	US-09-567-969-5
22	6	23.1	7257	4	US-09-568-480-5
23	6	23.1	7257	4	US-09-568-486-5
24	6	23.1	7257	4	US-09-568-472-5
25	5	19.2	7	4	US-09-057-897-20
26	5	19.2	7	4	US-08-159-339A-1184
27	5	19.2	9	3	US-08-159-339A-95

28	5	19.2	10	1	US-08-164-839-66	Sequence 66, Appl
29	5	19.2	10	1	US-08-583-799-66	Sequence 583, Appl
30	5	19.2	10	3	US-08-159-339A-593	Sequence 18, Appl
31	5	19.2	11	4	US-09-057-897-18	Sequence 9, Appl
32	5	19.2	12	4	US-09-060-039-9	Sequence 5169933-6
33	5	19.2	14	6	US-07-918-181A-17	Sequence 1183, Ap
34	5	19.2	15	1	US-07-918-181A-21	Sequence 21, Appl
35	5	19.2	15	1	US-08-231-575-17	Sequence 21, Appl
36	5	19.2	15	1	US-08-231-575-21	Sequence 21, Appl
37	5	19.2	15	3	US-08-159-339A-1183	Sequence 1183, Ap
38	5	19.2	15	3	PCT-US93-08328-17	Sequence 17, Appl
39	5	19.2	15	5	PCT-US93-06328-21	Sequence 21, Appl
40	5	19.2	15	5	US-09-162-934-18	Sequence 18, Appl
41	5	19.2	20	4	US-09-057-897-1	Sequence 1, Appl
42	5	19.2	21	4	US-09-057-897-32	Sequence 32, Appl
43	5	19.2	21	4	US-09-248-588-24	Sequence 24, Appl
44	5	19.2	22	4	US-09-162-934-17	Sequence 17, Appl
45	5	19.2	22	4	US-08-220-378-3	Sequence 2, Appl
46	5	19.2	25	2	US-08-696-012-3	Sequence 3, Appl
47	5	19.2	25	2	US-08-126-587C-2	Sequence 2, Appl
48	5	19.2	35	1	US-08-868-435-10	Sequence 10, Appl
49	5	19.2	36	4	US-08-744-231-10	Sequence 10, Appl
50	5	19.2	36	4	US-09-227-357-227	Sequence 227, Appl
51	5	19.2	60	4	US-08-928-692-64	Sequence 64, Appl
52	5	19.2	83	2	US-08-928-692-65	Sequence 65, Appl
53	5	19.2	83	2	US-08-278-089A-29	Sequence 29, Appl
54	5	19.2	100	1	US-08-838-957A-28	Sequence 28, Appl
55	5	19.2	102	2	US-09-142-469-6	Sequence 6, Appl
56	5	19.2	102	4	US-08-858-207A-397	Sequence 397, Appl
57	5	19.2	119	4	US-08-458-516-5	Sequence 5, Appl
58	5	19.2	127	1	US-08-943-136-2	Sequence 2, Appl
59	5	19.2	129	4	US-08-973-518-2	Sequence 2, Appl
60	5	19.2	129	4	US-07-874-848B-2	Sequence 2, Appl
61	5	19.2	143	3	US-09-096-244-2	Sequence 2, Appl
62	5	19.2	144	1	US-09-193-877-1	Sequence 1, Appl
63	5	19.2	145	4	US-08-362-453-10	Sequence 10, Appl
64	5	19.2	148	2	US-08-362-453-11	Sequence 11, Appl
65	5	19.2	150	1	US-08-362-453-12	Sequence 12, Appl
66	5	19.2	150	1	5310729-2	Sequence 49, Appl
67	5	19.2	150	6	US-08-946-339A-49	Sequence 110, Appl
68	5	19.2	154	4	US-09-247-155-110	Sequence 2, Appl
69	5	19.2	154	4	US-08-205-264-2	Sequence 15, Appl
70	5	19.2	161	3	US-08-362-453-15	Sequence 1, Appl
71	5	19.2	162	1	US-08-024-330-1	Sequence 1, Appl
72	5	19.2	165	1	US-07-952-840-1	Sequence 1, Appl
73	5	19.2	165	1		
74	5	19.2	165	1		

ALIGNMENTS

RESULT 1
US-08-879-565-14
: Sequence 14, Application US/08879565A
: Patent No. 6093573
: GENERAL INFORMATION:
: APPLICANT: Beamer, Lesa J.
: APPLICANT: Carroll, Stephen F.
: APPLICANT: Eisenberg, David
: TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF
: BACTERICIDAL/PERMEABILITY-INCREASING PROTEIN
: FILE REFERENCE: 1103/11034US01
: CURRENT APPLICATION NUMBER: US/08/879,565A
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 14
: LENGTH: 470
: TYPE: PRT
: ORGANISM: Human
: FEATURE:

OTHER INFORMATION: cholesteryl ester transfer protein (CEP) (Figure
OTHER INFORMATION: 5)
US-08-879-565-14

Query Match 100.0%; Score 26; DB 3; Length 470;
Best Local Similarity 100.0%; Pred. No. 8.8e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLOMDGFPPEHLVDFLOSL 26
DB 445 RDGFLLOMDGFPPEHLVDFLOSL 470

RESULT 2

US-09-171-969-4
Sequence 4, Application US/09171969
Patent No. 6284533
GENERAL INFORMATION:
APPLICANT: Thomas, Lawrence J.
TITLE OF INVENTION: PLASMIN-BASED VACCINE FOR TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 75 State Street, Suite 2300
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1807
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,969
FILING DATE: 01 May 1997 (01.05.97)
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/640,713
FILING DATE: 01 May 1996 (01.05.96)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/802,967
FILING DATE: 21 February 1997 (21.02.97)
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: TCS 414.1 PCT (05872)
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL:
ANTI-SENSE:
FEATURE:
NAME/KEY: Amino acid sequence of mature human
NAME/KEY: CEP
LOCATION:
PUBLICATION INFORMATION:
AUTHORS: Drayna, Dennis, et al.
TITLE: Cloning and sequencing of human
TITLE: cholesteryl ester transfer CDNA
JOURNAL: Nature
VOLUME: 327
ISSUE:
PAGES: 632 - 634
DATE: 18-JUN-1987
RELEVANT RESIDUES IN SEQ ID NO: 4: FROM 1 TO 476
US-09-171-969-4

Query Match 100.0%; Score 26; DB 4; Length 476;
Best Local Similarity 100.0%; Pred. No. 8.9e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGFLLOMDGFPPEHLVDFLOSL 26
DB 451 RDGFLLOMDGFPPEHLVDFLOSL 476

RESULT 3

US-09-171-969-7
Sequence 7, Application US/09171969
Patent No. 6284533
GENERAL INFORMATION:
APPLICANT: Thomas, Lawrence J.
TITLE OF INVENTION: PLASMIN-BASED VACCINE FOR TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 75 State Street, Suite 2300
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1807
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,969
FILING DATE: 01 May 1997 (01.05.97)
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/640,713
FILING DATE: 01 May 1996 (01.05.96)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/802,967
FILING DATE: 21 February 1997 (21.02.97)
ATTORNEY/AGENT INFORMATION:
NAME: Leon R. Yankwich
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: TCS 414.1 PCT (05872)
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL:
ANTI-SENSE:
FEATURE: amino acid sequence of peptide encoded
FEATURE: by bases 10 to 159 of SEQ ID NO:5
NAME/KEY:
LOCATION:
US-09-171-969-7

Query Match 42.3%; Score 11; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 HLLVDFLOSL 26
DB 40 HLLVDFLOSL 50

RESULT 4
US-09-171-969-2
Sequence 2, Application US/09171969
Patent No. 6284533
GENERAL INFORMATION:
APPLICANT: Thomas, Lawrence J.


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? TITLE OF INVENTION: PLASMID-BASED VACCINE FOR TREATING ATHEROSCLEROSIS
? NUMBER OF SEQUENCES: 10
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Banner & Witcoff, Ltd
? STREET: 75 State Street, Suite 2300
? CITY: Boston
? STATE: Massachusetts
? COUNTRY: USA
? ZIP: 02109-1807
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Wordperfect 6.1
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/171,969
? FILING DATE: 01 May 1997 (01.05.97)
? CLASSIFICATION: 514
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/640,713
? FILING DATE: 01 May 1996 (01.05.96)
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/802,967
? FILING DATE: 21 February 1997 (21.02.97)
? ATTORNEY/AGENT INFORMATION:
? NAME: Leon R. Yankwich
? REGISTRATION NUMBER: 30,237
? REFERENCE/DOCKET NUMBER: TCS 414.1 PCT (05872)
? INFORMATION FOR SEQ. ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 496 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? HYPOTHEICAL:
? ANTI-SENSE:
? FEATURE:
? NAME/KEY: Amino acid sequence for mature
? LOCATION: rabbit CDP protein.
? PUBLICATION INFORMATION:
? AUTHORS: Nagashima, Mariko, et al.
? TITLE: Cloning and mRNA tissue
? TITLE: distribution of rabbit
? TITLE: cholesteryl ester transfer
? JOURNAL: J. Lipid Res.
? VOLUME: 29
? ISSUE:
? PAGES: 1643 - 1649
? DATE: 1988
? RELEVANT RESIDUES IN SEQ. ID NO: 2: FROM 1 TO 496
? US-09-171-969-2

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? Query Match 42.3%; Score 11; DB 4; Length 496;
? Best Local Similarity 100.0%; Pred. No. 0.0022;
? Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 HLLVDFLOSL 26
DB 486 HLLVDFLOSL 496

RESULT 5
US-08-403-852D-17
? Sequence 17, Application US/08403852D
? Patent No. 5891695
? GENERAL INFORMATION:
? APPLICANT: Blanc, Veronique
? APPLICANT: Bianche, Francis
? APPLICANT: Crouzet, Joel
? APPLICANT: Jacques, Nathalie

```

```

? APPLICANT: Lacroix, Patricia
? APPLICANT: Thibaut, Denis
? APPLICANT: Zagorec, Monique
? APPLICANT: Debussche, Laurent
? TITLE OF INVENTION: Polypeptides Involved In The
? TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
? NUMBER OF SEQUENCES: 43
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
? STREET: 1300 I Street, N.W., Suite 700
? CITY: Washington
? STATE: D.C.
? COUNTRY: USA
? ZIP: 20005-3315
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/403,852D
? FILING DATE: 10-MAY-1995
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: PCT/FR 93/00923
? FILING DATE: 25-SEP-1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: FR 92/11441
? FILING DATE: 25-SEP-1992
? ATTORNEY/AGENT INFORMATION:
? NAME: Meyers, Kenneth J.
? REGISTRATION NUMBER: 25,146
? REFERENCE/DOCKET NUMBER: 03806, 0054-00000
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202) 408-4400
? TELEFAX: (202) 408-4400
? INFORMATION FOR SEQ. ID NO: 17:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 422 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? US-08-403-852D-17

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? Query Match 26.9%; Score 7; DB 2; Length 422;
? Best Local Similarity 100.0%; Pred. No. 13;
? Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 FGPEHL 17
DB 143 FGPEHL 149

RESULT 6
US-08-510-646B-18
? Sequence 18, Application US/08510646B
? Patent No. 6077699
? GENERAL INFORMATION:
? APPLICANT: Blanc, Veronique
? APPLICANT: Bianche, Francis
? APPLICANT: Crouzet, Joel
? APPLICANT: Jacques, Nathalie
? APPLICANT: Lacroix, Patricia
? APPLICANT: Thibaut, Denis
? APPLICANT: Zagorec, Monique
? APPLICANT: Debussche, Laurent
? APPLICANT: De Crecy-Lagard, Valerie
? TITLE OF INVENTION: Polypeptides Involved In The
? TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
? NUMBER OF SEQUENCES: 45

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Finegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,646B
FILING DATE: 03-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806,0054-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-510-646B-18

Query Match 26.9%; Score 7; DB 3; Length 422;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 FGFPEHL 17
|111111|
DB 143 FGFPEHL 149

RESULT 7
US-09-231-818-17
; Sequence 17, Application US/09231818
; Patent No. 6171846
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; APPLICANT: Blanche, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; APPLICANT: De Crecy-Lagard, Valerie
; TITLE OF INVENTION: Polypeptides Involved in The
; TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
; TITLE OF INVENTION: Coding For These Polypeptides And Their Use
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.

COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,818
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852
FILING DATE: 10-MAY-1995
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806,0054-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-231-818-17

Query Match 26.9%; Score 7; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 FGFPEHL 17
|111111|
DB 143 FGFPEHL 149

RESULT 8
US-09-339-913B-79
; Sequence 79, Application US/09339913B
; Patent No. 6303344
; GENERAL INFORMATION:
; APPLICANT: Patten, Phillip
; APPLICANT: Stemmer, William P.C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR POLYPEPTIDE ENGINEERING
; FILE REFERENCE: 02-02050305
; CURRENT APPLICATION NUMBER: US/09/339,913B
; CURRENT FILING DATE: 1999-06-24
; PRIOR APPLICATION NUMBER: 08/769,062
; PRIOR FILING DATE: 1996-12-18
; PRIOR APPLICATION NUMBER: 08/196,431
; PRIOR FILING DATE: 1994-02-17
; PRIOR APPLICATION NUMBER: 08/425,684
; PRIOR FILING DATE: 1995-04-18
; PRIOR APPLICATION NUMBER: 08/537,874
; PRIOR FILING DATE: 1995-10-30
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 79
; LENGTH: 166
; TYPE: PRT
; ORGANISM: human alpha interferon
US-09-339-913B-79

Query Match 23.1%; Score 6; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 49;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 DFGFPE 15
Db 35 DFGFPE 40

RESULT 9
US-09-339-904A-79
; Sequence 79, Application US/09339904A
; Patent No. 6319713
; GENERAL INFORMATION:
; APPLICANT: Patten, Phillip
; APPLICANT: Stemmer, William P.C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR POLYPEPTIDE ENGINEERING
; FILE REFERENCE: 02-020504US
; CURRENT APPLICATION NUMBER: US/09/339,904A
; PRIOR FILING DATE: 1999-06-24
; PRIOR APPLICATION NUMBER: 08/769,062
; PRIOR FILING DATE: 1996-12-18
; PRIOR APPLICATION NUMBER: 08/198,431
; PRIOR FILING DATE: 1994-02-17
; PRIOR APPLICATION NUMBER: 08/425,684
; PRIOR FILING DATE: 1995-04-18
; PRIOR APPLICATION NUMBER: 08/537,874
; PRIOR FILING DATE: 1995-10-30
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 79
; LENGTH: 166
; TYPE: PRT
; ORGANISM: human alpha Interferon
US-09-339-904A-79

Query Match 23.1%; Score 6; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 DFGFPE 15
Db 35 DFGFPE 40

RESULT 10
US-08-769-062B-79
; Sequence 79, Application US/08769062B
; Patent No. 6335160
; GENERAL INFORMATION:
; APPLICANT: Patten, Phillip
; APPLICANT: Stemmer, William P.C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR POLYPEPTIDE ENGINEERING
; FILE REFERENCE: 02-020500US
; CURRENT APPLICATION NUMBER: US/08/769,062B
; PRIOR FILING DATE: 1996-12-18
; PRIOR APPLICATION NUMBER: 08/198,431
; PRIOR FILING DATE: 1994-02-17
; PRIOR APPLICATION NUMBER: 08/425,684
; PRIOR FILING DATE: 1995-04-18
; PRIOR APPLICATION NUMBER: 08/537,874
; PRIOR FILING DATE: 1995-10-30
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 79
; LENGTH: 166
; TYPE: PRT
; ORGANISM: human alpha Interferon
US-08-769-062B-79

Query Match 23.1%; Score 6; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DFGFPE 15
Db 35 DFGFPE 40

RESULT 11
US-09-344-002B-79
; Sequence 79, Application US/09344002B
; Patent No. 6355484
; GENERAL INFORMATION:
; APPLICANT: Patten, Phillip
; APPLICANT: Stemmer, William P.C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR POLYPEPTIDE ENGINEERING
; FILE REFERENCE: 02-020502US
; CURRENT APPLICATION NUMBER: US/09/344,002B
; PRIOR FILING DATE: 1999-06-24
; PRIOR APPLICATION NUMBER: 08/769,062
; PRIOR FILING DATE: 1996-12-18
; PRIOR APPLICATION NUMBER: 08/198,431
; PRIOR FILING DATE: 1994-02-17
; PRIOR APPLICATION NUMBER: 08/425,684
; PRIOR FILING DATE: 1995-04-18
; PRIOR APPLICATION NUMBER: 08/537,874
; PRIOR FILING DATE: 1995-10-30
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 79
; LENGTH: 166
; TYPE: PRT
; ORGANISM: human alpha Interferon
US-09-344-002B-79

Query Match 23.1%; Score 6; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 DFGFPE 15
Db 35 DFGFPE 40

RESULT 12
US-08-026-758-11
; Sequence 11, Application US/08026758
; Patent No. 5780021
; GENERAL INFORMATION:
; APPLICANT: SOBEL, DOUGLAS O.
; TITLE OF INVENTION: A METHOD FOR TREATING AUTOIMMUNE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/026,758
; FILING DATE: 19930305
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: OBION, NO. 5780021man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1126-096-0

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 24..189
OTHER INFORMATION: /note= "IFN-alpha-4b"
US-08-026-758-11

Query Match 23.1%; Score 6; DB 1; Length 189;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DFGPPE 15
|||||
DB 58 DFGPPE 63

RESULT 13
US-08-026-758-20
Sequence 20, Application US/08026758
Patent No. 5780021
GENERAL INFORMATION:
APPLICANT: SOBEL, DOUGLAS O.
TITLE OF INVENTION: A METHOD FOR TREATING AUTOIMMUNE
DISEASES USING ALPHA-INTERFERON AND/OR BETA-INTERFERON
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/026,758
FILING DATE: 19930305
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Obion, No. 5780021man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-096-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 24..189
OTHER INFORMATION: /note= "IFN-alpha-76"
US-08-026-758-20

Query Match 23.1%; Score 6; DB 1; Length 189;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DFGPPE 15
|||||
DB 58 DFGPPE 63

RESULT 14
US-09-206-935-10
Sequence 10, Application US/09206935
Patent No. 629877
GENERAL INFORMATION:
APPLICANT: Chen, Jian
APPLICANT: Godowski, Paul
APPLICANT: Wood, William I.
APPLICANT: Zhang, Dong-Xiao
TITLE OF INVENTION: NOVEL TYPE I INTERFERONS
FILE REFERENCE: 1169, 500S05
CURRENT APPLICATION NUMBER: US/09/206,935
CURRENT FILING DATE: 1998-12-07
EARLIER APPLICATION NUMBER: 60/084,045
EARLIER FILING DATE: 1998-05-04
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 189
TYPE: PRT
ORGANISM: Homo sapiens
US-09-206-935-10

Query Match 23.1%; Score 6; DB 4; Length 189;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DFGPPE 15
|||||
DB 58 DFGPPE 63

RESULT 15
US-09-206-936-10
Sequence 10, Application US/09206936A
Patent No. 630475
GENERAL INFORMATION:
APPLICANT: Chen, Jian
APPLICANT: Wood, William I.
TITLE OF INVENTION: NO. 6300475el Interferon
FILE REFERENCE: P1224R1
CURRENT APPLICATION NUMBER: US/09/206,936A
CURRENT FILING DATE: 1998-12-07
EARLIER APPLICATION NUMBER: US 60/067,897
EARLIER FILING DATE: 1998-12-08
NUMBER OF SEQ ID NOS: 22
SEQ ID NO 10
LENGTH: 189
TYPE: PRT
ORGANISM: Homo sapiens
US-09-206-936-10

Query Match 23.1%; Score 6; DB 4; Length 189;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 DFGPPE 15
|||||
DB 58 DFGPPE 63

RESULT 16

5463025-1
 ; Patent No. 5463025
 ; APPLICANT: Sumi, Yoshihiko; Ichikawa, Yataro; Naki, Nobuo
 ; Muramatsu, Masami
 ; TITLE OF INVENTION: PROTEIN HAVING HUMAN PLASMIN INHIBITING
 ; ACTIVITY
 ; NUMBER OF SEQUENCES: 7
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/185,162
 ; FILING DATE: 24-JAN-1994
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 60,691
 ; FILING DATE: 13-MAY-1993
 ; APPLICATION NUMBER: 419,913
 ; FILING DATE: 05-SEP-1989
 ; SEQ ID NO:1:
 ; LENGTH: 464
 5463025-1

Query Match 23.1%; Score 6; DB 6; Length 464;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 20 DFFLLS 25
 Db 428 DFFLLS 433

RESULT 17
 US-08-928-692-59
 ; Sequence 59, Application US/08928692
 ; Patent No. 5958727
 ; GENERAL INFORMATION:
 ; APPLICANT: Brody, Howard
 ; APPLICANT: Yaver, Deborah S.
 ; APPLICANT: Hansen, Kim
 ; TITLE OF INVENTION: Methods for Modifying the Production of
 ; TITLE OF INVENTION: a Polypeptide
 ; NUMBER OF SEQUENCES: 80
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NO. 59587270 No. 59587270sk of No. 5958727th America, Inc.
 ; STREET: 405 Lexington Avenue
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10174
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/928,692
 ; FILING DATE: 12-SEPT-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lambiris, Elias J
 ; REGISTRATION NUMBER: 33,728
 ; REFERENCE/DOCKET NUMBER: 4444, 200-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-867-0123
 ; TELEFAX: 212-878-9655
 ; INFORMATION FOR SEQ ID NO: 59:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 911 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: NO. 5958727e
 ; US-08-928-692-59

Query Match 23.1%; Score 6; DB 2; Length 911;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GFFLLQ 8
 Db 635 GFFLLQ 640

RESULT 18
 US-09-413-814-42
 ; Sequence 42, Application US/09413814
 ; Patent No. 6225064
 ; GENERAL INFORMATION:
 ; APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
 ; APPLICANT: Bristol-Myers Squibb, CO.
 ; APPLICANT: Beyer, Stefan
 ; APPLICANT: Bioecker, Helmut
 ; APPLICANT: Brandt, Petra
 ; APPLICANT: Cino, Paul M
 ; APPLICANT: Dougherty, Brian A
 ; APPLICANT: Goldberg, Steven L
 ; APPLICANT: Hofle, Gerhard
 ; APPLICANT: Mueller, Joachim
 ; APPLICANT: Reichenbach, Hans
 ; TITLE OF INVENTION: DNA sequences for enzymatic syntheses of polypeptide or
 ; TITLE OF INVENTION: heteropolypeptide compounds
 ; FILE REFERENCE: PCT/US 99/23535
 ; CURRENT APPLICATION NUMBER: US/09/413,814
 ; CURRENT FILING DATE: 1999-10-07
 ; EARLIER APPLICATION NUMBER: DE 198 46 493.2
 ; EARLIER FILING DATE: 1998-10-09
 ; NUMBER OF SEQ ID NOS: 107
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 42
 ; LENGTH: 2539
 ; TYPE: PRT
 ; ORGANISM: Sorangium cellulosum
 ; US-09-413-814-42

Query Match 23.1%; Score 6; DB 4; Length 2539;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DGFLL 7
 Db 1319 DGFLL 1324

RESULT 19
 US-09-335-409-5
 ; Sequence 5, Application US/09335409
 ; Patent No. 6121029
 ; GENERAL INFORMATION:
 ; APPLICANT: Schupp, Thomas
 ; APPLICANT: Ligon, James
 ; APPLICANT: Molnar, Istvan
 ; APPLICANT: Zirkle, Ross
 ; APPLICANT: Cyr, Devon
 ; APPLICANT: Gerlach, Joern
 ; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
 ; FILE REFERENCE: 4-30582A
 ; CURRENT APPLICATION NUMBER: US/09/335,409
 ; CURRENT FILING DATE: 1999-06-17
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 7257
 ; TYPE: PRT
 ; ORGANISM: Sorangium cellulosum
 ; US-09-335-409-5

Query Match 23.1%; Score 6; DB 3; Length 7257;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 EHLVD 20
|||||
DB 2999 EHLVD 3004

RESULT 20
US-09-568-102-5
; Sequence 5, Application US/09568102
; Patent No. 6346404
; GENERAL INFORMATION:
; APPLICANT: Schnupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,102
; CURRENT FILING DATE: 2000-05-10
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5
; LENGTH: 7257
; TYPE: PR1
; ORGANISM: Sorangium cellulosum
US-09-568-102-5

Query Match 23.1%; Score 6; DB 4; Length 7257;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 EHLVD 20
|||||
DB 2999 EHLVD 3004

RESULT 21
US-09-567-969-5
; Sequence 5, Application US/09567969
; Patent No. 6355457
; GENERAL INFORMATION:
; APPLICANT: Schnupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/567,969
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5
; LENGTH: 7257
; TYPE: PR1
; ORGANISM: Sorangium cellulosum
US-09-567-969-5

Query Match 23.1%; Score 6; DB 4; Length 7257;

Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 EHLVD 20
|||||
DB 2999 EHLVD 3004

RESULT 22
US-09-568-480-5
; Sequence 5, Application US/09568480
; Patent No. 6355458
; GENERAL INFORMATION:
; APPLICANT: Schnupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,480
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5
; LENGTH: 7257
; TYPE: PR1
; ORGANISM: Sorangium cellulosum
US-09-568-480-5

Query Match 23.1%; Score 6; DB 4; Length 7257;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 EHLVD 20
|||||
DB 2999 EHLVD 3004

RESULT 23
US-09-568-486-5
; Sequence 5, Application US/09568486
; Patent No. 6355459
; GENERAL INFORMATION:
; APPLICANT: Schnupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,486
; CURRENT FILING DATE: 2000-05-10
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5
; LENGTH: 7257
; TYPE: PR1
; ORGANISM: Sorangium cellulosum
US-09-568-486-5

Query Match 23.1%; Score 6; DB 4; Length 7257;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 EHLVD 20
DB 2999 EHLVD 3004

RESULT 24

US-09-568-472-5
; Sequence 5, Application US/09568472
; Patent No. 6358719
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHIONINES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,472
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 7257
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-568-472-5

Query Match 23.1%; Score 6; DB 4; Length 7257;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 EHLVD 20
DB 2999 EHLVD 3004

RESULT 25
US-09-057-897-20
; Sequence 20, Application US/09057897
; Patent No. 6300476
; GENERAL INFORMATION:
; APPLICANT: Lu, Anthony Y. H.
; APPLICANT: Wang, Regina W.
; TITLE OF INVENTION: Anti-Peptide Antibody Against Human
; TITLE OF INVENTION: Cytochrome P450 3A4
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P. O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,897
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 19902
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (732)594-3905
; TELEFAX: (732)594-4720

; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-057-897-20

Query Match 19.2%; Score 5; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 VDFLQ 23
DB 3 VDFLQ 7

RESULT 26

US-08-159-339A-1184
; Sequence 1184, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: PasteSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1184:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-1184

Query Match 19.2%; Score 5; DB 3; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFLIL 7
| | | | |
Db 3 GFLIL 7

RESULT 27
US-08-159-339A-95

; Sequence 95, Application US/08159339A
; Patent No. 6037135

; GENERAL INFORMATION:

; APPLICANT: Kubo, Ralph T.

; APPLICANT: Grey, Howard M.

; APPLICANT: Sette, Alessandro

; APPLICANT: Celis, Esteban

; TITLE OF INVENTION: HLA Binding peptides and Their

; TITLE OF INVENTION: Uses

; NUMBER OF SEQUENCES: 1254

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; FILING DATE: 29-NOV-1993

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/926,666

; FILING DATE: 07-AUG-1992

; APPLICATION NUMBER: US 08/027,746

; FILING DATE: 05-MAR-1993

; APPLICATION NUMBER: US 08/103,396

; FILING DATE: 06-AUG-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Weber, Ellen Lauver

; REGISTRATION NUMBER: 32,762

; REFERENCE/DOCKET NUMBER: 018623-005030US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; TELEX:

; INFORMATION FOR SEQ ID NO: 95:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-159-339A-95

Query Match 19.2%; Score 5; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.7e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GFLIL 7
| | | | |
Db 4 GFLIL 8

RESULT 28

US-08-164-839-66
; Sequence 66, Application US/08164839

; Patent No. 5514573

; GENERAL INFORMATION:

; APPLICANT: YASUEDA, HISASHI

; APPLICANT: NAKANISHI, KAZUO

; APPLICANT: MOTOKI, MASAO

; APPLICANT: NAGASE, KAZUO

; APPLICANT: MATSUI, HIROSHI

; TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED

; TITLE OF INVENTION: FROM FISH

; NUMBER OF SEQUENCES: 72

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; ADDRESS: P.C.

; STREET: 1755 Jefferson Davis Highway, Fourth Floor

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/164,839

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/004,729

; FILING DATE: 14-JAN-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Oblon, No. 5514573man F.

; REGISTRATION NUMBER: 24,618

; REFERENCE/DOCKET NUMBER: 10-599-0

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)412-3000

; TELEFAX: (703)413-2220

; TELEX: 248855 OPAT UR

; INFORMATION FOR SEQ ID NO: 66:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-164-839-66

Query Match 19.2%; Score 5; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 34;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 LLVDF 21
| | | | |
Db 1 LLVDF 5

RESULT 29

US-08-583-799-66

; Sequence 66, Application US/08583799

; Patent No. 5607849

; GENERAL INFORMATION:

; APPLICANT: YASUEDA, HISASHI

; APPLICANT: NAKANISHI, KAZUO

; APPLICANT: MOTOKI, MASAO

; APPLICANT: NAGASE, KAZUO

; APPLICANT: MATSUI, HIROSHI

; TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED

; TITLE OF INVENTION: FROM FISH

; NUMBER OF SEQUENCES: 72

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; ADDRESS: P.C.

; STREET: 1755 Jefferson Davis Highway, Fourth Floor

CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,799
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5607849man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)412-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-583-799-66

Query Match 19.2%; Score 5; DB 1; Length 10;
Best local similarity 100.0%; Pred. No. 34;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LLVDF 21
Db 1 LLVDF 5

RESULT 30
US-08-159-339A-593
Sequence 593, Application US/08159339A
Patent No. 6037135
GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992

APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:
INFORMATION FOR SEQ ID NO: 593:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-593

Query Match 19.2%; Score 5; DB 3; Length 10;
Best local similarity 100.0%; Pred. No. 34;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFLLL 7
Db 5 GFLLL 9

RESULT 31
US-09-057-897-18
Sequence 18, Application US/09057897
Patent No. 6300476
GENERAL INFORMATION:
APPLICANT: Lu, Anthony Y.H.
APPLICANT: Wang, Regina W.
TITLE OF INVENTION: Anti-Peptide Antibody Against Human
TITLE OF INVENTION: Cytochrome P450 3A4
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: NJ
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,897
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 19902
TELECOMMUNICATION INFORMATION:
TELEPHONE: (732)594-3905
TELEFAX: (732)594-4720
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-057-897-18

Query Match 19.2%; Score 5; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 19 VDFLQ 23
DB 7 VDFLQ 11

RESULT 32
US-09-060-039-9
; Sequence 9, Application US/09060039
; Patent No. 6130036
; GENERAL INFORMATION:
; APPLICANT: Loeb, Lawrence A.
; APPLICANT: Kim, Baek
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
; TITLE OF INVENTION: FOR ANTI-AIDS DRUGS
; FILE REFERENCE: 920010.410C3
; CURRENT APPLICATION NUMBER: US/09/060.039
; CURRENT FILING DATE: 1998-04-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Randomly generated mutation of segment of HIV RT
; OTHER INFORMATION: gene which encodes a portion of the putative
; OTHER INFORMATION: nucleotide binding site
US-09-060-039-9

Query Match 19.2%; Score 5; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LVDVF 21
DB 7 LVDVF 11

RESULT 33
5169933-6
; Patent No. 5169933
; APPLICANT: ANDERSON, DAVID C.; MORGAN, CHARLES JR.; FRITZBERG,
; ALAN R.; NICHOLS, EVERETT J.
; TITLE OF INVENTION: CAVALENTLY-LINKED COMPLEXES AND METHODS
; FOR ENHANCED CYTOTOXICITY AND IMAGING
; NUMBER OF SEQUENCES: 45
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/390,241
; FILING DATE: 07-AUG-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 232,337
; FILING DATE: 15-AUG-1988
; SEQ ID NO: 6
; LENGTH: 14
5169933-6

Query Match 19.2%; Score 5; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFLL 7
DB 7 GFLL 11

RESULT 34

US-07-918-181A-17
; Sequence 17, Application US/07918181A
; Patent No. 5338833
; GENERAL INFORMATION:
; APPLICANT: Fowlkes, Dana M.
; TITLE OF INVENTION: C-Terminal IL-6 Mutelins
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Imclone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/918,181A
; FILING DATE: 23-JUL-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sheets, Eric J.
; REGISTRATION NUMBER: 30,326
; REFERENCE/DOCKET NUMBER: FOW-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: C-terminal
US-07-918-181A-17

Query Match 19.2%; Score 5; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DFLOS 24
DB 3 DFLOS 7

RESULT 35
US-07-918-181A-21
; Sequence 21, Application US/07918181A
; Patent No. 5338833
; GENERAL INFORMATION:
; APPLICANT: Fowlkes, Dana M.
; TITLE OF INVENTION: C-Terminal IL-6 Mutelins
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Imclone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/918,181A
FILING DATE: 23-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sheets, Eric J.
REGISTRATION NUMBER: 30,326
REFERENCE/DOCKET NUMBER: FOW-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
AMT-SENSE: NO
FRAGMENT TYPE: C-terminal
US-07-918-181A-21

Query Match 19.2%; Score 5; DB 1;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DFLQS 24
|||||
DB 3 DFLQS 7

RESULT 36
US-08-231-575-17
Sequence 17, Application US/08231575
Patent No. 5565336
GENERAL INFORMATION:
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: C-Terminal IL-6 Mutelins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,575
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/918,181
FILING DATE: 23-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Sheets, Eric J.
REGISTRATION NUMBER: 30,326
REFERENCE/DOCKET NUMBER: FOW-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
US-08-231-575-17

Query Match 19.2%; Score 5; DB 1;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DFLQS 24
|||||
DB 3 DFLQS 7

RESULT 37
US-08-231-575-21
Sequence 21, Application US/08231575
Patent No. 5565336
GENERAL INFORMATION:
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: C-Terminal IL-6 Mutelins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,575
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/918,181
FILING DATE: 23-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Sheets, Eric J.
REGISTRATION NUMBER: 30,326
REFERENCE/DOCKET NUMBER: FOW-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
US-08-231-575-21

Query Match 19.2%; Score 5; DB 1;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DFLQS 24
|||||
DB 3 DFLQS 7

RESULT 38
US-08-159-339A-1183

Sequence 1183, Application US/08159339A
Patent No. 6037135
GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Cells, Esteban
TITLE OF INVENTION: HLA Binding peptides and their
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:
INFORMATION FOR SEQ ID NO: 1183:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-1183

Query Match 19.2%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFLLL 7
DB 10 GFLLL 14

RESULT 39
PCT-US93-06928-17
Sequence 17, Application PC/TUS9306928
GENERAL INFORMATION:
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: Carboxy Terminal IL-6 Mutelins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.

ZIP: 11014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06928
FILING DATE: 19930723
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/918,181
FILING DATE: 23-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fell, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: FOW-2-T
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYDROTHERICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
PCT-US93-06928-17

Query Match 19.2%; Score 5; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DELQS 24
DB 3 DELQS 7

RESULT 40
PCT-US93-06928-21
Sequence 21, Application PC/TUS9306928
GENERAL INFORMATION:
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: Carboxy Terminal IL-6 Mutelins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 11014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06928
FILING DATE: 19930723
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/918,181
FILING DATE: 23-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fell, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: FOW-2-T
TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
PCT-US93-06928-21

Query Match 19.2%; Score 5; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DFLQS 24
11111
DB 3 DFLQS 7

RESULT 41
US-09-162-934-18
Sequence 18, Application US/09162934
Patent No. 6258597
GENERAL INFORMATION:
APPLICANT: Bachovchin, William
APPLICANT: 71 Marwick Road
APPLICANT: Melrose, MA 02176
APPLICANT: U.S.A.
APPLICANT: Wallner, Barbara
APPLICANT: 64 Arrowhead Road
APPLICANT: Weston, MA 02193
APPLICANT: U.S.A.
TITLE OF INVENTION: STIMULATION OF HEMATOPOIETIC CELLS IN
FILE REFERENCE: 10248/7005
CURRENT APPLICATION NUMBER: US/09/162,934
CURRENT FILING DATE: 1998-09-29
EARLIER APPLICATION NUMBER: US 60/060,306
EARLIER FILING DATE: 1997-09-29
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 18
LENGTH: 20
TYPE: PRT
ORGANISM: homo sapiens
US-09-162-934-18

Query Match 19.2%; Score 5; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LQWDF 11
11111
DB 11 LQWDF 15

RESULT 42
US-09-057-897-1
Sequence 1, Application US/09057897
Patent No. 6300476
GENERAL INFORMATION:
APPLICANT: Lu, Anthony Y.H.
APPLICANT: Wang, Regina W.
TITLE OF INVENTION: Anti-Peptide Antibody Against Human
CYCLOCHROME P450 3A4
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: NJ
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/057,897
APPLICATION NUMBER: US/09/057,897
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 19902
TELECOMMUNICATION INFORMATION:
TELEPHONE: (732)594-4720
TELEFAX: (732)594-3905
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-057-897-1

Query Match 19.2%; Score 5; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 VDFLQ 23
11111
DB 17 VDFLQ 21

RESULT 43
US-09-057-897-32
Sequence 32, Application US/09057897
Patent No. 6300476
GENERAL INFORMATION:
APPLICANT: Lu, Anthony Y.H.
APPLICANT: Wang, Regina W.
TITLE OF INVENTION: Anti-Peptide Antibody Against Human
CYCLOCHROME P450 3A4
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: NJ
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/057,897
APPLICATION NUMBER: US/09/057,897
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 19902
TELECOMMUNICATION INFORMATION:
TELEPHONE: (732)594-3905

TELEFAX: (732)594-4720
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-057-897-32

Query Match 19.2%; Score 5; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 VDFLQ 23
11111
DB 17 VDFLQ 21

RESULT 44
US-09-248-588-24
; Sequence 24, Application US/09248588
; Patent No. 6231864
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: Strategically Modified Hepatitis B Core Proteins and
; FILE REFERENCE: their Derivatives
; CURRENT APPLICATION NUMBER: US/09/248,588
; EARLIER FILING DATE: 1999-02-11
; EARLIER FILING DATE: 1998-02-12
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-248-588-24

Query Match 19.2%; Score 5; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 VDFLQ 23
11111
DB 18 VDFLQ 22

RESULT 45
US-09-162-934-17
; Sequence 17, Application US/09162934
; Patent No. 6238597
; GENERAL INFORMATION:
; APPLICANT: Bachovchin, William
; APPLICANT: 71 Warwick Road
; APPLICANT: Melrose, MA 02176
; APPLICANT: U.S.A.
; APPLICANT: Waliner, Barbara
; APPLICANT: 64 Arrowhead Road
; APPLICANT: Weston, MA 02193
; APPLICANT: U.S.A.
; TITLE OF INVENTION: STIMULATION OF HEMATOPOIETIC CELLS IN
; TITLE OF INVENTION: VITRO
; FILE REFERENCE: 10248/7005
; CURRENT APPLICATION NUMBER: US/09/162,934
; EARLIER FILING DATE: 1998-09-29
; EARLIER APPLICATION NUMBER: US 60/060,306
; EARLIER FILING DATE: 1997-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 17
; LENGTH: 22
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-162-934-17

Query Match 19.2%; Score 5; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 LQDMF 11
11111
DB 13 LQDMF 17

RESULT 46
US-09-057-897-2
; Sequence 2, Application US/09057897
; Patent No. 6300476
; GENERAL INFORMATION:
; APPLICANT: Lu, Anthony Y.H.
; TITLE OF INVENTION: Anti-Peptide Antibody Against Human
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: US
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,897
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 19902
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (732)594-3905
; TELEFAX: (732)594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-057-897-2

Query Match 19.2%; Score 5; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 VDFLQ 23
11111
DB 18 VDFLQ 22

RESULT 47
US-08-220-378-3
; Sequence 3, Application US/08220378
; Patent No. 5545716
; GENERAL INFORMATION:

APPLICANT: Johnson, Howard M.
APPLICANT: Pontzer, Carol H.
APPLICANT: Griggs, Nathan D.
TITLE OF INVENTION: Superantigen Agonist and Antagonist
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,378
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,497
FILING DATE: 08-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF126.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-220-378-3

Query Match 19.2%; Score 5; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 17 LLYDF 21
|||||
DB 6 LLYDF 10

RESULT 48
US-08-696-012-3
Sequence 3, Application US/08696012
Patent No. 5859207
GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.
APPLICANT: Pontzer, Carol H.
APPLICANT: Griggs, Nathan D.
TITLE OF INVENTION: Superantigen Agonist and Antagonist
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,012
FILING DATE: 12-AUG-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/220,378
FILING DATE: 29-MAR-1994
APPLICATION NUMBER: US 07/941,497
FILING DATE: 08-SEP-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF126.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-696-012-3

Query Match 19.2%; Score 5; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 17 LLYDF 21
|||||
DB 6 LLYDF 10

RESULT 49
US-08-126-587C-2
Sequence 2, Application US/08126587C
Patent No. 5534438
GENERAL INFORMATION:
APPLICANT: Hayden, Michael
APPLICANT: Goldberg, Paul
APPLICANT: Andrew, Susan
APPLICANT: Rommens, Johanna M.
APPLICANT: Lin, Biaoyang
TITLE OF INVENTION: Process for Isolating Genes and the Gene
TITLE OF INVENTION: Causative of Huntington's Disease and Differential 3'
TITLE OF INVENTION: Polydenylation in the Gene
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell Seltzer Park & Gibson
STREET: 1211 E. Morehead Street
CITY: Charlotte
STATE: No. 5534438th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/126,587C
FILING DATE: 24-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Layton Jr., Samuel G.
REGISTRATION NUMBER: 22,807
REFERENCE/DOCKET NUMBER: 3477-84
TELECOMMUNICATION INFORMATION:
TELEPHONE: 704-377-1561

TELEFAX: 704-334-2014
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-126-587C-2

Query Match 19.2%; Score 5; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 22 LOSLS 26
Db 16 LOSLS 20

RESULT 50
US-08-868-435-10
Sequence 10 Application US/08868435
Patent No. 6291221
GENERAL INFORMATION:
APPLICANT: Van Loon, Adolphus
APPLICANT: Mitchell, David
TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/868,435
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/744,231
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
REFERENCE/DOCKET NUMBER: Case Docket 9339
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4205
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-868-435-10

Query Match 19.2%; Score 5; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 22 LOSLS 26
Db 16 LOSLS 20

Db 30 LOSLS 34

Search completed: June 19, 2002, 11:07:59
Job time: 124 sec

, and support the concept that inhibition of CETP activity in vivo can be anti-atherogenic. Currently, this vaccine is in clin. trials.

ST **atherosclerosis vaccine cholesteryl ester transfer protein peptide HDL cholesterol**

IT **Proteins**

RL: BSU (Biological study, unclassified); BIOL (Biological study) (cholesterol ester-exchanging, peptide, conjugate with tetanus toxin peptide; vaccine contg. a cholesteryl ester transfer protein peptide for treatment of low plasma HDL-Cholesterol and atherosclerosis)

IT **Lipoproteins**

RL: BSU (Biological study, unclassified); BIOL (Biological study) (high-d., cholesterol; vaccine contg. a cholesteryl ester transfer protein peptide for treatment of low plasma HDL-Cholesterol and atherosclerosis)

IT **Toxins**

RL: PAC (Pharmacological activity); THU (Therapeutic use); BIOL (Biological study); USES (Uses) (tetanus, peptide, conjugate with CETP peptide; vaccine contg. a cholesteryl ester transfer protein peptide for treatment of low plasma HDL-Cholesterol and atherosclerosis)

IT **Atherosclerosis**

Immunotherapy

Vaccines

(vaccine contg. a cholesteryl ester transfer protein peptide for treatment of low plasma HDL-Cholesterol and atherosclerosis)

IT **57-88-5, Cholesterol**

RL: BSU (Biological study, unclassified); BIOL (Biological study) (HDL; vaccine contg. a cholesteryl ester transfer protein peptide for treatment of low plasma HDL-Cholesterol and atherosclerosis)

IT **430455-98-4**

RL: PAC (Pharmacological activity); THU (Therapeutic use); BIOL (Biological study); USES (Uses) (vaccine contg. a cholesteryl ester transfer protein peptide for treatment of low plasma HDL-Cholesterol and atherosclerosis)

RE.CNT 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD

RE

- (1) Agellon, L; J Biol Chem 1991, V266(17), P10796 HCAPLUS
- (2) Anon; Lancet 1994, V344(8934), P1383
- (3) Brown, M; Nature 1989, V342(6248), P448 HCAPLUS
- (4) Cashin-Hemphill, L; Online J Curr Clin Trials 1992, Doc No 26
- (5) Cashin-Hemphill, L; published erratum appears in Online J Curr Clin Trials 1992, Doc No 29
- (6) Gaynor, B; Atherosclerosis 1994, V110(1), P101 HCAPLUS
- (7) Gordon, D; N Engl J Med 1989, V321(19), P1311 MEDLINE
- (8) Herrera, V; Nat Med 1999, V5(12), P1383 HCAPLUS
- (9) Murphy, S; Natl Vital Stat Rep 2000, V48(11), P1 MEDLINE
- (10) Okamoto, H; Nature 2000, V406(6792), P203 HCAPLUS
- (11) Rittershaus, C; Arterioscler Thromb Vasc Biol 2000, V20(9), P2106 HCAPLUS
- (12) Sugano, M; J Biol Chem 1998, V273(9), P5033 HCAPLUS
- (13) Whitlock, M; J Clin Invest 1989, V84(1), P129 HCAPLUS

L42 ANSWER 2 OF 15 HCAPLUS COPYRIGHT 2002 ACS

AN 2001:651566 HCAPLUS

DN 135:225853

TI Plasmid-based **vaccine** for treating **atherosclerosis**
 IN **Thomas, Lawrence J.**
 PA AVANT Immunotherapeutics, Inc., USA
 SO U.S., 35 pp., Cont.-in-part of U.S. Ser. No. 802,967.
 CODEN: USXXAM
 DT Patent
 LA English
 IC ICM C12N018-88
 ICS A61K048-00
 NCL 435320100
 CC 15-2 (Immunochemistry)
 Section cross-reference(s): 3, 63

FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 6284533	B1	20010904	US 1998-171969	19981002
	WO 9741227	A1	19971106	WO 1997-US7294	19970501
	W: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
PRAI	US 1996-52983P	P	19960501		
	US 1997-802967	A2	19970221		
	WO 1997-US7294	W	19970501		
	US 1996-640713	A	19960501		
AB	A plasmid-based vaccine is provided herein based on the combination of DNA segments coding for one or more B cell epitopes of cholesteryl ester transfer protein (CETP) and one or more broad range helper T cell epitopes . Administration of the plasmids as a vaccine to a vertebrate subject provides an immune response to the subject's endogenous CETP and modulation of CETP activity, leading to prevention or reversal of various manifestations of heart disease. The vaccines provide an advantageous strategy for the prevention or treatment of atherosclerosis .				
ST	plasmid vaccine cholesteryl ester transfer protein; atherosclerosis autoantibody cholesteryl ester transfer protein				
IT	Histocompatibility antigens RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process) (MHC (major histocompatibility complex), class II; plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)				
IT	Antibodies RL: BSU (Biological study, unclassified); MFM (Metabolic formation); THU (Therapeutic use); BIOL (Biological study); FORM (Formation, nonpreparative); USES (Uses) (autoantibodies; plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)				
IT	Proteins, specific or class RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)				

(cholesterol ester-exchanging;
 plasmid-based vaccine encoding B cell epitope of
 cholesteryl ester transfer protein
 and helper T cell epitope of tetanus toxoid
 or diphtheria toxoid for treating
 atherosclerosis)

IT Toxoids

RL: BSU (Biological study, unclassified); PRP (Properties); THU
 (Therapeutic use); BIOL (Biological study); USES (Uses)
 (diphtheria; plasmid-based vaccine encoding B cell
 epitope of cholesteryl ester
 transfer protein and helper T cell epitope
 of tetanus toxoid or diphtheria
 toxoid for treating atherosclerosis)

IT B cell (lymphocyte)

(epitope; plasmid-based vaccine encoding B cell
 epitope of cholesteryl ester
 transfer protein and helper T cell epitope
 of tetanus toxoid or diphtheria
 toxoid for treating atherosclerosis)

IT T cell (lymphocyte)

(helper cell; plasmid-based vaccine encoding B cell
 epitope of cholesteryl ester
 transfer protein and helper T cell epitope
 of tetanus toxoid or diphtheria
 toxoid for treating atherosclerosis)

IT Influenza

(hemagglutinin; plasmid-based vaccine encoding B cell
 epitope of cholesteryl ester
 transfer protein and helper T cell epitope
 of tetanus toxoid or diphtheria
 toxoid for treating atherosclerosis)

IT Fissurella

(hemocyanin; plasmid-based vaccine encoding B cell
 epitope of cholesteryl ester
 transfer protein and helper T cell epitope
 of tetanus toxoid or diphtheria
 toxoid for treating atherosclerosis)

IT Lipoproteins

RL: BOC (Biological occurrence); BSU (Biological study, unclassified); THU
 (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (high-d., increase; plasmid-based vaccine encoding B cell
 epitope of cholesteryl ester
 transfer protein and helper T cell epitope
 of tetanus toxoid or diphtheria
 toxoid for treating atherosclerosis)

IT Gene, microbial

RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL
 (Biological study); USES (Uses)
 (immediate early, enhancer; plasmid-based vaccine encoding B
 cell epitope of cholesteryl ester
 transfer protein and helper T cell epitope
 of tetanus toxoid or diphtheria
 toxoid for treating atherosclerosis)

IT Enhancer (genetic element)

Promoter (genetic element)

RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL
 (Biological study); USES (Uses)
 (immediate early; plasmid-based vaccine encoding B cell
 epitope of cholesteryl ester
 transfer protein and helper T cell epitope
 of tetanus toxoid or diphtheria
 toxoid for treating atherosclerosis)

- IT Hemagglutinins
RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(influenza; plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)
- IT Drug delivery systems
(injections, i.m.; plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)
- IT Drug delivery systems
(intradermal; plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)
- IT Hemocyanins
RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(keyhole limpet; plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)
- IT Lipoproteins
RL: BSU (Biological study, unclassified); REM (Removal or disposal); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
(low-d., decrease; plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)
- IT Animal cell
(mammalian; plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)
- IT Infection
(measles, vaccine; plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)
- IT Lipids, processes
RL: REM (Removal or disposal); PROC (Process)
(neutral; plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)
- IT Salivary gland
(parotid, mumps, vaccine; plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)

- IT **Atherosclerosis**
DNA sequences
 Epitopes
 Heart, disease
 Molecular cloning
 Mycobacterium BCG
 Plasmids
 Protein sequences
 T cell (lymphocyte)
 Vaccines
 Vertebrate (Vertebrata)
 (plasmid-based vaccine encoding B cell epitope of
 cholesteryl ester transfer protein
 and helper T cell epitope of tetanus toxoid
 or diphtheria toxoid for treating
 atherosclerosis)
- IT DNA
RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified);
PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP
(Preparation); USES (Uses)
 (plasmid-based vaccine encoding B cell epitope of
 cholesteryl ester transfer protein
 and helper T cell epitope of tetanus toxoid
 or diphtheria toxoid for treating
 atherosclerosis)
- IT Fusion proteins (chimeric proteins)
RL: BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic
use); BIOL (Biological study); PREP (Preparation); USES (Uses)
 (plasmid-based vaccine encoding B cell epitope of
 cholesteryl ester transfer protein
 and helper T cell epitope of tetanus toxoid
 or diphtheria toxoid for treating
 atherosclerosis)
- IT TCR (T cell receptors)
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL
(Biological study); PROC (Process)
 (plasmid-based vaccine encoding B cell epitope of
 cholesteryl ester transfer protein
 and helper T cell epitope of tetanus toxoid
 or diphtheria toxoid for treating
 atherosclerosis)
- IT Invariant chain (class II antigen)
RL: BSU (Biological study, unclassified); PRP (Properties); THU
(Therapeutic use); BIOL (Biological study); USES (Uses)
 (plasmid-based vaccine encoding B cell epitope of
 cholesteryl ester transfer protein
 and helper T cell epitope of tetanus toxoid
 or diphtheria toxoid for treating
 atherosclerosis)
- IT Human herpesvirus 5
 (promoter; plasmid-based vaccine encoding B cell
 epitope of cholesteryl ester
 transfer protein and helper T cell epitope
 of tetanus toxoid or diphtheria
 toxoid for treating atherosclerosis)
- IT Tuberculin
RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL
(Biological study); USES (Uses)
 (purified protein deriv.; plasmid-based vaccine
 encoding B cell epitope of cholesteryl
 ester transfer protein and helper T cell
 epitope of tetanus toxoid or
 diphtheria toxoid for treating

- atherosclerosis)**
- IT **Toxoids**
 RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (tetanus; plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)
- IT **Pertussis**
Poliomyelitis
Rubella
Tuberculosis
 (vaccine; plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)
- IT **111274-16-9 122525-86-4**, Sialoglycoprotein **CETP**
 (rabbit clone .lambda.RCETP.2/.lambda.RCETP.1 protein moiety reduced) **199062-33-4**
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
 (amino acid sequence; plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)
- IT **199063-97-3 359035-23-7 359035-24-8**
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
 (nucleotide sequence; plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)
- IT **172273-70-0P 172273-71-1P 172273-72-2P 172273-73-3P 172273-74-4P 172273-75-5P 253309-86-3P 359016-11-8P**
 RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
 (plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)
- IT **119260-99-0 184882-09-5 359016-20-9 359016-22-1**
 RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (plasmid-based vaccine encoding B cell epitope of cholesteryl ester transfer protein and helper T cell epitope of tetanus toxoid or diphtheria toxoid for treating atherosclerosis)
- IT **359035-61-3, 6: PN: US6284533 SEQID: 6 unclaimed DNA 359035-62-4, 8: PN: US6284533 SEQID: 8 unclaimed DNA**
 RL: PRP (Properties)
 (unclaimed nucleotide sequence; plasmid-based vaccine for treating atherosclerosis)
- IT **88265-18-3, Toxin (Corynebacterium diphtheriae strain C7 reduced)**
 RL: PRP (Properties)
 (unclaimed protein sequence; plasmid-based vaccine for

treating atherosclerosis)
IT 126779-14-4
RL: PRP (Properties)
(unclaimed sequence; plasmid-based vaccine for treating
atherosclerosis)

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L42 ANSWER 3 OF 15 HCAPLUS COPYRIGHT 2002 ACS

AN 2000:709161 HCAPLUS

DN 134:40763

TI Vaccine-induced antibodies inhibit CETP activity in vivo and reduce aortic lesions in a rabbit model of

atherosclerosis

- AU **Rittershaus, Charles W.; Miller, David P.; Thomas, Lawrence J.; Picard, Michele D.; Honan, Christopher M.; Emmett, Constance D.; Pettey, Carolyn L.; Adari, Hedy; Hammond, Russell A.; Beattie, David T.; Callow, Allan D.; Marsh, Henry C.; Ryan, Una S.**
- CS AVANT Immunotherapeutics, Inc, Needham, MA, 02494, USA
- SO Arteriosclerosis, Thrombosis, and Vascular Biology (2000), 20(9), 2106-2112
- CODEN: ATVBFA; ISSN: 1079-5642
- PB Lippincott Williams & Wilkins
- DT Journal
- LA English
- CC 15-2 (Immunochemistry)
- Section cross-reference(s): 14
- AB Using a **vaccine** approach, the authors immunized New Zealand White rabbits with a peptide contg. a region of **cholesteryl ester transfer protein (CETP)** known to be required for neutral lipid **transfer** function. These rabbits had significantly reduced plasma **CETP** activity and an altered lipoprotein profile. In a **cholesterol**-fed rabbit model of **atherosclerosis**, the fraction of plasma **cholesterol** in HDL was 42% higher and the fraction of plasma **cholesterol** in LDL was 24% lower in the **CETP-vaccinated** group than in the control-**vaccinated** group. Moreover, the percentage of the aorta surface exhibiting **atherosclerotic** lesion was 39.6% smaller in the **CETP-vaccinated** rabbits than in controls. The data reported here demonstrate that **CETP** activity can be reduced in vivo by **vaccination** with a peptide derived from **CETP** and support the concept that inhibition of **CETP** activity in vivo can be anti-atherogenic. In addn., these studies suggest that **vaccination** against a self-antigen is a viable therapeutic strategy for disease management.
- ST **vaccine antibody cholesteryl ester transfer protein atherosclerosis**
- IT **Antiarteriosclerotics**
(**antiatherosclerotics**; **vaccination** with **cholesteryl ester transfer protein** alters lipoprotein profiles and ameliorates lesions in **atherosclerosis** model in relation to)
- IT **Proteins, specific or class**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(**cholesterol ester-exchanging**; **vaccination** with **cholesteryl ester transfer protein** alters lipoprotein profiles and ameliorates lesions in **atherosclerosis** model)
- IT **Lipoproteins**
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(high-d.; **vaccination** with **cholesteryl ester transfer protein** alters **cholesterol** content of)
- IT **Lipoproteins**
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(low-d.; **vaccination** with **cholesteryl ester transfer protein** alters **cholesterol** content of)
- IT **Vaccines**
(**synthetic**; **vaccination** with **cholesteryl ester transfer protein** alters lipoprotein profiles and ameliorates lesions in **atherosclerosis** model)

- IT Antibodies
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(to **cholesteryl ester transfer protein** in relation to immunotherapy of **atherosclerosis**)
- IT **Atherosclerosis**
(**vaccination with cholesteryl ester transfer protein** alters lipoprotein profiles and ameliorates lesions in **atherosclerosis** model)
- IT 57-88-5, **Cholesterol**, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(**vaccination with cholesteryl ester transfer protein** alters plasma lipoprotein content of)

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L42 ANSWER 4 OF 15 HCAPLUS COPYRIGHT 2002 ACS

AN 2000:588130 HCAPLUS

DN 134:36572

TI Current, new and future treatments in dyslipidemia and
atherosclerosis

AU Chong, Pang H.; Bachenheimer, Bonnie S.

CS College of Pharmacy, Cook County Hospital, University of Illinois,
Chicago, IL, USA

SO Drugs (2000), 60(1), 55-93

CODEN: DRUGAY; ISSN: 0012-6667

PB Adis International Ltd.

DT Journal; General Review

LA English

CC 1-0 (Pharmacology)

AB A review with 294 refs. The new therapeutic options available to clinicians treating dyslipidemia in the last decade have enabled effective treatment for many patients. The development of the HMG-CoA reductase inhibitors (statins) have been a major advance in that they possess multiple pharmacol. effects (pleiotropic effects) resulting in potent redns. of low d. lipoproteins (LDL) and prevention of the **atherosclerotic** process. More recently, the newer fibric acid derivs. have also reduced LDL to levels comparable to those achieved with statins, have reduced triglycerides, and gemfibrozil has been shown to increase high d. lipoprotein (HDL) levels. Nicotinic acid has been made tolerable with sustained-release formulations, and is still considered an excellent choice in elevating HDL **cholesterol** and is potentially effective in reducing lipoprotein(a) [Lp(a)] levels, an emerging risk factor for coronary heart disease (CHD). Furthermore, recent studies have reported pos. lipid-lowering effects from estrogen and/or progestogen in postmenopausal women but there are still conflicting reports on the use of these agents in dyslipidemia and in females at risk for CHD. In addn. to lowering lipid levels, these antihyperlipidemic agents may have directly or indirectly targeted thrombogenic, fibrinolytic and **atherosclerotic** processes which may have been unaccounted for in their overall success in clin. trails. Although LDL **cholesterol** is still the major target for therapy, it is likely that over the next several years other lipid/lipoprotein and nonlipid parameters will become more generally accepted targets for specific therapeutic interventions. Some important emerging lipid/lipoprotein parameters that have been assocd. with CHD include elevated triglyceride, oxidized LDL **cholesterol** and Lp(a) levels, and low HDL levels. The nonlipid parameters include elevated homocysteine and fibrinogen, and decreased endothelial-derived nitric oxide prodn. Among the new investigational agents are inhibitors of squalene synthetase, acylCoA: **cholesterol** acyltransferase, **cholesteryl ester transfer protein**, monocyte-macrophages and LDL **cholesterol** oxidn. Future applications may include thyromimetic therapy, **cholesterol** **vaccination**, somatic gene therapy, and recombinant **proteins**, in particular, apolipoproteins A-I and E. Non-LDL-related targets such as peroxisome proliferator-activating receptors, matrix metalloproteinases and scavenger receptor class B type I may also have clin. significance in the treatment of **atherosclerosis** in the near future. Before lipid-lowering therapy, dietary and lifestyle modification is and should be the first therapeutic intervention in the management of dyslipidemia. Although current recommendations from the US and Europe are slightly different,

adherence to these recommendations is essential to lower the risk of **atherosclerotic** vascular disease, more specifically CHD. New guidelines that are expected in the near future will encompass global opinions from the expert scientific community addressing the issue of target LDL goal (aggressive vs. moderate lowering) and the application of therapy for newer emerging CHD risk factors.

ST review antilipidemic agent dyslipidemia **atherosclerosis**

IT **Atherosclerosis**

Hypolipemic agents

(current, new and future treatments in dyslipidemia and **atherosclerosis**)

IT Lipids, biological studies

RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)

(dyslipidemia; current, new and future treatments in dyslipidemia and **atherosclerosis**)

RE.CNT 294 THERE ARE 294 CITED REFERENCES AVAILABLE FOR THIS RECORD

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TI Artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens

IN Wang, Chang Yi

PA United Biomedical Inc., USA

SO PCT Int. Appl., 129 pp.

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DT Patent

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IC ICM A61K045-00

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CC 15-2 (Immunochemistry)

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FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9966957	A2	19991229	WO 1999-US13975	19990621
	W:				
	AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
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	R:				
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PRAI	US 1998-100412	A2	19980620		
	WO 1999-US13975	W	19990621		
AB	Disclosed are immunogenic peptide compns. comprising a T helper epitope linked to a target antigenic site or a synthetic B cell epitope , and optionally with a immunostimulatory sequence for inducing T helper cell-mediated immune response and producing high level of antibodies directed against the "target antigen". The disclosed immunogenic peptide compns. are useful for contraception or control of hormone-dependent tumor (with LH-releasing hormone as target), growth promotion in farm animal (with somatostatin as target), treatment of allergy (with IgE as target), prevention of HIV infection (with CD4 receptor as target), prevention of foot-and-mouth disease (with FMDV capsid protein as target), treatment of malaria (with circumsporozoite antigen of Plasmodium falciparum as target), and treatment of arteriosclerosis (with cholesteryl ester transport protein as target).				
ST	T helper cell epitope antigen immunostimulant; vaccine T B cell epitope				

- IT Antigens
 RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (CS (circumsporozoite); artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)
- IT Immunoglobulins
 RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (E; artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)
- IT Proteins, specific or class
 RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (VPl; artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)
- IT Measles virus
 (antigen; artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)
- IT Allergy
Arteriosclerosis
Epitopes
 Foot-and-mouth disease virus
 Human immunodeficiency virus
 Human immunodeficiency virus 1
 Human immunodeficiency virus 2
 Immunotherapy
 Infection
 Livestock
 Malaria
 Neoplasm
 Pathogen
 Plasmodium falciparum
 Protein sequences
 Rat
 Simian immunodeficiency virus
Vaccines
 Veterinary medicine
 (artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)
- IT Antibodies
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)
- IT CD4 (antigen)
 Haptens
 RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)
- IT Antigens
 RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (autoantigens; artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)
- IT **Proteins**, specific or class
 RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (**cholesterol ester-exchanging**; artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)
- IT **Vaccines**
 (contraceptive; artificial T helper cell **epitopes** as immune

stimulators for synthetic peptide immunogens)

IT Cardiovascular system
(disease; artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)

IT Immunity
(disorder; artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)

IT B cell (lymphocyte)
(**epitope**; artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)

IT T cell (lymphocyte)
(helper cell, **epitope**; artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)

IT Fissurella
(hemocyanin; artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)

IT Antigens
RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(hepatitis B surface; artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)

IT CD4-positive T cell
(immune response mediated by; artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)

IT Castration
(immuno-; artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)

IT Proteins, specific or class
RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(invasins; artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)

IT Hemocyanins
RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(**keyhole limpet**; artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)

IT Antibodies
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(neutralizing; artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)

IT Antigens
RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(peptide; artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)

IT Growth, animal
(promotion; artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)

IT Immunostimulants
(sequence; artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)

IT Amino acids, biological studies
RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(stimulatory; artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)

IT Swine
(taint; artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)

IT Antigens
 RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (tumor-assocd.; artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)

IT Contraceptives
 (vaccines; artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)

IT 9034-40-6, LH-releasing hormone 40958-31-4, Somatostatin (sheep reduced)
 51110-01-1, Somatostatin 60556-70-9 92463-35-9 109489-04-5
 123202-49-3 130540-86-2 143201-20-1 150241-81-9 159347-89-4
 160824-82-8 184882-09-5 221550-30-7 232933-99-2 232934-00-8
 232934-04-2 232934-05-3 253196-73-5 253196-75-7 253196-76-8
 253196-77-9 253196-78-0 253196-79-1 253196-81-5 253196-82-6
 253196-84-8 253196-85-9 253196-86-0 253196-87-1 253196-88-2
 253196-89-3 253196-90-6 253196-91-7 253196-92-8 253196-94-0
 253196-95-1 253196-96-2 253196-97-3 253196-98-4 253196-99-5
 253197-01-2 253197-03-4 253197-05-6 253197-07-8 253197-09-0
 253197-11-4 253197-13-6 253197-15-8 253197-18-1 253197-20-5
 253197-22-7 253197-24-9 253197-26-1 253197-27-2 253197-28-3
 253197-29-4 253197-30-7 253197-31-8 253197-32-9 253273-61-9
 253273-62-0 253274-37-2 253309-62-5 253309-63-6 253309-64-7
 253309-65-8 253309-66-9 253309-67-0 253309-68-1 253309-69-2
 253309-70-5 253309-71-6 253309-72-7 253309-73-8 253309-74-9
 253309-75-0 253309-76-1 253309-77-2 253309-78-3 253309-79-4
 253309-80-7 253309-81-8 253309-82-9 253309-83-0 253309-84-1
 253309-85-2 253309-86-3 253309-87-4 253309-88-5 253309-89-6
 253332-84-2 253332-85-3 253332-86-4 253332-87-5 253332-88-6
 253332-89-7 253332-91-1 253332-93-3 253332-94-4 253332-95-5
 253332-99-9 253333-01-6 253333-14-1 253333-25-4 253333-32-3
 253333-33-4 253333-34-5 253333-37-8 253333-38-9 253333-39-0
 253333-40-3 253333-41-4 253335-01-2 253335-03-4 253335-04-5
 253335-24-9 253335-66-9 253335-70-5 253335-82-9 253335-96-5
 253336-07-1 253336-50-4 253336-54-8 253336-57-1 253336-62-8
 253336-67-3 253336-69-5 253336-70-8 253336-71-9 253336-73-1
 253336-75-3 253336-76-4 253336-81-1 253336-96-8 253336-97-9
 253336-99-1 253337-01-8 253337-02-9 253337-03-0 253337-04-1
 253337-05-2 253337-07-4 253337-15-4 253337-67-6 253602-91-4
 RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (artificial T helper cell **epitopes** as immune stimulators for synthetic peptide immunogens)

L42 ANSWER 6 OF 15 HCAPLUS COPYRIGHT 2002 ACS

AN 1999:454264 HCAPLUS

DN 131:83997

TI Assay for predicting the angiographic response to LDL cholesterol-lowering therapy in patients, and **cholesterol ester transfer protein** gene for the use thereof

IN Kuivenhoven, Jan Albert; Kastelein, Johannes Jacobus Pieter

PA Academisch Ziekenhuis bij de Universiteit van Amsterdam, Neth.

SO PCT Int. Appl., 25 pp.

CODEN: PIXXD2

DT Patent

LA English

IC ICM C12Q001-68

ICS C07K014-47

CC 3-3 (Biochemical Genetics)

Section cross-reference(s): 1, 13

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9935286	A2	19990715	WO 1999-EP150	19990106

W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

EP 939136 A1 19990901 EP 1998-200022 19980107

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO

CA 2317940 AA 19990715 CA 1999-2317940 19990106

AU 9922791 A1 19990726 AU 1999-22791 19990106

EP 1049805 A2 20001108 EP 1999-902536 19990106

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI

JP 2002504315 T2 20020212 JP 2000-527668 19990106

PRAI EP 1998-200022 A 19980107

WO 1999-EP150 W 19990106

AB The present invention relates to an assay for testing a genetic predisposition in patients with coronary artery disease (CAD) to respond to LDL **cholesterol**-lowering therapy. The method comprises screening for the presence (B1) or absence (B2) of a TaqI restriction site in intron 1 of both alleles of the **cholesterol ester transfer protein (CETP)** gene. A novel interaction was revealed between pravastatin treatment for CAD, this **CETP** gene polymorphism, and predicting the progression of coronary **atherosclerosis**. The response to pravastatin with regard to coronary **atherosclerosis** was greatest for homozygotes for B1B1 while B2B2 homozygotes did not appear to benefit from this treatment. Thus, according to the invention, the TaqIB polymorphism of **CETP** is found to be a genetic marker for identifying subjects who will or will not exhibit regression of coronary **atherosclerosis** in response to LDL **cholesterol**-lowering therapy, such as pravastatin.

ST therapy coronary **atherosclerosis cholesterol ester transfer protein** gene

IT Gene, animal

RL: ANT (Analyte); BOC (Biological occurrence); BSU (Biological study, unclassified); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(**CETP**; assay for predicting the angiog. response to LDL **cholesterol**-lowering therapy in patients, and **cholesterol ester transfer protein** gene for the use thereof)

IT Primers (nucleic acid)

RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(PCR; assay for predicting the angiog. response to LDL **cholesterol**-lowering therapy in coronary artery disease patients, and **cholesterol ester transfer protein** gene for the use thereof)

IT Genetic polymorphism

(TaqIB restriction site in intron 1 of **CETP** gene; assay for predicting the angiog. response to LDL **cholesterol**-lowering therapy in coronary artery disease patients, and **cholesterol ester transfer protein** gene for the use thereof)

IT DNA sequences

PCR (polymerase chain reaction)

Test kits

(assay for predicting the angiog. response to LDL **cholesterol**-lowering therapy in coronary artery disease patients, and **cholesterol ester transfer protein**)

- gene for the use thereof)
- IT Anticholesteremic agents
Susceptibility (genetic)
(assay for predicting the angiog. response to LDL cholesterol-lowering therapy in patients, and **cholesterol ester transfer protein** gene for the use thereof)
- IT **Proteins**, specific or class
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(**cholesterol ester-exchanging**, gene;
assay for predicting the angiog. response to LDL cholesterol-lowering therapy in patients, and **cholesterol ester transfer protein** gene for the use thereof)
- IT Artery, disease
(coronary; assay for predicting the angiog. response to LDL cholesterol-lowering therapy in coronary artery disease patients, and **cholesterol ester transfer protein** gene for the use thereof)
- IT Genetic markers
(use of **CETP** gene as; assay for predicting the angiog. response to LDL cholesterol-lowering therapy in coronary artery disease patients, and **cholesterol ester transfer protein** gene for the use thereof)
- IT 81093-37-0, Pravastatin
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(assay for predicting the angiog. response to LDL cholesterol-lowering therapy in coronary artery disease patients, and **cholesterol ester transfer protein** gene for the use thereof)
- IT 140027-68-5, DNA (human **CETP** gene fragment)
RL: ANT (Analyte); BOC (Biological occurrence); BSU (Biological study, unclassified); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(nucleotide sequence; assay for predicting the angiog. response to LDL cholesterol-lowering therapy in coronary artery disease patients, and **cholesterol ester transfer protein** gene for the use thereof)
- IT 229482-34-2 229482-35-3
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(primer; assay for predicting the angiog. response to LDL cholesterol-lowering therapy in coronary artery disease patients, and **cholesterol ester transfer protein** gene for the use thereof)

L42 ANSWER 7 OF 15 HCAPLUS COPYRIGHT 2002 ACS

AN 1999:282118 HCAPLUS

DN 130:310673

TI Xenogeneic **cholesteryl ester transfer protein (CETP)** for modulation of **CETP** activity in treatment of **atherosclerosis**

IN **Rittershaus, Charles W.; Thomas, Lawrence J.**

PA Avant Immunotherapeutics, Inc., USA

SO PCT Int. Appl., 62 pp.

CODEN: PIXXD2

DT Patent

LA English

IC ICM A61K039-00

ICS A61K039-39; A61K048-00; C07K014-47

CC 15-2 (Immunochemistry)

Section cross-reference(s): 3, 63

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PI	WO 9920302	A1	19990429	WO 1998-US22145	19981020

W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

CA 2307012 AA 19990429 CA 1998-2307012 19981020
AU 9911048 A1 19990510 AU 1999-11048 19981020
EP 1024825 A1 20000809 EP 1998-953762 19981020

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI

JP 2001520204 T2 20011030 JP 2000-516697 19981020

PRAI US 1997-954643 A2 19971020
WO 1998-US22145 W 19981020

AB Methods for modulating **cholesteryl ester transfer protein (CETP)** activity and the plasma levels of lipoproteins involved in heart disease involve administration of a non-endogenous **CETP** or a plasmid-based **vaccine** for expression of such non-endogenous **CETP** to elicit prodn. in a mammal of antibodies that recognize (bind to) the mammal's native (endogenous) **CETP**.

ST **cholesteryl ester transfer protein antiatherosclerotic** sequence

IT Promoter (genetic element)
RL: PEP (Physical, engineering or chemical process); PROC (Process) (Cytomegalovirus immediate early promoter/enhancer; xenogeneic **cholesteryl ester transfer protein (CETP)** for modulation of **CETP** activity in treatment of **atherosclerosis**)

IT Immunostimulants (adjuvants, Freund's; xenogeneic **cholesteryl ester transfer protein (CETP)** for modulation of **CETP** activity in treatment of **atherosclerosis**)

IT Immunostimulants (adjuvants, Ribi; xenogeneic **cholesteryl ester transfer protein (CETP)** for modulation of **CETP** activity in treatment of **atherosclerosis**)

IT Immunostimulants (adjuvants; xenogeneic **cholesteryl ester transfer protein (CETP)** for modulation of **CETP** activity in treatment of **atherosclerosis**)

IT **Antiartherosclerotics** (antiatherosclerotics; xenogeneic **cholesteryl ester transfer protein (CETP)** for modulation of **CETP** activity in treatment of **atherosclerosis**)

IT Antibodies
RL: BPN (Biosynthetic preparation); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PREP (Preparation); PROC (Process) (**cholesteryl ester transfer protein-binding**; xenogeneic **cholesteryl ester transfer protein (CETP)** for modulation of **CETP** activity in treatment of **atherosclerosis**)

IT Transport proteins
RL: BAC (Biological activity or effector, except adverse); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses) (**cholesteryl ester**; xenogeneic **cholesteryl ester transfer protein (CETP)** for

- modulation of CESTP activity in treatment of
atherosclerosis)
- IT Cytomegalovirus
(immediate early promoter/enhancer of; xenogeneic **cholesteryl ester transfer protein (CESTP)** for modulation of CESTP activity in treatment of **atherosclerosis)**
- IT Gene, microbial
RL: PEP (Physical, engineering or chemical process); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
(immediate early, promoter of; xenogeneic **cholesteryl ester transfer protein (CESTP)** for modulation of CESTP activity in treatment of **atherosclerosis)**
- IT Lipoproteins
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(low-d., **cholesterol** conjugates, metab. of; xenogeneic **cholesteryl ester transfer protein (CESTP)** for modulation of CESTP activity in treatment of **atherosclerosis)**
- IT Anticholesteremic agents
Genetic polymorphism
Immunostimulants
Monkey
Mouse
Plasmid vectors
Protein sequences
Rabbit
Vaccines
cDNA sequences
(xenogeneic **cholesteryl ester transfer protein (CESTP)** for modulation of CESTP activity in treatment of **atherosclerosis)**
- IT **223577-55-7P**
RL: BAC (Biological activity or effector, except adverse); BOC (Biological occurrence); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses)
(amino acid sequence; xenogeneic **cholesteryl ester transfer protein (CESTP)** for modulation of CESTP activity in treatment of **atherosclerosis)**
- IT **57-88-5D, Cholesterol, LDL** conjugates
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(metab. of; xenogeneic **cholesteryl ester transfer protein (CESTP)** for modulation of CESTP activity in treatment of **atherosclerosis)**
- IT **81669-55-8P, Cholesteryl ester transferase**
RL: BAC (Biological activity or effector, except adverse); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(xenogeneic **cholesteryl ester transfer protein (CESTP)** for modulation of CESTP activity in treatment of **atherosclerosis)**

RE.CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE

- (1) Hesler, C; J BIOL CHEM 1987, V262(5), P2275 HCAPLUS
- (2) Hesler, C; J BIOL CHEM 1988, V263(11), P5020 HCAPLUS
- (3) Immune Response Corp Inc; WO 9639168 A 1996 HCAPLUS
- (4) Smith, A; MEDICAL SCIENCE RESEARCH 1993, V21(24), P911 HCAPLUS
- (5) T Cell Sciences Inc; WO 9634888 A 1996 HCAPLUS

- (6) T Cell Sciences Inc; WO 9741227 A 1997 HCAPLUS
 (7) Thomas, L; FASEB JOURNAL 1998, V12(4), Pa310

L42 ANSWER 8 OF 15 HCAPLUS COPYRIGHT 2002 ACS
 AN 1999:223038 HCAPLUS
 DN 130:250711

TI Vector vaccines against cholesterol ester
 transfer protein for the treatment of
 atherosclerosis

IN Needleman, Philip; Glenn, Kevin

PA Monsanto Company, USA

SO PCT Int. Appl., 99 pp.

CODEN: PIXXD2

DT Patent

LA English

IC ICM C12N015-12

ICS A61K048-00

CC 14-5 (Mammalian Pathological Biochemistry)

FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9915655	A1	19990401	WO 1998-US19366	19980917
W:	AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
CA 2302778	AA	19990401	CA 1998-2302778	19980917
AU 9892317	A1	19990412	AU 1998-92317	19980917
EP 1015584	A1	20000705	EP 1998-944877	19980917
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, PT, IE, FI			
JP 2002516656	T2	20020611	JP 2000-512947	19980917
PRAI US 1997-934367	A	19970919		
WO 1998-US19366	W	19980917		

AB Expression vectors for manuf. of antigenic fragments of
 cholesteryl ester transfer protein (CETP) that can be used to inactivate the protein are described. The protein plays a key role in the transfer of cholesterol from HDL to LDL and VLDL and inhibition of CETP synthesis can be used to prevent LDL and VLDL formation in the prophylaxis of atherosclerosis. Immunogens, inocula, DNA segments, and recombinant DNA mol. vectors useful for carrying out the invention are also disclosed. The use of antigenic fragments of rabbit CETP to raise autoantibodies in rabbits is demonstrated. Antibodies to three such peptides cross-reacted with human CETP. Rabbits vaccinated with these antigens showed a .apprx.10% increase in serum HDL. Antigens were manufd. as fusion proteins with hepatitis B core antigens in Escherichia coli, in a baculovirus system, and in mammalian cell culture.

ST cholesteryl ester transfer protein
 antigen vaccine atherosclerosis; autoantibody
 cholesteryl ester transfer protein
 atherosclerosis HDL

IT Antibodies

RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (autoantibodies, to cholesteryl ester
 transfer protein; vector vaccines against
 cholesterol ester transfer protein
 for treatment of atherosclerosis)

IT Proteins, specific or class

- RL: ADV (Adverse effect, including toxicity); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(cholesterol ester-exchanging; vector
vaccines against cholesterol ester
transfer protein for treatment of
atherosclerosis)
- IT Toxoids
RL: BPN (Biosynthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(diphtheria, fusion proteins with cholesteryl
ester transfer protein, as antigens; vector
vaccines against cholesterol ester
transfer protein for treatment of
atherosclerosis)
- IT Antigens
RL: BPN (Biosynthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(hepatitis B core, fusion proteins with cholesteryl
ester transfer protein, as antigens; vector
vaccines against cholesterol ester
transfer protein for treatment of
atherosclerosis)
- IT Lipoproteins
RL: ADV (Adverse effect, including toxicity); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(high-d., prevention of cholesterol ester
transfer from; vector vaccines against
cholesterol ester transfer protein
for treatment of atherosclerosis)
- IT Lipoproteins
RL: ADV (Adverse effect, including toxicity); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(low-d., prevention of cholesterol ester
transfer to; vector vaccines against
cholesterol ester transfer protein
for treatment of atherosclerosis)
- IT Plasmid vectors
(pCMV-SPORT-HBcAg/CETP/HBcAg, vector vaccine
against cholesteryl ester transfer
protein; vector vaccines against cholesterol
ester transfer protein for treatment of
atherosclerosis)
- IT Plasmid vectors
(pcDNA1/AMP-HBcAg/CETP/HBcAg-1, vector vaccine
against cholesteryl ester transfer
protein; vector vaccines against cholesterol
ester transfer protein for treatment of
atherosclerosis)
- IT Plasmid vectors
(pcDNA1/AMP-HBcAg/CETP/HBcAg-2, vector vaccine
against cholesteryl ester transfer
protein; vector vaccines against cholesterol
ester transfer protein for treatment of
atherosclerosis)
- IT Vaccines
(synthetic; vector vaccines against cholesterol
ester transfer protein for treatment of
atherosclerosis)
- IT Toxoids
RL: BPN (Biosynthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)

(tetanus, fusion **proteins with cholesteryl ester transfer protein**, as antigens; vector **vaccines against cholesterol ester transfer protein** for treatment of **atherosclerosis**)

IT **Atherosclerosis**

(vector **vaccines against cholesterol ester transfer protein** for treatment of **atherosclerosis**)

IT **Lipoproteins**

RL: ADV (Adverse effect, including toxicity); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)

(very-low-d., prevention of **cholesterol ester transfer to; vector vaccines against cholesterol ester transfer protein** for treatment of **atherosclerosis**)

IT 123202-49-3 221550-30-7

RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(antigenic peptide of **cholesteryl ester transfer protein; vector vaccines against cholesterol ester transfer protein** for treatment of **atherosclerosis**)

IT 221550-31-8 221550-32-9 221550-33-0 221550-34-1 221550-35-2 221550-37-4

RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(antigenic peptide of rabbit **cholesteryl ester transfer protein; vector vaccines against cholesterol ester transfer protein** for treatment of **atherosclerosis**)

RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE

- (1) Evans, E; Journal of Lipid Research 1994, P1634
- (2) Gaynor, E; Atherosclerosis 1994, V110, P101
- (3) Melchior, E; Journal of Biological Chemistry 1995, V270, P21068
- (4) Melchior, E; Trends in Cardiovascular Medicine 1995, V5, P83
- (5) O'Brien, C; Molecular Medicine Today 1997, V3(6), P231 MEDLINE
- (6) Schodel, E; Journal of Virology 1992, V66, P106
- (7) Sugano, E; Journal of Biological Chemistry 1996, V271, P19080
- (8) T Cell Sciences Inc; WO 9634888 A 1996 HCAPLUS
- (9) Thomas, L; WO 9741227 A 1997 HCAPLUS
- (10) Thomas, L; Journal of Allergy and Clinical Immunology 1997, V99(1)

L42 ANSWER 9 OF 15 HCAPLUS COPYRIGHT 2002 ACS

AN 1999:127088 HCAPLUS

DN 130:192774

TI Cholesterylester transfer protein (CETP)-mRNA as target molecule in therapy of **atherosclerosis**, transcription constructs and drug screening

IN Budzinski, Ralph; Krist, Bernd; Mark, Michael; Mueller, Peter

PA Boehringer Ingelheim Pharma K.-G., Germany

SO Ger. Offen., 24 pp.

CODEN: GWXXBX

DT Patent

LA German

IC ICM C12N015-11

ICS C12N015-54; C07H021-00; C12Q001-68; A61K048-00

CC 3-3 (Biochemical Genetics)

Section cross-reference(s): 1

FAN.CNT 1

PATENT NO. KIND DATE APPLICATION NO. DATE

 PI DE 19731609 A1 19990218 DE 1997-19731609 19970723
 DE 19731609 C2 19991230
 AB The invention concerns the **cholesteryl ester transfer protein-mRNA (CETP-mRNA)** as target mol. for gene therapy; transcription constructs of the human **CETP** gene contg. 5'-non-translating regions with regulatory sequences; the usage of the transcription constructs for mol. recognition in high throughput screening of drugs for **atherosclerosis** therapy via the suppression of **CETP** gene expression; and therapeutic antisense oligonucleotides that inhibit the translation of **CETP**. **CETP** expression can be inhibited by antisense nucleotides including 3'-dideoxynucleosides, phosphorothioate, methoxy and methylphosphonate derivs; or non nucleotide mols. Drug screening is performed in a cell free system contg. reticulocyte lysate, aminoacids, radiolabeled leucin, synthesized **CETP-mRNA** and the antisense nucleotide; after incubation the presence of radiolabeled **CETP** is measured using monoclonal antibodies to **CETP**. Similar screening is performed when hepatoma cells are incubated with the therapeutic oligonucleotide; the **CETP** expression is measured using RIA. Binding of the prospective drug substance to the nucleic acid can also be tested in a BiaCore system using surface plasmon resonance detection .
 ST **cholesteryl ester transfer protein**
CETP mRNA gene therapy atherosclerosis
 IT **Proteins, specific or class**
 RL: BUU (Biological use, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (cholesterol ester-exchanging;
cholesteryl ester-transfer protein
 -mRNA (**CETP-mRNA**) as target mol. in therapy of
atherosclerosis, transcription constructs and drug screening)
 IT **Atherosclerosis**
 Drug screening
 Gene therapy
 Molecular recognition
 Transcriptional regulation
 (cholesteryl ester-transfer
protein-mRNA (CETP-mRNA) as target mol. in therapy of
atherosclerosis, transcription constructs and drug screening)
 IT Antisense oligonucleotides
 RL: BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (cholesteryl ester-transfer
protein-mRNA (CETP-mRNA) as target mol. in therapy of
atherosclerosis, transcription constructs and drug screening)
 IT mRNA
 RL: BUU (Biological use, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (cholesteryl ester-transfer
protein-mRNA (CETP-mRNA) as target mol. in therapy of
atherosclerosis, transcription constructs and drug screening)
 IT Translation, genetic
 (in reticulocyte lysates, for screening of antisense mRNAs;
cholesteryl ester-transfer protein
 -mRNA (**CETP-mRNA**) as target mol. in therapy of
atherosclerosis, transcription constructs and drug screening)
 IT Animal tissue culture
 (mammalian; **cholesteryl ester-transfer**
protein-mRNA (CETP-mRNA) as target mol. in therapy of
atherosclerosis, transcription constructs and drug screening)
 IT Antibodies
 RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)

- (monoclonal, for quantifying CETP prodn.; **cholesteryl ester-transfer protein-mRNA (CETP -mRNA)** as target mol. in therapy of **atherosclerosis**, transcription constructs and drug screening)
- IT Immunoassay
(radioimmunoassay, for quantifying CETP prodn.; **cholesteryl ester-transfer protein -mRNA (CETP-mRNA)** as target mol. in therapy of **atherosclerosis**, transcription constructs and drug screening)
- IT Surface plasmon
(resonance for detecting mol. recognition; **cholesteryl ester-transfer protein-mRNA (CETP -mRNA)** as target mol. in therapy of **atherosclerosis**, transcription constructs and drug screening)
- IT 220791-39-9
RL: BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antisense oligonucleotide binding to the 5'-non-translating region of the transcription construct at -11 to 4 position; **cholesteryl ester-transfer protein-mRNA (CETP -mRNA)** as target mol. in therapy of **atherosclerosis**)
- IT 220791-30-0
RL: BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antisense oligonucleotide binding to the 5'-non-translating region of the transcription construct at -18 to 2 position; **cholesteryl ester-transfer protein-mRNA (CETP -mRNA)** as target mol. in therapy of **atherosclerosis**)
- IT 220791-32-2
RL: BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antisense oligonucleotide binding to the 5'-non-translating region of the transcription construct at -23 to 15 position; **cholesteryl ester-transfer protein-mRNA (CETP -mRNA)** as target mol. in therapy of **atherosclerosis**)
- IT 220791-37-7
RL: BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antisense oligonucleotide binding to the 5'-non-translating region of the transcription construct at -24 to -13 position; **cholesteryl ester-transfer protein-mRNA (CETP -mRNA)** as target mol. in therapy of **atherosclerosis**)
- IT 220791-45-7
RL: BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antisense oligonucleotide binding to the 5'-non-translating region of the transcription construct at -26 to -12 position; **cholesteryl ester-transfer protein-mRNA (CETP -mRNA)** as target mol. in therapy of **atherosclerosis**)
- IT 220791-28-6
RL: BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antisense oligonucleotide binding to the 5'-non-translating region of the transcription construct at -26 to 3 position; **cholesteryl ester-transfer protein-mRNA (CETP -mRNA)** as target mol. in therapy of **atherosclerosis**)
- IT 220791-44-6
RL: BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antisense oligonucleotide binding to the 5'-non-translating region of the transcription construct at 1584 to 1594 position; **cholesteryl ester-transfer protein -mRNA (CETP-mRNA)** as target mol. in therapy of

- atherosclerosis)**
- IT 220791-41-3
 RL: BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (antisense oligonucleotide binding to the 5'-non-translating region of the transcription construct at 168 to 183 position; **cholesteryl ester-transfer protein-mRNA (CETP**
-mRNA) as target mol. in therapy of **atherosclerosis)**
- IT 220791-36-6
 RL: BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (antisense oligonucleotide binding to the 5'-non-translating region of the transcription construct at 568 to 584 position; **cholesteryl ester-transfer protein-mRNA (CETP**
-mRNA) as target mol. in therapy of **atherosclerosis)**
- IT 220735-58-0
 RL: BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (antisense oligonucleotide binding to the 5'-non-translating region of the transcription construct at 64 to 71 position; **cholesteryl ester-transfer protein-mRNA (CETP**
-mRNA) as target mol. in therapy of **atherosclerosis)**
- IT 220791-43-5
 RL: BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (antisense oligonucleotide binding to the 5'-non-translating region of the transcription construct at 743 to 760 position; **cholesteryl ester-transfer protein-mRNA (CETP**
-mRNA) as target mol. in therapy of **atherosclerosis)**
- IT 220791-46-8
 RL: BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (antisense oligonucleotide binding to the 5'-non-translating region of the transcription construct at 753 to 768 position; **cholesteryl ester-transfer protein-mRNA (CETP**
-mRNA) as target mol. in therapy of **atherosclerosis)**
- IT 220791-40-2
 RL: BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (antisense oligonucleotide binding to the 5'-non-translating region of the transcription construct at 9 to 24 position; **cholesteryl ester-transfer protein-mRNA (CETP**
-mRNA) as target mol. in therapy of **atherosclerosis)**
- IT 220791-48-0 220791-49-1 220791-50-4 220791-51-5
 RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
 (nucleotide sequence, 5'-non-translating region of human **CETP**
; cholesteryl ester-transfer
protein-mRNA (CETP-mRNA) as target mol. in therapy of
atherosclerosis, transcription constructs and drug screening)
- IT 220791-47-9
 RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
 (nucleotide sequence, coding for human **CETP**;
cholesteryl ester-transfer protein
-mRNA (CETP-mRNA) as target mol. in therapy of
atherosclerosis, transcription constructs and drug screening)

PA T Cell Sciences, Inc., USA; Thomas, Lawrence J.
 SO PCT Int. Appl., 66 pp.
 CODEN: PIXXD2

DT Patent

LA English

IC ICM C12N015-12

ICS A61K031-70

CC 1-7 (Pharmacology)

Section cross-reference(s): 3, 14, 63

FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	WO 9741227	A1	19971106	WO 1997-US7294	19970501	
	W:			AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM		
	RW:			GH, KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG		
	CA 2250428	AA	19971106	CA 1997-2250428	19970501	
	AU 9729946	A1	19971119	AU 1997-29946	19970501	
	AU 721729	B2	20000713			
	EP 914427	A1	19990512	EP 1997-924549	19970501	
	R:			AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI		
	JP 2001508760	T2	20010703	JP 1997-539202	19970501	
	US 6284533	B1	20010904	US 1998-171969	19981002	
PRAI	US 1996-640713	A	19960501			
	US 1997-802967	A2	19970221			
	US 1996-52983P	P	19960501			
	WO 1997-US7294	W	19970501			
AB	A plasmid-based vaccine is provided that is based on the combination of DNA segments coding for one or more B cell epitopes of CETP and one or more broad range helper T cell epitopes . Administration of the plasmids as a vaccine to a vertebrate subject provides an immune response to the subject's endogenous CETP and modulation of CETP activity, leading to prevention or reversal of various manifestations of heart disease. The vaccines provide an advantageous strategy for the prevention or treatment of atherosclerosis .					
ST	atherosclerosis plasmid vaccine treatment sequence CETP ; cholesteryl ester transfer protein vaccine atherosclerosis ; epitope CETP fusion protein vaccine atherosclerosis					
IT	B cell (lymphocyte) (CETP B-cell epitope ; plasmid vaccine for atherosclerosis treatment)					
IT	Protein motifs (CETP neutral lipid binding domain or neutral lipid transfer domain; plasmid vaccine for atherosclerosis treatment)					
IT	Fissurella (Keyhole limpet hemocyanin ; plasmid vaccine for atherosclerosis treatment)					
IT	Hemocyanins RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses) (Keyhole limpet hemocyanin ; helper T cell epitope derived from; plasmid vaccine for atherosclerosis treatment)					
IT	Antiarteriosclerotics					

- (**antiatherosclerotics, vaccine as; plasmid vaccine for atherosclerosis treatment**)
- IT Antibodies
 RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL (Biological study); FORM (Formation, nonpreparative)
 (autoantibodies, **CETP** induces formation of autoantibodies which inhibit **CETP** activity; plasmid **vaccine** for **atherosclerosis treatment**)
- IT Lipids, biological studies
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (blood, **CETP** domains for binding and transfer of; plasmid **vaccine** for **atherosclerosis treatment**)
- IT Proteins, specific or class
 RL: BPN (Biosynthetic preparation); BPR (Biological process); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); PROC (Process); USES (Uses)
 (**cholesterol ester-exchanging, CETP** induces formation of autoantibodies which inhibit **CETP** activity; plasmid **vaccine** for **atherosclerosis treatment**)
- IT Toxins
 RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (**diphtheria, helper T cell epitope** derived from; plasmid **vaccine** for **atherosclerosis treatment**)
- IT Cardiovascular system
 (disease, method for treatment of; plasmid **vaccine** for **atherosclerosis treatment**)
- IT Tuberculin
 RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (helper T cell **epitope** derived from; plasmid **vaccine** for **atherosclerosis treatment**)
- IT Antigens
 RL: BPN (Biosynthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
 (helper T cell **epitope**; plasmid **vaccine** for **atherosclerosis treatment**)
- IT T cell (lymphocyte)
 (helper cell, **vaccine** comprising **CETP** B cell **epitope** and broad range helper T cell **epitopes**; plasmid **vaccine** for **atherosclerosis treatment**)
- IT Lipoproteins
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (high-d., method to reducing circulating ratio of HDL and LDL and VLDL to cholesterol; plasmid **vaccine** for **atherosclerosis treatment**)
- IT Lipoproteins
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (low-d., method to reducing circulating ratio of HDL and LDL and VLDL to cholesterol; plasmid **vaccine** for **atherosclerosis treatment**)
- IT Animal cell
 (mammalian, promoter for transcription in mammalian cells; plasmid **vaccine** for **atherosclerosis treatment**)
- IT Heart, disease
 (method for treatment of; plasmid **vaccine** for **atherosclerosis treatment**)
- IT Salivary gland
 (parotid, diseases, **mumps, vaccines**; helper T cell **epitope** derived from; plasmid **vaccine** for

- atherosclerosis treatment)**
- IT Salivary gland
 - (parotid, **mumps**, **vaccines**; helper T cell
 - epitope** derived from; plasmid **vaccine** for
 - atherosclerosis treatment)**
- IT **Atherosclerosis**
 - Plasmid vectors
 - Protein sequences
 - Vertebrate (Vertebrata)
 - cDNA sequences
 - (plasmid **vaccine** for **atherosclerosis treatment)**
- IT Transcription, genetic
 - (promoter for transcription in mammalian cells; plasmid **vaccine**
 - for **atherosclerosis treatment)**
- IT Promoter (genetic element)
 - RL: BUU (Biological use, unclassified); BIOL (Biological study); USES
 - (Uses)
 - (promoter for transcription in mammalian cells; plasmid **vaccine**
 - for **atherosclerosis treatment)**
- IT **Vaccines**
 - RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL
 - (Biological study); USES (Uses)
 - (synthetic, rubella and **mumps** and measles; helper T cell
 - epitope** derived from; plasmid **vaccine** for
 - atherosclerosis treatment)**
- IT **Toxoids**
 - RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES
 - (Uses)
 - (**tetanus**, helper T cell **epitope** derived from;
 - plasmid **vaccine** for **atherosclerosis treatment)**
- IT **Epitopes**
 - (**vaccine** comprising CESTP B cell **epitope**
 - and broad range helper T cell **epitopes**; plasmid
 - vaccine** for **atherosclerosis treatment)**
- IT Fusion proteins (chimeric proteins)
 - RL: BPN (Biosynthetic preparation); THU (Therapeutic use); BIOL
 - (Biological study); PREP (Preparation); USES (Uses)
 - (**vaccine** comprising CESTP B cell **epitope**
 - and broad range helper T cell **epitopes**; plasmid
 - vaccine** for **atherosclerosis treatment)**
- IT Pertussis
 - (**vaccine**; helper T cell **epitope** derived from;
 - plasmid **vaccine** for **atherosclerosis treatment)**
- IT Rubella
 - (**vaccines**; helper T cell **epitope** derived from;
 - plasmid **vaccine** for **atherosclerosis treatment)**
- IT Lipoproteins
 - RL: BOC (Biological occurrence); BSU (Biological study, unclassified); THU
 - (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 - (very-low-d., method to reducing circulating ratio of HDL and LDL and
 - VLDL to cholesterol; plasmid **vaccine** for
 - atherosclerosis treatment)**
- IT 111274-16-9P, Cholesteryl ester
 - transfer protein** (human clone .lambda.CESTP
 - .10/.lambda.CESTP.307) 199062-23-2P
 - 199062-31-2P
 - RL: BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic
 - use); BIOL (Biological study); PREP (Preparation); USES (Uses)
 - (amino acid sequence; plasmid **vaccine** for
 - atherosclerosis treatment)**
- IT 199062-11-8 199062-33-4
 - RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES
 - (Uses)

(amino acid sequence; plasmid **vaccine** for **atherosclerosis** treatment)

IT 57-88-5, Cholesterol, biological studies
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
 (method to reducing circulating ratio of HDL and LDL and VLDL to cholesterol; plasmid **vaccine** for **atherosclerosis** treatment)

IT 111274-10-3P, DNA (human clone .lambda.CETP.10/.lambda.CETP.307 **cholesterol ester-exchanging protein** cDNA) 199063-45-1P 199063-46-2P 199063-97-3P 199063-98-4P 199063-99-5P
 RL: BPN (Biosynthetic preparation); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
 (nucleotide sequence; plasmid **vaccine** for **atherosclerosis** treatment)

L42 ANSWER 11 OF 15 HCAPLUS COPYRIGHT 2002 ACS
 AN 1997:97190 HCAPLUS
 DN 126:99323
 TI Immunostimulation method for increasing HDL **cholesterol** level using **cholesterol ester transfer protein** (CETP) or fragments thereof
 IN Kwoh, Deborah Y.; Brostoff, Steven W.; Carlo, Dennis J.
 PA The Immune Response Corporation, USA
 SO PCT Int. Appl., 25 pp.
 CODEN: PIXXD2
 DT Patent
 LA English
 IC ICM A61K038-17
 CC 1-10 (Pharmacology)
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	WO 9639168	A1	19961212	WO 1996-US9143	19960605	<--
	W:	AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG				
	RW:	KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN				
	CA 2223177	AA	19961212	CA 1996-2223177	19960605	<--
	AU 9660912	A1	19961224	AU 1996-60912	19960605	<--
	AU 715410	B2	20000203			
	EP 831881	A1	19980401	EP 1996-918201	19960605	<--
	R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	JP 11507910	T2	19990713	JP 1996-501533	19960605	<--
PRAI	US 1995-482454		19950606	<--		
	WO 1996-US9143		19960605			
AB	A method is provided for increasing HDL cholesterol in a mammal by stimulating an immune response that inhibits the function of CETP . Such an immune response can be induced by immunizing with CETP or fragments of CETP (together termed CETP peptides) which contain an epitope capable of stimulating such a response. The peptides can be conjugated to a carrier, e.g. KLH or ovalbumin, in order to increase immunogenicity. Adjuvants can also be administered.					
ST	CETP peptide immunostimulation HDL cholesterol					
IT	Antigens Peptides, biological studies RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses) (CETP immunogenic epitopes ; immunostimulation					

- method for increasing HDL **cholesterol** with **cholesterol ester transfer protein (CETP)** or fragments)
- IT Antiarteriosclerotics
(antiatherosclerotics; immunostimulation method for increasing HDL **cholesterol** with **cholesterol ester transfer protein (CETP)** or fragments)
- IT **Proteins**, specific or class
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(**cholesterol ester-exchanging, CETP** immunogenic **epitope**; immunostimulation method for increasing HDL **cholesterol** with **cholesterol ester transfer protein (CETP)** or fragments)
- IT Hemocyanins
Ovalbumin
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(conjugates, with **CETP** peptides; immunostimulation method for increasing HDL **cholesterol** with **cholesterol ester transfer protein (CETP)** or fragments)
- IT **Toxoids**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(**diphtheria**, conjugates with **CETP** peptides; immunostimulation method for increasing HDL **cholesterol** with **cholesterol ester transfer protein (CETP)** or fragments)
- IT B cell (lymphocyte)
(**epitope**; immunostimulation method for increasing HDL **cholesterol** with **cholesterol ester transfer protein (CETP)** or fragments)
- IT Lipoproteins
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(high-d.; immunostimulation method for increasing HDL **cholesterol** with **cholesterol ester transfer protein (CETP)** or fragments)
- IT Immunostimulants
(immunostimulation method for increasing HDL **cholesterol** with **cholesterol ester transfer protein (CETP)** or fragments)
- IT **Toxoids**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(**tetanus**, conjugates with **CETP** peptides; immunostimulation method for increasing HDL **cholesterol** with **cholesterol ester transfer protein (CETP)** or fragments)
- IT Antibodies
RL: BPN (Biosynthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(to **CETP**; immunostimulation method for increasing HDL **cholesterol** with **cholesterol ester transfer protein (CETP)** or fragments)
- IT 155381-67-2D, conjugates
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(immunostimulation method for increasing HDL **cholesterol** with **cholesterol ester transfer protein**)

(CETP) or fragments)
 IT 57-88-5, **Cholesterol**, biological studies
 RL: BOC (Biological occurrence); BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); OCCU (Occurrence); PROC (Process)
 (immunostimulation method for increasing HDL **cholesterol** with **cholesterol ester transfer protein** (CETP) or fragments)
 IT 125377-61-9 125377-61-9D, conjugates 155381-67-2 186002-92-6 186002-92-6D, conjugates
 RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (immunostimulation method for increasing HDL **cholesterol** with **cholesterol ester transfer protein** (CETP) or fragments)

L42 ANSWER 12 OF 15 HCAPLUS COPYRIGHT 2002 ACS

AN 1997:12606 HCAPLUS

DN 126:46315

TI Modulation of **cholesteryl ester transfer protein** (CETP) activity

IN Rittershaus, Charles W.; Thomas, Lawrence J.

PA T Cell Sciences, Inc., USA; Rittershaus, Charles W.; Thomas, Lawrence J.

SO PCT Int. Appl., 81 pp.

CODEN: PIXXD2

DT Patent

LA English

IC ICM C07K014-775

ICS C07K014-47; A61K038-17; A61K039-00

CC 15-2 (Immunochemistry)

Section cross-reference(s): 14

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	WO 9634888	A1	19961107	WO 1996-US6147	19960501	<--
	W:	AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK				
	RW:	KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	CA 2219795	AA	19961107	CA 1996-2219795	19960501	<--
	AU 9656360	A1	19961121	AU 1996-56360	19960501	<--
	AU 707752	B2	19990722			
	EP 827509	A1	19980311	EP 1996-913320	19960501	<--
	R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	JP 11504635	T2	19990427	JP 1996-533487	19960501	<--
	US 2002042364	A1	20020411	US 2001-943548	20010830	<--
PRAI	US 1995-432483	A	19950501			<--
	WO 1996-US6147	W	19960501			
	US 1997-945289	A3	19971017			
AB	This invention relates to peptides comprising a helper T cell epitope portion and a B cell epitope portion for eliciting an immune response against endogenous cholesteryl ester transfer protein (CETP) activity, to prevent or treat cardiovascular disease, such as atherosclerosis. The T helper T cell epitope may be derived from an antigenic peptide selected from the group consisting tetanus toxoid, diphtheria toxoid, pertussis vaccine, Bacille Calmette-Guerin, polio vaccine, measles vaccine, mumps vaccine, rubella vaccine, purified					

- protein deriv. of tuberculin, keyhole
limpet hemocyanin, hsp70 and combination thereof.
- ST cholesteryl ester transfer protein
antigen vaccine; atherosclerosis helper T cell
epitope vaccine
- IT Heat-shock proteins
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(HSP 70; peptide vaccine comprising helper T cell
epitope and B cell epitope that inhibits
cholesteryl ester transfer protein
activity for treating atherosclerosis)
- IT Proteins, specific or class
RL: ADV (Adverse effect, including toxicity); BSU (Biological study,
unclassified); BIOL (Biological study)
(cholesterol ester-exchanging; peptide
vaccine comprising helper T cell epitope and B cell
epitope that inhibits cholesteryl ester
transfer protein activity for treating
atherosclerosis)
- IT Toxoids
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(diphtheria; peptide vaccine comprising helper T
cell epitope and B cell epitope that inhibits
cholesteryl ester transfer protein
activity for treating atherosclerosis)
- IT Cardiovascular system
(disease; peptide vaccine comprising helper T cell
epitope and B cell epitope that inhibits
cholesteryl ester transfer protein
activity for treating atherosclerosis)
- IT B cell (lymphocyte)
(epitope; peptide vaccine comprising helper T cell
epitope and B cell epitope that inhibits
cholesteryl ester transfer protein
activity for treating atherosclerosis)
- IT T cell (lymphocyte)
(helper cell, epitope; peptide vaccine comprising
helper T cell epitope and B cell epitope that
inhibits cholesteryl ester transfer
protein activity for treating atherosclerosis)
- IT Lipoproteins
RL: ADV (Adverse effect, including toxicity); BOC (Biological occurrence);
BSU (Biological study, unclassified); BIOL (Biological study); OCCU
(Occurrence)
(high-d.; peptide vaccine comprising helper T cell
epitope and B cell epitope that inhibits
cholesteryl ester transfer protein
activity for treating atherosclerosis)
- IT Hemocyanins
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(keyhole limpet; peptide vaccine
comprising helper T cell epitope and B cell epitope
that inhibits cholesteryl ester transfer
protein activity for treating atherosclerosis)
- IT Lipoproteins
RL: ADV (Adverse effect, including toxicity); BOC (Biological occurrence);
BSU (Biological study, unclassified); BIOL (Biological study); OCCU
(Occurrence)
(low-d.; peptide vaccine comprising helper T cell
epitope and B cell epitope that inhibits
cholesteryl ester transfer protein
activity for treating atherosclerosis)
- IT Infection

- (measles, vaccine; peptide vaccine comprising helper T cell epitope and B cell epitope that inhibits cholesteryl ester transfer protein activity for treating atherosclerosis)
- IT Lipids, biological studies
 RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
 (neutral, binding; peptide vaccine comprising helper T cell epitope and B cell epitope that inhibits cholesteryl ester transfer protein activity for treating atherosclerosis)
- IT Salivary gland
 (parotid, diseases, mumps, vaccine; peptide vaccine comprising helper T cell epitope and B cell epitope that inhibits cholesteryl ester transfer protein activity for treating atherosclerosis)
- IT Salivary gland
 (parotid, mumps, vaccine; peptide vaccine comprising helper T cell epitope and B cell epitope that inhibits cholesteryl ester transfer protein activity for treating atherosclerosis)
- IT Atherosclerosis
 Hypercholesterolemia
 Mycobacterium BCG
 Protein sequences
 (peptide vaccine comprising helper T cell epitope and B cell epitope that inhibits cholesteryl ester transfer protein activity for treating atherosclerosis)
- IT Antibodies
 RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (peptide vaccine comprising helper T cell epitope and B cell epitope that inhibits cholesteryl ester transfer protein activity for treating atherosclerosis)
- IT Vaccines
 (peptide; peptide vaccine comprising helper T cell epitope and B cell epitope that inhibits cholesteryl ester transfer protein activity for treating atherosclerosis)
- IT Toxoids
 RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (pertussis; peptide vaccine comprising helper T cell epitope and B cell epitope that inhibits cholesteryl ester transfer protein activity for treating atherosclerosis)
- IT Tuberculin
 RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (protein deriv.; peptide vaccine comprising helper T cell epitope and B cell epitope that inhibits cholesteryl ester transfer protein activity for treating atherosclerosis)
- IT Toxoids
 RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (tetanus; peptide vaccine comprising helper T cell epitope and B cell epitope that inhibits cholesteryl ester transfer protein activity for treating atherosclerosis)
- IT Poliomyelitis
 Rubella
 (vaccine; peptide vaccine comprising helper T cell epitope and B cell epitope that inhibits

cholesteryl ester transfer protein
activity for treating **atherosclerosis**)

IT Peptides, biological studies
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(**vaccine**; peptide **vaccine** comprising helper T cell
epitope and B cell **epitope** that inhibits
cholesteryl ester transfer protein
activity for treating **atherosclerosis**)

IT Lipoproteins
RL: ADV (Adverse effect, including toxicity); BOC (Biological occurrence);
BSU (Biological study, unclassified); BIOL (Biological study); OCCU
(Occurrence)
(very-low-d.; peptide **vaccine** comprising helper T cell
epitope and B cell **epitope** that inhibits
cholesteryl ester transfer protein
activity for treating **atherosclerosis**)

IT 57-88-5, **Cholesterol**, biological studies
RL: ADV (Adverse effect, including toxicity); BOC (Biological occurrence);
BSU (Biological study, unclassified); BIOL (Biological study); OCCU
(Occurrence)
(peptide **vaccine** comprising helper T cell **epitope**
and B cell **epitope** that inhibits **cholesteryl**
ester transfer protein activity for
treating **atherosclerosis**)

IT 111274-16-9, **Protein** (human clone .lambda.CETP
.10/.lambda.CETP.307 **cholesterol ester-**
exchanging reduced)
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP
(Properties); THU (Therapeutic use); BIOL (Biological study); PROC
(Process); USES (Uses)
(peptide **vaccine** comprising helper T cell **epitope**
and B cell **epitope** that inhibits **cholesteryl**
ester transfer protein activity for
treating **atherosclerosis**)

IT 80295-45-0, Complement C3d
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(peptide **vaccine** comprising helper T cell **epitope**
and B cell **epitope** that inhibits **cholesteryl**
ester transfer protein activity for
treating **atherosclerosis**)

IT 119260-99-0 123202-49-3 126779-14-4 184882-08-4 184882-09-5
184882-10-8 184882-11-9
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(peptide **vaccine** comprising helper T cell **epitope**
and B cell **epitope** that inhibits **cholesteryl**
ester transfer protein activity for
treating **atherosclerosis**)

L42 ANSWER 13 OF 15 HCAPLUS COPYRIGHT 2002 ACS
AN 1995:541414 HCAPLUS
DN 122:299055
TI **Cholesteryl ester transfer protein**
inhibitor polypeptide, antibodies against the synthetic polypeptide and
prophylactic and therapeutic anti-**atherosclerosis** treatments
IN Kushwaha, Rampratap S.; McGill, Henry C., Jr.; Kanda, Patrick
PA Southwest Foundation for Biomedical Research, USA
SO PCT Int. Appl., 47 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C07K014-435
ICS C07K016-18; A61K038-17
CC 63-3 (Pharmaceuticals)

FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9504755	A1	19950216	WO 1994-US8624	19940802 <--
	W: AU, CA, JP, KR				
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	CA 2145767	AA	19950216	CA 1994-2145767	19940802 <--
	AU 9475526	A1	19950228	AU 1994-75526	19940802 <--
	AU 683295	B2	19971106		
	EP 664813	A1	19950802	EP 1994-925711	19940802 <--
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
	JP 08502525	T2	19960319	JP 1994-506464	19940802 <--
	US 5519001	A	19960521	US 1995-394066	19950224 <--
PRAI	US 1993-102160		19930804	<--	
	US 1991-811049		19911219	<--	
	WO 1994-US8624		19940802	<--	
AB	A polypeptide and analogs thereof inhibit cholesteryl ester transfer protein (CETP) . An anti- atherosclerosis compn. comprises an anti- atherosclerosis effective amt. of the polypeptide and a pharmaceutically acceptable carrier. An anti- atherosclerosis kit comprises in sep. sterile containers at least one unit of the compn. contg. the polypeptide, one syringe, and one needle. An antibody has specificity for the polypeptide of the invention, the baboon CETP 4-kDa polypeptide inhibitor, the 1-36 amino acid N-terminal fragment of apoC-I, modified apo A-I (mol. wt. 31 kDa), or modified apoE (mol. wt. 41 kDa). A method of preventing atherosclerosis in a mammal being predisposed to that condition comprises administering to the mammal a prophylactically effective amt. of the polypeptide of the invention, and a method of treating a mammal afflicted with atherosclerosis comprises the administration of a therapeutically effective amt. of the polypeptide. The peptides consist of the N-terminal 36 residues of baboon apoC-I, a synthetic peptide adding an N-terminal Ala-Pro dipeptide, the human 38-residue analog, and active fragments and substituted analogs.				
ST	atherosclerosis inhibitor peptide; cholesteryl ester transfer protein inhibitor peptide				
IT	Peptides, biological studies				
	RL: BAC (Biological activity or effector, except adverse); THU (Therapeutic use); BIOL (Biological study); USES (Uses)				
	(cholesterol ester-exchanging protein-inhibiting; cholesteryl ester transfer protein inhibitor polypeptide, antibodies against the synthetic polypeptide and prophylactic and therapeutic anti- atherosclerosis treatments)				
IT	Baboon				
	(cholesteryl ester transfer protein inhibitor polypeptide, antibodies against the synthetic polypeptide and prophylactic and therapeutic anti- atherosclerosis treatments)				
IT	Antibodies				
	RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)				
	(cholesteryl ester transfer protein inhibitor polypeptide, antibodies against the synthetic polypeptide and prophylactic and therapeutic anti- atherosclerosis treatments)				
IT	Protein sequences				
	(of cholesteryl ester transfer protein inhibitor polypeptide from baboon and human)				
IT	Antiarteriosclerotics				
	(antiatherosclerotics, cholesteryl ester transfer protein inhibitor polypeptide, antibodies against the synthetic polypeptide and prophylactic and therapeutic				

anti-atherosclerosis treatments)

IT Lipoproteins
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(apo-, A-I, **cholesteryl ester transfer protein** inhibitor polypeptide, antibodies against the synthetic polypeptide and prophylactic and therapeutic anti-**atherosclerosis** treatments)

IT Lipoproteins
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(apo-, C-I, **cholesteryl ester transfer protein** inhibitor polypeptide, antibodies against the synthetic polypeptide and prophylactic and therapeutic anti-**atherosclerosis** treatments)

IT Lipoproteins
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(apo-, E, **cholesteryl ester transfer protein** inhibitor polypeptide, antibodies against the synthetic polypeptide and prophylactic and therapeutic anti-**atherosclerosis** treatments)

IT **Proteins**, specific or class
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(**cholesterol ester-exchanging, cholesteryl ester transfer protein** inhibitor polypeptide, antibodies against the synthetic polypeptide and prophylactic and therapeutic anti-**atherosclerosis** treatments)

IT 150027-05-7 161051-55-4 163062-88-2
RL: BAC (Biological activity or effector, except adverse); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(**cholesteryl ester transfer protein** inhibitor polypeptide, antibodies against the synthetic polypeptide and prophylactic and therapeutic anti-**atherosclerosis** treatments)

L42 ANSWER 14 OF 15 HCAPLUS COPYRIGHT 2002 ACS

AN 1993:552092 HCAPLUS

DN 119:152092

TI **Cholesteryl ester transfer protein**
(**CETP**) inhibitor polypeptide, antibodies against the synthetic polypeptide, and prophylactic and therapeutic anti-**atherosclerosis** treatments

IN Kushwaha, Rampratap; Born, Kathleen; McGill, Henry C., Jr.; Kanda, Patrick; Dunham, Raymond G.

PA Southwest Foundation for Biomedical Research, USA

SO PCT Int. Appl., 46 pp.

CODEN: PIXXD2

DT Patent

LA English

IC ICM A61K037-00

ICS A61K037-02; A61K037-64; A61K037-04

CC 1-8 (Pharmacology)

Section cross-reference(s): 15

FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9311782	A1	19930624	WO 1992-US10846	19921215 <--
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	EP 618803	A1	19941012	EP 1993-901360	19921215 <--
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
	US 5512548	A	19960430	US 1994-193515	19940208 <--
	US 5519001	A	19960521	US 1995-394066	19950224 <--
PRAI	US 1991-811049		19911219	<--	
	WO 1992-US10846		19921215	<--	
	US 1993-102160		19930804	<--	

- AB A polypeptide and analogs thereof inhibit **CETP**. Also disclosed are methods using the polypeptide of the invention for prevention and treatment of **atherosclerosis**, an **anti-atherosclerosis** compn., and an **anti-atherosclerosis** kit. An antibody is disclosed which has specificity for the polypeptide of the invention, the baboon **CETP** 4 kDa polypeptide inhibitor, the 1-36 apo C-I amino-terminal fragment, modified apo A-I (31 kDa mol. wt.), or modified apo E (41 kDa mol. wt.). Sequences of polypeptide inhibitors are included. Detection of the **CETP** inhibitor peptide in the plasma of baboons with a high HDL1 phenotype is described, as is **CETP** inhibition by various peptide fragments.
- ST **cholesteryl ester transfer protein**
inhibitor peptide; antibody **cholesteryl ester transfer protein** inhibitor
- IT Antibodies
RL: BIOL (Biological study)
(to **cholesteryl ester transfer protein** inhibitor peptides)
- IT Sialoglycoproteins
RL: BIOL (Biological study)
(**CETP** (**cholesterol ester-transfer protein**), peptide inhibitor of)
- IT **Antiartherosclerotics**
(**antiatherosclerotics**, **cholesteryl ester transfer protein** inhibitor peptides)
- IT Lipoproteins
RL: BIOL (Biological study)
(apo-, A-I, modified, antibody specific for **cholesteryl ester transfer protein** inhibitor peptide reactive with)
- IT Lipoproteins
RL: BIOL (Biological study)
(apo-, C-I, antibody specific for **cholesteryl ester transfer protein** inhibitor peptide reactive with)
- IT Lipoproteins
RL: BIOL (Biological study)
(apo-, E, modified, antibody specific for **cholesteryl ester transfer protein** inhibitor peptide reactive with)
- IT Lipoproteins
RL: BIOL (Biological study)
(high-d., 1, **cholesteryl ester transfer protein** inhibitory peptide in baboon with high)
- IT 149930-28-9 149930-29-0 149930-30-3 150027-05-7
RL: BIOL (Biological study)
(**cholesteryl ester transfer protein** inhibitor peptide amino acid sequence)
- IT 150027-05-7D, analogs
RL: BIOL (Biological study)
(**cholesteryl ester transfer protein** inhibitor peptides)
- L42 ANSWER 15 OF 15 HCAPLUS COPYRIGHT 2002 ACS
- AN 1993:36917 HCAPLUS
- DN 118:36917
- TI Molecular cloning, sequence, and expression of cynomolgus monkey **cholesteryl ester transfer protein**.
Inverse correlation between hepatic **cholesteryl ester transfer protein** mRNA levels and plasma high density lipoprotein levels
- AU Pape, Michael E.; Rehberg, Edward F.; Marotti, Keith R.; Melchior, George W.
- CS Upjohn Co., Kalamazoo, MI, 49001, USA

- SO Arterioscler. Thromb. (1991), 11(6), 1759-71
CODEN: ARTTE5; ISSN: 1049-8834
- DT Journal
- LA English
- CC 14-5 (Mammalian Pathological Biochemistry)
Section cross-reference(s): 3, 6
- AB A cDNA clone contg. the coding region for cynomolgus monkey **cholesteryl ester transfer protein (CETP)** was isolated by the polymerase chain reaction with primers based on the human **CETP** cDNA sequence and cDNA synthesized from liver poly (A+) RNA. Anal. of that cDNA indicated that the nucleotide and amino acid sequences of cynomolgus monkey **CETP** were greater than 95% homologous with the human sequences. A fragment of the cDNA was used to develop an internal-std./RNase protection assay that allowed precise quantification of **CETP** mRNA levels. Anal. of total RNA from various tissues with this assay revealed that the liver and thoracic aorta expressed high levels of **CETP** mRNA; the mesenteric fat, adrenal gland, spleen, and abdominal aorta had low but detectable levels of the mRNA; and the brain, kidney, intestine, and skeletal muscle had undetectable levels of that mRNA. When the monkeys were made hypercholesterolemic by a high-fat, high-**cholesterol** (HFHC) diet, hepatic levels of **CETP** mRNA increased from 1.6 pg/.mu.g total RNA to 4.1 pg/.mu.g; mesenteric fat **CETP** mRNA increased from 0.4 pg/.mu.g total RNA to 5.3 pg/.mu.g; and plasma CET activity increased approx. fourfold. The **CETP** mRNA levels in the thoracic and abdominal aortas were not significantly increased in monkeys fed the HFHC diet, even though those animals had gross **atherosclerosis**. The apoprotein E mRNA levels, however, were markedly increased in the aortas of monkeys with **atherosclerosis**, with the largest increase occurring in the abdominal aorta. Taken together, these data suggest that lipid deposition in the artery was not accompanied by increased expression of the **CETP** gene in that tissue. Statistical anal. showed that a strong, neg. correlation existed between hepatic **CETP** mRNA levels and both high d. lipoprotein **cholesterol** and apoprotein A-I. These data suggest that HFHC diet-induced changes in high d. lipoprotein metab. may be linked to altered expression of a functional **CETP** gene.
- ST **cholesterol ester transfer protein atherosclerosis** monkey; **cholesterol ester transfer protein** sequence monkey
- IT Adipose tissue, composition
(**cholesteryl ester transfer protein** mRNA of mesenteric, in **atherosclerosis** in cynomolgus monkey)
- IT Liver, composition
Organ
(**cholesteryl ester transfer protein** mRNA of, in **atherosclerosis** in cynomolgus monkey)
- IT Blood plasma
(**cholesteryl ester transfer protein** of, in **atherosclerosis** in cynomolgus monkey)
- IT Macaca irus
(**cholesteryl ester transfer protein** of, mol. cloning and sequence and expression of, in **atherosclerosis**)
- IT Gene, animal
RL: BIOL (Biological study)
(for **cholesteryl ester transfer protein**, nucleotide sequence of and predicted amino acid sequence from and expression of, in **atherosclerosis** in cynomolgus monkey)
- IT Ribonucleic acids, messenger

- RL: BIOL (Biological study)
(for **cholesteryl ester transfer protein**, of liver in **atherosclerosis** in cynomolgus monkey, high-d. lipoproteins of blood plasma in relation to)
- IT Molecular cloning
(of **cholesteryl ester transfer protein** cDNA of cynomolgus monkey)
- IT Protein sequences
(of **cholesteryl ester transfer protein**, of cynomolgus monkey liver)
- IT Lipoproteins
RL: BIOL (Biological study)
(apo-, A-I, mRNA for, of liver, in **atherosclerosis** in cynomolgus monkey, **cholesteryl ester transfer protein** in relation to)
- IT Lipoproteins
RL: BIOL (Biological study)
(apo-, E, mRNA for, of aorta and liver, in **atherosclerosis** in cynomolgus monkey, **cholesteryl ester transfer protein** in relation to)
- IT Arteriosclerosis
(**atherosclerosis**, **cholesteryl ester transfer protein** mRNA of aorta and liver and other organs in, in cynomolgus monkey)
- IT Deoxyribonucleic acid sequences
(complementary, for **cholesteryl ester transfer protein**, of cynomolgus monkey liver)
- IT Lipoproteins
RL: BIOL (Biological study)
(high-d., **cholesterol** of, of blood plasma in **atherosclerosis** in cynomolgus monkey, **cholesteryl ester transfer protein** in relation to)
- IT Proteins, specific or class
RL: BIOL (Biological study)
(lipid-exchanging I, gene for, nucleotide sequence of and predicted amino acid sequence from and expression of, in **atherosclerosis** in cynomolgus monkey)
- IT 145170-17-8, Glycoprotein (Macaca irus **cholesterol ester-exchanging protein** moiety reduced)
RL: PRP (Properties)
(amino acid sequence of, complete)
- IT 145170-15-6
RL: PRP (Properties)
(nucleotide sequence of)
- IT 145170-16-7, Deoxyribonucleic acid (Macaca irus **cholesterol ester-exchanging glycoprotein messenger RNA-complementary**)
RL: PRP (Properties)
(nucleotide sequence of, complete)
- IT 57-88-5D, Cholest-5-en-3-ol (3.beta.)-, esters
RL: BIOL (Biological study)
(transfer protein for, gene for, nucleotide sequence of and predicted amino acid sequence from and expression of, in **atherosclerosis** in cynomolgus monkey)

=> fil biosis

FILE 'BIOSIS' ENTERED AT 11:58:18 ON 19 JUN 2002

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FILE COVERS 1969 TO DATE.

CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNs) PRESENT
FROM JANUARY 1969 TO DATE.

RECORDS LAST ADDED: 12 June 2002 (20020612/ED)

=> d all tot

L60 ANSWER 1 OF 6 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 2001:517733 BIOSIS
DN PREV200100517733
TI Plasmid-based **vaccine** for treating **atherosclerosis**.
AU **Thomas, Lawrence J. (1)**
CS (1) Easton, MA USA
ASSIGNEE: AVANT Immunotherapeutics, Inc.
PI US 6284533 September 04, 2001
SO Official Gazette of the United States Patent and Trademark Office Patents,
(Sep. 4, 2001) Vol. 1250, No. 1, pp. No Pagination. e-file.
ISSN: 0098-1133.
DT Patent
LA English
AB A plasmid-based **vaccine** is provided herein based on the
combination of DNA segments coding for one or more B cell epitopes of
cholesteryl ester transfer protein (CETP) and one or more broad range helper T cell epitopes.
Administration of the plasmids as a **vaccine** to a vertebrate
subject provides an immune response to the subject's endogenous
CETP and modulation of **CETP** activity, leading to
prevention or reversal of various manifestations of heart disease. The
vaccines provide an advantageous strategy for the prevention or
treatment of **atherosclerosis**.
NCL 435320000
IT Major Concepts
Cardiovascular Medicine (Human Medicine, Medical Sciences);
Pharmacology
IT Diseases
atherosclerosis: vascular disease
IT Chemicals & Biochemicals
plasmid-based **vaccine**: **vaccine**
IT Alternate Indexing
Atherosclerosis (MeSH)

L60 ANSWER 2 OF 6 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 2001:298985 BIOSIS
DN PREV200100298985
TI An extended toxicologic evaluation of an immunoneutralizing
vaccine to produce anti-**CETP** antibodies for the
prevention/treatment of **atherosclerosis**.
AU **Thomas, Lawrence J. (1)**; Picard, Michele D. (1); Miller, David
P. (1); Emmett, Constance D. (1); Scesney, Susanne M. (1); Pisano, Milissa
L. (1); Adari, Hedy (1); Hammond, Russell A. (1); Marsh, Henry C. (1);
Rittershaus, Charles W. (1); Pettey, Carolyn L. (1)
CS (1) AVANT Immunotherapeutics, 119 Fourth Ave., Needham, MA, 02494 USA
SO FASEB Journal, (March 7, 2001) Vol. 15, No. 4, pp. A566. print.
Meeting Info.: Annual Meeting of the Federation of American Societies for
Experimental Biology on Experimental Biology 2001 Orlando, Florida, USA
March 31-April 04, 2001
ISSN: 0892-6638.
DT Conference
LA English
SL English
AB A toxicology study was conducted with an immunoneutralizing
vaccine designed to elicit antibodies that would bind to and block
the function of **cholesteryl ester transfer protein (CETP)**, in order to prevent
atherosclerosis. The **vaccine** consisted of a dimer of a

31 a.a. synthetic chimeric peptide containing an N-terminal cysteine, a T cell epitope (residues 830-843 of tetanus toxin), and a B cell epitope (residues 461-476 of human CETP), formulated with an alum adjuvant. In this study NZW rabbits were immunized with either 0 mg (4 males and 4 females), 0.1 mg (2 males and 2 females), 0.25 mg (4 males and 4 females) or 1.0 mg (4 males and 4 females) of the vaccine on days 1, 29 and 57. On day 197 (at a relative antibody minimum) half of the animals from groups 1, 3 and 4 were sacrificed. The remaining animals were reboosted and euthanized on day 211, at an expected antibody maximum. Blood samples were taken periodically throughout the study and were assessed for hematology, clinical chemistry, and antibody titers. All rabbits in the non-control groups developed anti-rabbit CETP antibody titers, thus validating the immunogenicity of the vaccine. In all other measurements the vaccinated groups were indistinguishable from the control group. All animals were monitored for clinical abnormalities throughout the study, and at necropsy, gross pathology was assessed, selected organs were weighed, and samples of 44 tissues were taken for histopathology. By all the above parameters, no significant test article-related pathology was observed. This study demonstrated the administration of this CETP immunoneutralizing vaccine produced specific self-reactive antibody titers but no detectable test article-related pathology.

- CC Cytology and Cytochemistry - Animal *02506
 General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
 Pathology, General and Miscellaneous - Therapy *12512
 Cardiovascular System - Blood Vessel Pathology *14508
 Blood, Blood-Forming Organs and Body Fluids - Blood and Lymph Studies *15002
 Blood, Blood-Forming Organs and Body Fluids - Blood Cell Studies *15004
 Pharmacology - General *22002
 Pharmacology - Immunological Processes and Allergy *22018
 Toxicology - General; Methods and Experimental *22501
 Toxicology - Pharmacological Toxicology *22504
 Immunology and Immunochemistry - General; Methods *34502
- BC Leporidae 86040
- IT Major Concepts
 Pharmacology; Toxicology
- IT Parts, Structures, & Systems of Organisms
 B cell: blood and lymphatics, immune system; T cell: blood and lymphatics, immune system; blood: blood and lymphatics
- IT Diseases
 atherosclerosis: prevention, treatment, vascular disease
- IT Chemicals & Biochemicals
 anti-cholesteryl ester transfer
 protein antibodies [anti-CETP antibodies];
 cholesteryl ester transfer protein
 [CETP]; cholesteryl ester
 transfer protein immunoneutralizing vaccine
 [CETP immunoneutralizing vaccine]: immunogenicity,
 immunostimulant - drug; immunoneutralizing vaccine:
 immunostimulant - drug, toxicity
- IT Alternate Indexing
 Atherosclerosis (MeSH)
- IT Methods & Equipment
 toxicology study
- IT Miscellaneous Descriptors
 Meeting Abstract
- ORGN Super Taxa
 Leporidae: Lagomorpha, Mammalia, Vertebrata, Chordata, Animalia
- ORGN Organism Name
 NZW rabbit (Leporidae): female, male
- ORGN Organism Superterms

Animals; Chordates; Lagomorphs; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Vertebrates

L60 ANSWER 3 OF 6 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 AN 2000:476466 BIOSIS
 DN PREV200000476466
 TI **Vaccine-induced antibodies inhibit CETP activity in vivo and reduce aortic lesions in a rabbit model of atherosclerosis.**
 AU **Rittershaus, Charles W. (1); Miller, David P.; Thomas, Lawrence J.; Picard, Michele D.; Honan, Christopher M.; Emmett, Constance D.; Pettey, Carolyn L.; Adari, Hedy; Hammond, Russell A.; Beattie, David T.; Callow, Allan D.; Marsh, Henry C.; Ryan, Una S.**
 CS (1) AVANT Immunotherapeutics, Inc, 119 Fourth Ave, Needham, MA, 02494 USA
 SO Arteriosclerosis Thrombosis and Vascular Biology, (September, 2000) Vol. 20, No. 9, pp. 2106-2112. print.
 ISSN: 1079-5642.
 DT Article
 LA English
 SL English
 AB Using a **vaccine** approach, we **immunized** New Zealand White rabbits with a peptide containing a region of **cholesteryl ester transfer protein (CETP)** known to be required for neutral lipid **transfer** function. These rabbits had significantly reduced plasma **CETP** activity and an altered lipoprotein profile. In a **cholesterol**-fed rabbit model of **atherosclerosis**, the fraction of plasma **cholesterol** in HDL was 42% higher and the fraction of plasma **cholesterol** in LDL was 24% lower in the **CETP-vaccinated** group than in the control-**vaccinated** group. Moreover, the percentage of the aorta surface exhibiting **atherosclerotic** lesion was 39.6% smaller in the **CETP-vaccinated** rabbits than in controls. The data reported here demonstrate that **CETP** activity can be reduced in vivo by **vaccination** with a peptide derived from **CETP** and support the concept that inhibition of **CETP** activity in vivo can be antiatherogenic. In addition, these studies suggest that **vaccination** against a self-antigen is a viable therapeutic strategy for disease management.
 CC Biochemical Studies - Proteins, Peptides and Amino Acids *10064
 Biochemical Studies - General *10060
 Biochemical Studies - Lipids *10066
 Cardiovascular System - Physiology and Biochemistry *14504
 Cardiovascular System - Blood Vessel Pathology *14508
 BC Leporidae 86040
 IT Major Concepts
 Biochemistry and Molecular Biophysics; Cardiovascular System (Transport and Circulation)
 IT Diseases
 atherosclerosis: vascular disease
 IT Chemicals & Biochemicals
 cholesteryl ester transfer protein: inhibition, plasma activity; **cholesteryl ester transfer protein vaccine**;
 high-density lipoprotein: plasma fraction; low-density lipoprotein: plasma fraction
 IT Alternate Indexing
 Atherosclerosis (MeSH)
 ORGN Super Taxa
 Leporidae: Lagomorpha, Mammalia, Vertebrata, Chordata, Animalia
 ORGN Organism Name
 rabbit (Leporidae): animal model
 ORGN Organism Superterms
 Animals; Chordates; Lagomorphs; Mammals; Nonhuman Mammals; Nonhuman

Vertebrates; Vertebrates

- L60 ANSWER 4 OF 6 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 AN 1999:282999 BIOSIS
 DN PREV199900282999
 TI A **vaccine** to produce anti-**cholesteryl ester transfer protein (CETP)** antibodies for the prevention/treatment of **atherosclerosis**.
 AU **Thomas, L. J. (1)**; Picard, M. D. (1); Miller, D. P. (1); Honan, C. M. (1); Adari, H. (1); Emmett, C. D. (1); Marsh, H. C. (1); Ryan, U. S. (1); Pettey, C. L. (1); **Rittershaus, C. W. (1)**
 CS (1) Avant Immunotherapeutics, Inc., Needham, MA, 02494 USA
 SO FASEB Journal, (March 15, 1999) Vol. 13, No. 5 PART 2, pp. A693.
 Meeting Info.: Annual Meeting of the Professional Research Scientists on Experimental Biology 99 Washington, D.C., USA April 17-21, 1999 Federation of American Societies for Experimental Biology
 . ISSN: 0892-6638.
 DT Conference
 LA English
 CC Pharmacology - General *22002
 Biochemical Studies - General *10060
 Nutrition - General Studies, Nutritional Status and Methods *13202
 Immunology and Immunochemistry - General; Methods *34502
 Cardiovascular System - General; Methods *14501
 General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
 BC Leporidae 86040
 IT Major Concepts
 Cardiovascular System (Transport and Circulation); Pharmacology
 IT Diseases
atherosclerosis: vascular disease; fatty streak lesion:
 vascular disease
 IT Chemicals & Biochemicals
anti-cholesteryl ester transfer protein; **anti-cholesteryl ester transfer protein** antibody producing **vaccine**
; cholesterol supplemented diet
 IT Alternate Indexing
Atherosclerosis (MeSH)
 IT Methods & Equipment
atherosclerosis prevention: prevention method;
atherosclerosis treatment: therapeutic method
 IT Miscellaneous Descriptors
 Meeting Abstract
 ORGN Super Taxa
 Leporidae: Lagomorpha, Mammalia, Vertebrata, Chordata, Animalia
 ORGN Organism Name
 New Zealand White rabbit (Leporidae)
 ORGN Organism Superterms
 Animals; Chordates; Lagomorphs; Mammals; Nonhuman Mammals; Nonhuman
 Vertebrates; Vertebrates
 RN 20910-06-9D (CHOLESTERYL)
 57-88-5 (CHOLESTEROL)
- L60 ANSWER 5 OF 6 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 AN 1998:200178 BIOSIS
 DN PREV199800200178
 TI Use of xenogeneic **cholesteryl ester transfer protein (CETP)** in a plasmid-based **vaccine** to produce anti-CETP autoantibodies for the prevention/treatment of **atherosclerosis**.
 AU **Thomas, L. J.**; Adari, H.; Picard, M. D.; Honan, C. M.; Miller, D. P.; **Rittershaus, C. W.**; Pettey, C. L.

- CS T Cell Sciences Inc., Needham, MA USA
 SO FASEB Journal, (March 17, 1998) Vol. 12, No. 4, pp. A310.
 Meeting Info.: Annual Meeting of the Professional Research Scientists on
 Experimental Biology 98, Part 1 San Francisco, California, USA April
 18-22, 1998 Federation of American Societies for Experimental Biology
 . ISSN: 0892-6638.
- DT Conference
 LA English
 CC Cardiovascular System - Blood Vessel Pathology *14508
 Biochemical Studies - General *10060
 General Biology - Symposia, Transactions and Proceedings of Conferences,
 Congresses, Review Annuals *00520
 Biochemical Studies - Proteins, Peptides and Amino Acids *10064
 IT Major Concepts
 Cardiovascular System (Transport and Circulation)
 IT Diseases
 atherosclerosis: prevention, treatment, vascular disease
 IT Chemicals & Biochemicals
 plasmid-based **vaccine**; xenogenic **cholesteryl**
 ester transfer protein: autoantibodies
 IT Miscellaneous Descriptors
 Meeting Abstract
 RN 20910-06-9D (CHOLESTERYL)
- L60 ANSWER 6 OF 6 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 AN 1997:144273 BIOSIS
 DN PREV199799443476
 TI A plasmid-based **vaccine** to elicit autoantibodies to
cholesteryl ester transfer protein (
CETP) for the prevention/treatment of **atherosclerosis**.
 AU Thomas, L. J.; Picard, M. D.; Stewart, S. E.; Waite, B. C. D.;
 Lin, A. Y.; Rittershaus, C. W.; Pettey, C. L.
 CS T Cell Sci. Inc., Needham, MA USA
 SO Journal of Allergy and Clinical Immunology, (1997) Vol. 99, No. 1 PART 2,
 pp. S187.
 Meeting Info.: Joint Meeting of the American Academy of Allergy, Asthma
 and Immunology, the American Association of Immunologists and the Clinical
 Immunology Society San Francisco, California, USA February 21-26, 1997
 ISSN: 0091-6749.
- DT Conference; Abstract
 LA English
 CC General Biology - Symposia, Transactions and Proceedings of Conferences,
 Congresses, Review Annuals 00520
 Biochemical Studies - Proteins, Peptides and Amino Acids 10064
 Biochemical Studies - Sterols and Steroids 10067
 Biochemical Studies - Carbohydrates 10068
 Metabolism - Carbohydrates *13004
 Metabolism - Sterols and Steroids *13008
 Metabolism - Proteins, Peptides and Amino Acids *13012
 Cardiovascular System - Blood Vessel Pathology *14508
 Pharmacology - Drug Metabolism; Metabolic Stimulators *22003
 Pharmacology - Cardiovascular System *22010
 Pharmacology - Immunological Processes and Allergy *22018
 Routes of Immunization, Infection and Therapy 22100
 Genetics of Bacteria and Viruses 31500
 Immunology and Immunochemistry - Immunopathology, Tissue Immunology
 ***34508**
- BC Leporidae *86040
 IT Major Concepts
 Cardiovascular System (Transport and Circulation); Immune System
 (Chemical Coordination and Homeostasis); Metabolism; Pharmacology
 IT Chemicals & Biochemicals
 CHOLESTERYL; CHOLESTEROL

IT Miscellaneous Descriptors
 ANIMAL MODEL; ATHEROSCLEROSIS; CARDIOVASCULAR SYSTEM;
 CHOLESTEROL ESTER TRANSFER PROTEIN
 AUTOANTIBODY INDUCTION; CHOLESTERYL ESTER
 TRANSFER PROTEIN; CYTOMEGALOVIRUS PROMOTER/ENHANCER
 GENE; IMMUNE SYSTEM; IMMUNOTHERAPEUTIC METHOD; PLASMID-BASED
 VACCINE TREATMENT; VACCINE PREVENTION;
 VACCINE TREATMENT; VASCULAR DISEASE

ORGN Super Taxa
 Leporidae: Lagomorpha, Mammalia, Vertebrata, Chordata, Animalia

ORGN Organism Name
 rabbit (Leporidae)

ORGN Organism Superterms
 animals; chordates; lagomorphs; mammals; nonhuman mammals; nonhuman
 vertebrates; vertebrates

RN 20910-06-9D (CHOLESTERYL)
 57-88-5D (CHOLESTEROL)

=> fil wpix

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http://www.derwent.com/userguides/dwpi_guide.html <<<

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L73 ANSWER 1 OF 4 WPIX (C) 2002 THOMSON DERWENT
 AN 1999-302645 [25] WPIX
 DNC C1999-088748
 TI Vaccine against cholesteryl ester
 transfer protein.
 DC B04 D16
 IN RITTERSHAUS, C W; THOMAS, L J
 PA (AVAN-N) AVANT IMMUNOTHERAPEUTICS INC
 CYC 83
 PI WO 9920302 A1 19990429 (199925)* EN 61p A61K039-00
 RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL
 OA PT SD SE SZ UG ZW
 W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE
 GH GM HR HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG
 MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG
 US UZ VN YU ZW
 AU 9911048 A 19990510 (199938)
 EP 1024825 A1 20000809 (200039) EN A61K039-00

R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE
 JP 2001520204 W 20011030 (200202) 67p A61K039-00
 ADT WO 9920302 A1 WO 1998-US22145 19981020; AU 9911048 A AU 1999-11048
 19981020; EP 1024825 A1 EP 1998-953762 19981020, WO 1998-US22145 19981020;
 JP 2001520204 W WO 1998-US22145 19981020, JP 2000-516697 19981020
 FDT AU 9911048 A Based on WO 9920302; EP 1024825 A1 Based on WO 9920302; JP
 2001520204 W Based on WO 9920302
 PRAI US 1997-954643 19971020
 IC ICM A61K039-00
 ICS A61K039-39; A61K048-00; A61P009-00; A61P009-10; C07K014-47;
 C12N015-09
 AB WO 9920302 A UPAB: 20011203
 NOVELTY - **Vaccine** that promotes production of antibodies that
 bind endogenous **cholesteryl ester transfer**
protein (CETP) in a mammal comprises a non-endogenous,
 optionally mammalianized, **CETP**, optionally combined with an
 adjuvant, for non-specific stimulation of the mammal's immune response.
 DETAILED DESCRIPTION - An INDEPENDENT CLAIM is also included for a
 plasmid-based **vaccine** comprising a promoter, functional in
 mammalian cells, linked to a sequence encoding a non-endogenous
CETP.
 ACTIVITY - Anti-atherosclerotic.
 MECHANISM OF ACTION - Antibodies raised against the **vaccine**
 recognize endogenous **CETP**, reducing its activity, and thus the
transfer of cholesterol from high-density lipoprotein
 (HDL) to (very) low-density lipoprotein (LDL).
 USE - The **vaccines** (and equivalent plasmid-based
vaccines) are used:
 (1) to increase the ratio of circulating high-density lipoprotein
 (HDL)-associated **cholesterol** to low-density lipoprotein
 (LDL)-associated **cholesterol**;
 (2) to decrease the level of endogenous **CETP** activity in
 humans or other animals;
 (3) to alter metabolism of LDL-associated **cholesterol**, for
 inhibiting development of **atherosclerotic** lesions;
 (4) to lower circulating levels of LDL and total **cholesterol**
 ;
 (5) to treat or prevent **atherosclerosis** (or more generally
 heart disease)
 FS CPI
 FA AB; DCN
 MC CPI: B04-C01G; B04-E08; B04-N02A; B05-A01A; B05-C05; B14-F06;
 B14-F07; B14-S11; D05-H07; D05-H12E
 TECH UPTX: 19990630
 TECHNOLOGY FOCUS - BIOTECHNOLOGY - Preferred **vaccine**: The
 non-endogenous **CETP** is from rabbit, mouse or monkey, or is a
 humanized form of these, or it is an allelic variant or polymorph of a
 human **CETP**. Particularly preferred is a humanized rabbit
CETP of 447 amino acids (sequence given in the specification. This
 lacks the region from 393Ala to 411Ala, so resembles the human protein
 more closely than the wild-type rabbit protein. Alternatively, where the
 host is a rabbit, the non-endogenous **CETP** is the human protein.
 Suitable adjuvants are alum, complete or incomplete Freund's adjuvant or
 the RIBI adjuvant system. Optionally the non-endogenous **CETP** is
 dimerized or linked to a related protein (e.g. phospholipid transfer
 protein) or other conventional carrier protein to increase its
 immunogenicity. It may also contain a source of T helper cells epitopes.
 Plasmid-based **vaccines** express the same **CETP** as above,
 and include a cytomegalovirus immediate-early promoter-enhancer.
 Preparation: **CETP** may be expressed by standard recombinant DNA
 methods. A typical expression vector is pCMV-**CETP**-TT (ATCC
 98038) in which the cytomegalovirus promoter controls expression of a
vaccinating peptide described in PCT/US96/06147. It is modified

conventionally to express full-length **CETP** proteins.
TECHNOLOGY FOCUS - PHARMACEUTICALS - Preferred vaccine: The non-endogenous **CETP** is from rabbit, mouse or monkey, or is a humanized form of these, or it is an allelic variant or polymorph of a human **CETP**. Particularly preferred is a humanized rabbit **CETP** of 447 amino acids (reproduced). This lacks the region from 393Ala to 411Ala, so resembles the human protein more closely than the wild-type rabbit protein. Alternatively, where the host is a rabbit, the non-endogenous **CETP** is the human protein. Suitable adjuvants are alum, complete or incomplete Freund's adjuvant or the RIBI adjuvant system. Optionally the non-endogenous **CETP** is dimerized or linked to a related protein (e.g. phospholipid transfer protein) or other conventional carrier protein to increase its immunogenicity. It may also contain a source of T helper cells epitopes. Plasmid-based **vaccines** express the same **CETP** as above, and include a cytomegalovirus immediate-early promoter-enhancer.

TECHNOLOGY FOCUS - ORGANIC CHEMISTRY - Preparation: **CETP** are produced by usual methods of automated peptide synthesis, and coupled to carriers or other peptides through usual bifunctional crosslinkers.

L73 ANSWER 2 OF 4 WPIX (C) 2002 THOMSON DERWENT
 AN 1999-276984 [23] WPIX
 DNC C1999-081276
 TI New recombinant DNA **vaccines** lessening **cholesterol ester transfer** contain DNA encoding **cholesteryl ester transfer protein**.
 DC B04 D16
 IN GLENN, K; NEEDLEMAN, P
 PA (MONS) MONSANTO CO
 CYC 83
 PI WO 9915655 A1 19990401 (199923)* EN 98p C12N015-12
 RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL
 OA PT SD SE SZ UG ZW
 W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE
 GH GM HR HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG
 MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG
 US UZ VN YU ZW
 AU 9892317 A 19990412 (199934) C12N015-12
 EP 1015584 A1 20000705 (200035) EN C12N015-12
 R: AT BE CH DE DK ES FI FR GB GR IE IT LI LU NL PT SE
 ADT WO 9915655 A1 WO 1998-US19366 19980917; AU 9892317 A AU 1998-92317
 19980917; EP 1015584 A1 EP 1998-944877 19980917, WO 1998-US19366 19980917
 FDT AU 9892317 A Based on WO 9915655; EP 1015584 A1 Based on WO 9915655
 PRAI US 1997-934367 19970919
 IC ICM C12N015-12
 ICS A61K048-00
 AB WO 9915655 A UPAB: 19991103
 NOVELTY - New recombinant DNA **vaccines** contain DNA encoding **cholesteryl ester transfer protein**, for producing antibodies to lessen the **transfer of cholesteryl esters** from HDL.
 DETAILED DESCRIPTION - A novel process for producing antibodies to **cholesteryl ester transfer protein** (**CETP**) in a mammal comprises:
 (a) **immunizing** the mammal with an inoculum containing a vehicle in which is dissolved or dispersed a recombinant DNA molecule comprising a DNA sequence that contains:
 (i) a sequence encoding a **CETP** immunogen linked to;
 (ii) a promoter sequence that controls the expression of the **CETP** immunogen DNA sequence in the mammal, the **CETP** immunogen being an immunogenic polypeptide having a **CETP** amino acid residue sequence, the **immunization** providing an amount of

the recombinant DNA molecule to induce antibodies to **CETP**;

(b) maintaining the **immunized** mammal for the production of antibodies that bind to **CETP**.

INDEPENDENT CLAIMS are also included for:

(1) a process for increasing the concentration of high density lipoprotein (HDL) **cholesterol** in the blood of a mammal whose blood contains **CETP** comprising:

(a) step (a) as above;

(b) maintaining the **immunized** mammal for the **CETP** immunogen to be expressed and for the production of antibodies that bind to **CETP** and lessen the **transfer** of **cholesteryl esters** from HDL;

(2) an inoculum that comprises a recombinant DNA molecule comprising a DNA sequence that contains:

(1) a sequence encoding a **CETP** immunogen linked to;

(2) a promoter sequence that controls the expression of the **CETP** immunogen DNA sequence in a mammal, the recombinant DNA molecule being dissolved or dispersed in a vehicle.

USE - The method can provide an autogeneic immunological process for lessening the **transfer** of **cholesteryl esters** from HDL particles and for increasing the HDL **cholesterol** concentration of a mammal whose blood also contains **CETP**. The method may be useful in treating human pro-atherogenic dyslipoproteinemias characterized by low HDL/LDL **cholesterol** ratios.

ADVANTAGE - The method can have an effect that lasts for months as compared to the short-term effects of the small molecule drugs now available.

Dwg.0/0

FS CPI

FA AB; DCN

MC CPI: B04-B04D5; B04-E02F; B04-G01; B04-N02A0E; B14-F02; B14-S11;
D05-H07; D05-H12C; D05-H12E; D05-H17C

TECH UPTX: 20001114

TECHNOLOGY FOCUS - BIOTECHNOLOGY - The encoded **CETP** immunogen may comprise an immunogenic polypeptide fused to an exogenous antigen carrier polypeptide, e.g. hepatitis B core protein, tetanus toxoid, or diphtheria toxoid. The DNA may be dissolved or dispersed in a vehicle, e.g. PBS or isotonic saline.

In the process for producing antibodies the blood of the mammal contains **CETP**.

In (1) step (a) may be repeated several times, preferably at intervals of about 3 months to six months until the HDL cholesterol levels is increased by about 10%. In (1) the recombinant DNA encodes human or rabbit **CETP** as the immunogenic polypeptide. The immunogenic polypeptide may be fused (especially by either termini) to an exogenous antigenic carrier polypeptide, where the antigen is especially hepatitis B core protein, tetanus toxoid or diphtheria toxoid. The antigenic carriers may optionally be fused to the C terminus and N terminus of the immunogenic polypeptide. When the antigenic carriers are fused to both termini the immunogenic portion is 10-30 amino acids in length, and is fused to an amino terminal and carboxy-terminal flanking sequence where:

(a) the amino terminal flanking sequence consists of 70-90 amino acid residues of the hepatitis B core protein sequences from amino acids 1-90, the C terminal sequence is 65-85 amino acid residues in length having the hepatitis B core protein sequence from amino acids 80-183 (sic); or

(b) the amino terminal flanking sequence consists of 10-20 amino acid residues of the hepatitis B core protein sequences from amino acids 1-35 (sic), the C terminal sequence is 120-160 amino acid residues in length having the hepatitis B core protein sequence from amino acids 10-183 (sic).

When the antigenic carriers are fused to both termini the immunogenic portion is about equal in number to the number of amino acid residues absent from the hepatitis B core protein between the C termini of the

flanking sequence of the amino terminal flanking sequence and the amino termini of the flanking sequence of the C terminal flanking sequence. The encoded immunogenic polypeptide has one of the two 26 or amino acid sequences given in the specification.

L73 ANSWER 3 OF 4 WPIX (C) 2002 THOMSON DERWENT
 AN 1997-549731 [50] WPIX
 DNC C1997-175370
 TI DNA plasmid-based **vaccine** encodes **CETP** B cell and helper T cell epitope(s) - used for elevating high density lipoprotein levels, and for treating cardiovascular disease.
 DC B04 D16
 IN **THOMAS, L J**
 PA (TCEL-N) T CELL SCI INC; (AVAN-N) **AVANT IMMUNOTHERAPEUTICS INC**
 CYC 73
 PI WO 9741227 A1 19971106 (199750)* EN 67p C12N015-12
 RW: AT BE CH DE DK EA ES FI FR GB GH GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG
 W: AL AM AT AU AZ BB BG BR BY CA CH CN CZ DE DK EE ES FI GB GE GH HU IL IS JP KE KG KP KR KZ LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK TJ TM TR TT UA UG US UZ VN
 AU 9729946 A 19971119 (199812) C12N015-12
 EP 914427 A1 19990512 (199923) EN C12N015-12
 R: AT BE CH DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE
 AU 721729 B 20000713 (200039) C12N015-12
 JP 2001508760 W 20010703 (200142) 75p A61K039-00
 US 6284533 B1 20010904 (200154) C12N015-12
 ADT WO 9741227 A1 WO 1997-US7294 19970501; AU 9729946 A AU 1997-29946 19970501; EP 914427 A1 EP 1997-924549 19970501; WO 1997-US7294 19970501; AU 721729 B AU 1997-29946 19970501; JP 2001508760 W JP 1997-539202 19970501; WO 1997-US7294 19970501; US 6284533 B1 Provisional US 1996-52983P 19960501, CIP of US 1997-802967 19970221, WO 1997-US7294 19970501, US 1998-171969 19981002
 FDT AU 9729946 A Based on WO 9741227; EP 914427 A1 Based on WO 9741227; AU 721729 B Previous Publ. AU 9729946, Based on WO 9741227; JP 2001508760 W Based on WO 9741227; US 6284533 B1 Based on WO 9634888
 PRAI US 1997-802967 19970221; US 1996-640713 19960501; US 1996-52983P 19960501; US 1998-171969 19981002
 REP 2.Jnl.Ref; WO 9634888
 IC ICM A61K039-00; C12N015-12
 ICS A61K031-70; A61K048-00; A61P009-10; C12N005-10; C12N015-09
 AB WO 9741227 A UPAB: 19971217
 A novel DNA plasmid-based **vaccine** comprises a nucleotide sequence encoding an immunogenic polypeptide, which includes at least one segment encoding a B cell epitope of **cholesteryl ester transferase protein (CETP)** linked in frame with at least one segment encoding a broad range helper T cell epitope, where the nucleotide segment is operably linked to a promoter sequence suitable for directing the transcription of the nucleotide sequence in a mammalian cell.
 USE - The **vaccines** can be used to elevate the ratio of circulating high density lipoproteins (HDL) to circulating low density lipoproteins (LDL), very low density lipoproteins (VLDL) or total **cholesterol** in a human. It can also be used for decreasing the level of endogenous **CETP** activity in a human. The **vaccine** can also be used to produce anti-**CETP** antibodies in a human and for treating cardiovascular disease in a human (all claimed).
 Dwg.0/10
 FS CPI
 FA AB
 MC CPI: B04-E08; B04-F11; B14-S11; D05-H07; D05-H12E; D05-H17C

L73 ANSWER 4 OF 4 WPIX (C) 2002 THOMSON DERWENT
 AN 1996-506103 [50] WPIX
 DNC C1996-158783
 TI **Cholesteryl ester transfer protein**
 B cell epitope linked to T cell epitope - used to generate
vaccine to regulate **CETP** activity for decreasing the
 risk of developing a cardiovascular disease e.g. **atherosclerosis**

DC B04 C06 D16
 IN **RITTERSHAUS, C W; THOMAS, L J**
 PA (AVAN-N) **AVANT IMMUNOTHERAPEUTICS INC;** (TCEL-N) T CELL SCI INC;
 (RITT-I) **RITTERSHAUS C W;** (THOM-I) **THOMAS L J**

CYC 70
 PI WO 9634888 A1 19961107 (199650)* EN 72p C07K014-775
 RW: AT BE CH DE DK ES FI FR GB GR IE IT KE LS LU MC MW NL OA PT SD SE
 SZ UG
 W: AL AM AT AU AZ BB BG BR BY CA CH CN CZ DE DK EE ES FI GB GE HU IS
 JP KE KG KP KR KZ LK LR LT LU LV MD MG MK MN MW MX NO NZ PL PT RO
 RU SD SE SG SI SK TJ TM TR TT UA UG US UZ VN
 AU 9656360 A 19961121 (199711) C07K014-775
 EP 827509 A1 19980311 (199814) EN C07K014-775
 R: AT BE CH DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE
 JP 11504635 W 19990427 (199927) 87p C07K014-47
 AU 707752 B 19990722 (199940) C07K014-775
 CA 2219795 C 20000808 (200051) EN C12N009-96
 US 2002042364 A1 20020411 (200227) A61K039-00

ADT WO 9634888 A1 WO 1996-US6147 19960501; AU 9656360 A AU 1996-56360
 19960501; EP 827509 A1 EP 1996-913320 19960501, WO 1996-US6147 19960501;
 JP 11504635 W JP 1996-533487 19960501, WO 1996-US6147 19960501; AU 707752
 B AU 1996-56360 19960501; CA 2219795 C CA 1996-2219795 19960501, WO
 1996-US6147 19960501; US 2002042364 A1 CIP of US 1995-432483 19950501, Div
 ex WO 1996-US6147 19960501, Div ex US 1997-945289 19971017, US 2001-943548
 20010830

FDT AU 9656360 A Based on WO 9634888; EP 827509 A1 Based on WO 9634888; JP
 11504635 W Based on WO 9634888; AU 707752 B Previous Publ. AU 9656360,
 Based on WO 9634888; CA 2219795 C Based on WO 9634888

PRAI US 1995-432483 19950501; US 1997-945289 19971017; US 2001-943548
 20010830

REP 3.Jnl.Ref; WO 9425060

IC ICM A61K039-00; C07K014-47; C07K014-775; C12N009-96
 ICS A61K038-17; A61K038-45; A61K039-04; A61K039-05; A61K039-07;
 A61K039-08; A61K039-10; A61K039-13; A61K039-165; A61K039-20;
 A61K039-385; C07K014-33; C07K016-18; C12N009-10; C12N015-09

ICA C12P021-08

AB WO 9634888 A UPAB: 19961211
 An isolated peptide comprising a broad range helper T cell epitope and a B
 cell epitope of the **cholesteryl ester transfer
 protein (CETP)** is new. Also claimed is a method of
 making an anti-**CETP vaccine** to modulate endogenous
CETP activity or to treat **atherosclerosis**
 therapeutically or prophylactically by: (a) selecting a **CETP** B
 cell epitope which does not include a Class I major histocompatibility
 complex T cell antigen; (b) selecting a helper T cell epitope derived from
 a non-**CETP** antigenic peptide; and (c) linking the B and T cell
 epitopes to form an immunogenic moiety.
 USE - The peptide maybe used in a claimed **vaccine** to
 decrease the level of endogenous **CETP** activity in a human or
 animal so as to alter the catabolism of high density lipoprotein (HDL)-
cholesterol, resulting in an elevated ratio of HDL-
cholesterol versus low density (LDL)- or very LDL (VLDL)-
cholesterol (claimed). This leads to a decreased risk of
 developing a cardiovascular disease, esp. **atherosclerosis**.
 Dwg.0/13

FS CPI
FA AB; DCN
MC CPI: B04-B04C1; B04-C01G; B04-L05A; B04-N02B; B14-D02A2; **B14-F07**
; **B14-S11**; B04-B04C1; C04-B04C1; B04-C01G; C04-C01G;
B04-L05A; C04-L05A; B04-N02B; C04-N02B; B14-D02A2; C14-D02A2;
B14-F07; C14-F07; B14-S11;
C14-S11; C04-B04C1; C04-C01G; C04-L05A; C04-N02B; C14-D02A2;
C14-F07; C14-S11; D05-H07; D05-H17C

=> fil medline

FILE 'MEDLINE' ENTERED AT 12:14:46 ON 19 JUN 2002

FILE LAST UPDATED: 18 JUN 2002 (20020618/UP). FILE COVERS 1958 TO DATE.

On June 9, 2002, MEDLINE was reloaded. See HELP RLOAD for details.

MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the
MeSH 2002 vocabulary. Enter HELP THESAURUS for details.

THIS FILE CONTAINS CAS REGISTRY NUMBERS FOR EASY AND ACCURATE
SUBSTANCE IDENTIFICATION.

=> d all tot

L88 ANSWER 1 OF 5 MEDLINE
AN 2002099139 MEDLINE
DN 21687251 PubMed ID: 11828696
TI Down with the bad, up with the good. A biotech firm develops a
vaccine to raise good cholesterol levels.
AU Maeder Thomas
SO SCIENTIFIC AMERICAN, (2002 Feb) 286 (2) 32-3.
Journal code: 0404400. ISSN: 0036-8733.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200202
ED Entered STN: 20020207
Last Updated on STN: 20020222
Entered Medline: 20020221
CT Check Tags: Animal; Human
***Arteriosclerosis: PC, prevention & control**
***Biotechnology**
***Carrier Proteins: IM, immunology**
Clinical Trials, Phase II
***Lipoproteins, HDL Cholesterol: BL, blood**
Tetanus Toxin: IM, immunology
***Vaccines**
CN 0 (Carrier Proteins); 0 (Lipoproteins, HDL Cholesterol); 0 (Tetanus
Toxin); 0 (**Vaccines**); 0 (**cholesterol ester**
transfer proteins)

L88 ANSWER 2 OF 5 MEDLINE
AN 2001058876 MEDLINE
DN 20383755 PubMed ID: 10929930
TI Current, new and future treatments in dyslipidaemia and
atherosclerosis.
AU Chong P H; Bachenheimer B S
CS College of Pharmacy, University of Illinois, and Cook County Hospital,
Chicago 60612-3785, USA.. cpang@tigger.cc.uic.edu
SO DRUGS, (2000 Jul) 60 (1) 55-93. Ref: 294
Journal code: 7600076. ISSN: 0012-6667.

CY New Zealand
 DT Journal; Article; (JOURNAL ARTICLE)
 General Review; (REVIEW)
 (REVIEW, TUTORIAL)
 LA English
 FS Priority Journals
 EM 200012
 ED Entered STN: 20010322
 Last Updated on STN: 20010322
 Entered Medline: 20001222
 AB The new therapeutic options available to clinicians treating dyslipidaemia in the last decade have enabled effective treatment for many patients. The development of the HMG-CoA reductase inhibitors (statins) have been a major advance in that they possess multiple pharmacological effects (pleiotropic effects) resulting in potent reductions of low density lipoproteins (LDL) and prevention of the **atherosclerotic** process. More recently, the newer fibric acid derivatives have also reduced LDL to levels comparable to those achieved with statins, have reduced triglycerides, and gemfibrozil has been shown to increase high density lipoprotein (HDL) levels. Nicotinic acid has been made tolerable with sustained-release formulations, and is still considered an excellent choice in elevating HDL **cholesterol** and is potentially effective in reducing lipoprotein(a) [Lp(a)] levels, an emerging risk factor for coronary heart disease (CHD). Furthermore, recent studies have reported positive lipid-lowering effects from estrogen and/or progestogen in postmenopausal women but there are still conflicting reports on the use of these agents in dyslipidaemia and in females at risk for CHD. In addition to lowering lipid levels, these antihyperlipidaemic agents may have directly or indirectly targeted thrombogenic, fibrinolytic and **atherosclerotic** processes which may have been unaccounted for in their overall success in clinical trials. Although LDL **cholesterol** is still the major target for therapy, it is likely that over the next several years other lipid/lipoprotein and nonlipid parameters will become more generally accepted targets for specific therapeutic interventions. Some important emerging lipid/lipoprotein parameters that have been associated with CHD include elevated triglyceride, oxidised LDL **cholesterol** and Lp(a) levels, and low HDL levels. The nonlipid parameters include elevated homocysteine and fibrinogen, and decreased endothelial-derived nitric oxide production. Among the new investigational agents are inhibitors of squalene synthetase, acylCoA: **cholesterol** acyltransferase, **cholesteryl ester transfer protein**, monocyte-macrophages and LDL **cholesterol** oxidation. Future applications may include thromimetic therapy, **cholesterol** vaccination, somatic gene therapy, and recombinant **proteins**, in particular, apolipoproteins A-I and E. Non-LDL-related targets such as peroxisome proliferator-activating receptors, matrix metalloproteinases and scavenger receptor class B type I may also have clinical significance in the treatment of **atherosclerosis** in the near future. Before lipid-lowering therapy, dietary and lifestyle modification is and should be the first therapeutic intervention in the management of dyslipidaemia. Although current recommendations from the US and Europe are slightly different, adherence to these recommendations is essential to lower the risk of **atherosclerotic** vascular disease, more specifically CHD. New guidelines that are expected in the near future will encompass global opinions from the expert scientific community addressing the issue of target LDL goal (aggressive versus moderate lowering) and the application of therapy for newer emerging CHD risk factors.
 CT Check Tags: Human
 *Anticholesteremic Agents: TU, therapeutic use
 *Arteriosclerosis: DT, drug therapy
 Arteriosclerosis: PP, physiopathology
 Arteriosclerosis: PC, prevention & control

*Cholesterol: ME, metabolism
 Diet
 Forecasting
 *Hyperlipidemia: DT, drug therapy
 Hyperlipidemia: PP, physiopathology
 Hyperlipidemia: PC, prevention & control
 Life Style
 *Lipoproteins: DE, drug effects
 *Lipoproteins: ME, metabolism
 RN 57-88-5 (Cholesterol)
 CN 0 (Anticholesteremic Agents); 0 (Lipoproteins)

L88 ANSWER 3 OF 5 MEDLINE
 AN 2000482102 MEDLINE
 DN 20436374 PubMed ID: 10978256
 TI **Vaccine-induced antibodies inhibit CETP activity in vivo and reduce aortic lesions in a rabbit model of atherosclerosis.**
 CM Comment in: Arterioscler Thromb Vasc Biol. 2000 Sep;20(9):2029-31
 AU Rittershaus C W; Miller D P; Thomas L J; Picard M D; Honan C M; Emmett C D; Pettey C L; Adari H; Hammond R A; Beattie D T; Callow A D; Marsh H C; Ryan U S
 CS AVANT Immunotherapeutics, Inc, Needham, MA 02494, USA..
 crittershaus@avantimmune.com
 NC HL-59122 (NHLBI)
 SO ARTERIOSCLEROSIS, THROMBOSIS, AND VASCULAR BIOLOGY, (2000 Sep) 20 (9) 2106-12.
 Journal code: 9505803. ISSN: 1524-4636.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 200010
 ED Entered STN: 20001019
 Last Updated on STN: 20010521
 Entered Medline: 20001012

AB Using a **vaccine** approach, we **immunized** New Zealand White rabbits with a peptide containing a region of **cholesteryl ester transfer protein (CETP)** known to be required for neutral lipid **transfer** function. These rabbits had significantly reduced plasma **CETP** activity and an altered lipoprotein profile. In a **cholesterol**-fed rabbit model of **atherosclerosis**, the fraction of plasma **cholesterol** in HDL was 42% higher and the fraction of plasma **cholesterol** in LDL was 24% lower in the **CETP-vaccinated** group than in the control-**vaccinated** group. Moreover, the percentage of the aorta surface exhibiting **atherosclerotic** lesion was 39.6% smaller in the **CETP-vaccinated** rabbits than in controls. The data reported here demonstrate that **CETP** activity can be reduced in vivo by **vaccination** with a peptide derived from **CETP** and support the concept that inhibition of **CETP** activity in vivo can be antiatherogenic. In addition, these studies suggest that **vaccination** against a self-antigen is a viable therapeutic strategy for disease management.

CT Check Tags: Animal; Human; Support, U.S. Gov't, P.H.S.
 Antibodies: BL, blood
 *Aorta: PA, pathology
 Arteriosclerosis: IM, immunology
 *Arteriosclerosis: ME, metabolism
 Arteriosclerosis: PA, pathology
 Arteriosclerosis: TH, therapy
 Blotting, Western
 CHO Cells

Carrier Proteins: GE, genetics
 *Carrier Proteins: IM, immunology
 Carrier Proteins: ME, metabolism
 Cholesterol, Dietary: PD, pharmacology
 Disease Models, Animal
 Hamsters
 Kidney Function Tests
 Lipoproteins: AN, analysis
 Rabbits
 Recombinant Proteins: IM, immunology
 Recombinant Proteins: ME, metabolism
 Vaccines, Synthetic: AD, administration & dosage
 *Vaccines, Synthetic: IM, immunology
 CN 0 (Antibodies); 0 (Carrier Proteins); 0 (Cholesterol, Dietary); 0
 (Lipoproteins); 0 (Recombinant Proteins); 0 (Vaccines,
 Synthetic); 0 (cholesterol ester transfer
 proteins)

L88 ANSWER 4 OF 5 MEDLINE
 AN 1999307576 MEDLINE
 DN 99307576 PubMed ID: 10377515
 TI A vaccine approach to healthy lipoprotein levels.
 AU Fricker J
 SO MOLECULAR MEDICINE TODAY, (1999 Jul) 5 (7) 281.
 Journal code: 9508560. ISSN: 1357-4310.
 CY ENGLAND: United Kingdom
 DT News Announcement
 LA English
 FS Priority Journals
 EM 199909
 ED Entered STN: 19991005
 Last Updated on STN: 19991005
 Entered Medline: 19990921
 CT Check Tags: Animal; Human; Male
 Aged
 Aged, 80 and over
 Antibodies: CH, chemistry
 *Arteriosclerosis: PC, prevention & control
 Carrier Proteins: GE, genetics
 *Carrier Proteins: IM, immunology
 Clinical Trials
 Japan
 *Lipoproteins, HDL: BL, blood
 Peptides: CS, chemical synthesis
 Peptides: IM, immunology
 Rabbits
 Vaccines: AD, administration & dosage
 Vaccines: CS, chemical synthesis
 *Vaccines: IM, immunology
 CN 0 (Antibodies); 0 (Carrier Proteins); 0 (Lipoproteins, HDL); 0 (Peptides);
 0 (Vaccines); 0 (cholesterol ester
 transfer proteins)

L88 ANSWER 5 OF 5 MEDLINE
 AN 97355212 MEDLINE
 DN 97355212 PubMed ID: 9211407
 TI Vaccine for atherosclerosis.
 AU O'Brien C
 SO MOLECULAR MEDICINE TODAY, (1997 Jun) 3 (6) 231.
 Journal code: 9508560. ISSN: 1357-4310.
 CY ENGLAND: United Kingdom
 DT News Announcement
 LA English

FS Priority Journals
 EM 199708
 ED Entered STN: 19970908
 Last Updated on STN: 19970908
 Entered Medline: 19970822
 CT Check Tags: Animal; Human
 Apolipoproteins: BI, biosynthesis
 Apolipoproteins: IM, immunology
 *Arteriosclerosis: TH, therapy
 Carrier Proteins: BI, biosynthesis
 Carrier Proteins: GE, genetics
 *Carrier Proteins: IM, immunology
 Mice
 Mice, Transgenic
 Rabbits
 *Vaccines, DNA
 CN 0 (Apolipoproteins); 0 (Carrier Proteins); 0 (Vaccines, DNA); 0
 (cholesterol ester transfer proteins
)

=> d his

(FILE 'HOME' ENTERED AT 11:33:14 ON 19 JUN 2002)
 SET COST OFF

FILE 'REGISTRY' ENTERED AT 11:33:30 ON 19 JUN 2002
 E CHOLESTERYL ESTER TRANSFER PROTEIN/CN

L1 1 S E4
 E CETP/CN
 E CHOLESTER? (L) ESTER (L) TRANSFER? (L) PROTEIN
 L2 13 S CHOLESTER? (L) ESTER (L) TRANSFER? (L) PROTEIN
 L3 13 S CETP
 L4 13 S CHOLESTER? (L) ESTER (L) EXCHANG? (L) PROTEIN
 L5 1 S L1 AND L2-L4
 L6 24 S L2-L4 NOT L5

FILE 'HCAPLUS' ENTERED AT 11:37:36 ON 19 JUN 2002

L7 876 S CHOLESTER? (L) ESTER (L) EXCHANG? (L) PROTEIN
 E CHOLESTER? (L) ESTER (L) TRANSFER? (L) PROTEIN
 L8 883 S CETP
 L9 1325 S CHOLESTER? (L) ESTER (L) TRANSFER? (L) PROTEIN
 L10 16 S L5 OR L6
 L11 16 S L7-L9 AND L10
 L12 57 S ?ARTHEROSCLERO?
 L13 34932 S ?ATHEROSCLERO?
 L14 19 S ?ARTHERIOSCLERO?
 L15 13496 S ?ARTERIOSCLERO?
 L16 9 S L11 AND L12-L15
 L17 4 S L11 AND VACCIN?
 L18 4 S L17 AND L16
 E ATHEROSCLEROSIS/CT
 E E3+ALL
 L19 20165 S E7-E9,E6
 L20 32452 S E6,E8,E9/BI
 E E5+ALL
 L21 22555 S E5+NT
 L22 8925 S E5/BI
 L23 9 S L11 AND L19-L22
 L24 4 S L16,L23 AND VACCIN?
 L25 5 S L16,L23 NOT L24
 L26 9 S L23-L25
 L27 331 S L7-L9 AND L12-L15,L19-L22

L28 9 S L27 AND VACCIN?
L29 24 S L7-L9,L10 AND EPITOP?
L30 5 S L29 AND (TETANUS OR DIPHTHER? OR TOXOID OR TOXIN OR BCG OR BA
L31 15 S L26,L28,L30
L32 19 S L29 NOT L31
E RITTERSHAUS C/AU
L33 20 S E3-E6
E THOMAS L/AU
L34 219 S E3,E14,E15
E THOMAS LARRY/AU
L35 4 S E3
L36 23 S E26,E29
L37 6 S L33-L36 AND L7-L10
L38 6 S L31 AND L37
L39 9 S L31 NOT L38
L40 15 S L38,L39
L41 5 S L40 AND (PY<=1995 OR PRY<=1995 OR AY<=1995)
L42 15 S L40,L41

FILE 'HCAPLUS' ENTERED AT 11:52:33 ON 19 JUN 2002

FILE 'BIOSIS' ENTERED AT 11:52:55 ON 19 JUN 2002

L43 1 S L5 OR L6
L44 1529 S L7-L9
L45 1529 S L43,L44
L46 324 S L45 AND L12-L15,L20,L22
L47 8 S L45 AND VACCIN?
L48 7 S L45 AND (IMMUNIZ? OR IMMUNIS?)
L49 6 S L46 AND L47,L48
L50 17 S 22100/CC AND L45
L51 15 S 34508/CC AND L45
L52 3 S 22018/CC AND L45
L53 37 S L49-L52
L54 10 S L53 AND L46
SEL DN AN 1 5 9 10
L55 6 S L54 NOT E1-E8
E RITTERSHAUS C/AU
L56 37 S E3-E6
E THOMAS L/AU
L57 491 S E3,E16-E19
E THOMAS LAWRENCE/AU
L58 9 S E3,E5
L59 6 S L45 AND L56-L58
L60 6 S L55,L59

FILE 'BIOSIS' ENTERED AT 11:58:18 ON 19 JUN 2002

FILE 'WPIX' ENTERED AT 11:58:47 ON 19 JUN 2002

L61 94 S L7-L9
L62 64 S L61 AND L12-L15,L20,L22
L63 53 S L61 AND (B14-F07 OR C14-F07 OR B12-H03 OR C12-H03)/MC
L64 64 S L61 AND (?ATHEROSCLERO? OR ?ATHERIOSCLERO? OR ?ARTERIOSCLERO?
L65 65 S L62-L64
L66 4 S L61 AND (VACCIN? OR IMMUNIZ? OR IMMUNIS? OR (B14-S11 OR C14-S
L67 2 S L66 AND L65
L68 2 S L66 NOT L67
E RITTERSHAUS C/AU
L69 9 S E3,E4
E THOMAS L/AU
L70 95 S E3,E11
L71 3 S L61 AND L69,L70
L72 3 S AVANT?/PA AND L61
L73 4 S L66-L68,L71,L72

FILE 'WPIX' ENTERED AT 12:08:58 ON 19 JUN 2002

FILE 'MEDLINE' ENTERED AT 12:09:11 ON 19 JUN 2002

L74 1433 S L7-L10
L75 264 S L74 AND L12-L15,L19-L22
L76 253 S L74 AND (?ATHEROSCLERO? OR ?ATHERIOSCLERO? OR ?ARTERIOSCLERO?
E ATHEROSCLERO/CT
E E8+ALL
E E2+ALL
L77 89148 S E4+NT
L78 154 S L74 AND L77
L79 264 S L75,L76,L78
L80 5 S L79 AND (VACCIN? OR IMMUNIZ? OR IMMUNIS?)
E VACCINE/CT
E E4+ALL
E E2+ALL
L81 0 S L79 AND E44+NT
E E44+ALL
E VACCINES/CT
E E3+ALL
L82 4 S L79 AND E7+NT
L83 5 S L80,L82
L84 265 S L74 AND C14./CT
L85 47 S L74 AND A7./CT
L86 4 S L84,L85 AND (VACCIN? OR IMMUNIZ? OR IMMUNIS?)/CT
L87 4 S L84 AND VACCINES+NT/CT
L88 5 S L83,L86,L87

FILE 'MEDLINE' ENTERED AT 12:14:46 ON 19 JUN 2002

